

Nico Jehmlich

List of Publications by Year in descending order

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Version: 2024-02-01

169
papers

9,130
citations

53794

45
h-index

51608

86
g-index

181
all docs

181
docs citations

181
times ranked

11841
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	27.8	1,878
2	Land use driven change in soil pH affects microbial carbon cycling processes. <i>Nature Communications</i> , 2018, 9, 3591.	12.8	380
3	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016, 65, 225-237.	12.1	317
4	Soil Fungal:Bacterial Ratios Are Linked to Altered Carbon Cycling. <i>Frontiers in Microbiology</i> , 2016, 7, 1247.	3.5	292
5	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015, 524, 105-108.	27.8	231
6	Rational design of a microbial consortium of mucosal sugar utilizers reduces <i>Clostridiodes difficile</i> colonization. <i>Nature Communications</i> , 2020, 11, 5104.	12.8	177
7	The active microbial diversity drives ecosystem multifunctionality and is physiologically related to carbon availability in Mediterranean semi-arid soils. <i>Molecular Ecology</i> , 2016, 25, 4660-4673.	3.9	151
8	Differential sensitivity of total and active soil microbial communities to drought and forest management. <i>Global Change Biology</i> , 2017, 23, 4185-4203.	9.5	150
9	Widespread soil bacterium that oxidizes atmospheric methane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8515-8524.	7.1	149
10	Global ecological predictors of the soil priming effect. <i>Nature Communications</i> , 2019, 10, 3481.	12.8	148
11	Protein-based stable isotope probing (Protein-SIP) reveals active species within anoxic mixed cultures. <i>ISME Journal</i> , 2008, 2, 1122-1133.	9.8	126
12	Synergistic biodegradation of aromatic-aliphatic copolyester plastic by a marine microbial consortium. <i>Nature Communications</i> , 2020, 11, 5790.	12.8	122
13	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. <i>ISME Journal</i> , 2013, 7, 1877-1885.	9.8	107
14	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	3.8	107
15	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. <i>Molecular Metabolism</i> , 2019, 22, 96-109.	6.5	102
16	Combined Genomic and Proteomic Approaches Identify Gene Clusters Involved in Anaerobic 2-Methylnaphthalene Degradation in the Sulfate-Reducing Enrichment Culture N47. <i>Journal of Bacteriology</i> , 2010, 192, 295-306.	2.2	101
17	Protein-based stable isotope probing. <i>Nature Protocols</i> , 2010, 5, 1957-1966.	12.0	97
18	Oxygen and nitrogen production by an ammonia-oxidizing archaeon. <i>Science</i> , 2022, 375, 97-100.	12.6	91

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19	Identification of periodontitis associated changes in the proteome of whole human saliva by mass spectrometric analysis. <i>Journal of Clinical Periodontology</i> , 2013, 40, 825-832.	4.9	88
20	Improving protein extraction and separation methods for investigating the metaproteome of anaerobic benzene communities within sediments. <i>Biodegradation</i> , 2009, 20, 737-750.	3.0	86
21	Comparative evaluation of saliva collection methods for proteome analysis. <i>Clinica Chimica Acta</i> , 2013, 419, 42-46.	1.1	85
22	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	6.7	83
23	In situ protein SIP highlights Burkholderiaceae as key players degrading toluene by para ring hydroxylation in a constructed wetland model. <i>Environmental Microbiology</i> , 2016, 18, 1176-1186.	3.8	81
24	Incorporation of carbon and nitrogen atoms into proteins measured by protein-based stable isotope probing (Protein-SIP). <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 2889-2897.	1.5	77
25	Phenol Degradation in the Strictly Anaerobic Iron-Reducing Bacterium <i>Geobacter metallireducens</i> GS-15. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3912-3919.	3.1	74
26	The Proteome of the Isolated <i>Chlamydia trachomatis</i> Containing Vacuole Reveals a Complex Trafficking Platform Enriched for Retromer Components. <i>PLoS Pathogens</i> , 2015, 11, e1004883.	4.7	74
27	Exercise Training in Patients with Chronic Heart Failure Promotes Restoration of High-Density Lipoprotein Functional Properties. <i>Circulation Research</i> , 2013, 113, 1345-1355.	4.5	70
28	Metabolomics reveals impact of seven functional foods on metabolic pathways in a gut microbiota model. <i>Journal of Advanced Research</i> , 2020, 23, 47-59.	9.5	70
29	Biotransformation of Two Pharmaceuticals by the Ammonia-Oxidizing Archaeon <i>Nitrososphaera gargensis</i> . <i>Environmental Science & Technology</i> , 2016, 50, 4682-4692.	10.0	68
30	Anaerobic naphthalene degradation by sulfate-reducing Desulfobacteraceae from various anoxic aquifers. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	67
31	Protein-SIP in environmental studies. <i>Current Opinion in Biotechnology</i> , 2016, 41, 26-33.	6.6	67
32	Snake venomomics of the Siamese Russell's viper (<i>Daboia russelli siamensis</i>) Relation to pharmacological activities. <i>Journal of Proteomics</i> , 2009, 72, 256-269.	2.4	66
33	Effects of chronic dietary exposure of zinc oxide nanoparticles on the serum protein profile of juvenile common carp (<i>Cyprinus carpio</i> L.). <i>Science of the Total Environment</i> , 2017, 579, 1504-1511.	8.0	65
34	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. <i>Journal of Proteome Research</i> , 2015, 14, 619-627.	3.7	64
35	A Peroxygenase from <i>Chaetomium globosum</i> Catalyzes the Selective Oxygenation of Testosterone. <i>ChemBioChem</i> , 2017, 18, 563-569.	2.6	63
36	Dehalococcoides mccartyi Strain DCMB5 Respires a Broad Spectrum of Chlorinated Aromatic Compounds. <i>Applied and Environmental Microbiology</i> , 2015, 81, 587-596.	3.1	62

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37	Enhancing metaproteomicsâ€”The value of models and defined environmental microbial systems. <i>Proteomics</i> , 2016, 16, 783-798.	2.2	62
38	Proteinâ€”based stable isotope probing (proteinâ€”SIP) in functional metaproteomics. <i>Mass Spectrometry Reviews</i> , 2012, 31, 683-697.	5.4	61
39	An unusual strategy for the anoxic biodegradation of phthalate. <i>ISME Journal</i> , 2017, 11, 224-236.	9.8	61
40	Bacteria dominate the short-term assimilation of plant-derived N in soil. <i>Soil Biology and Biochemistry</i> , 2016, 96, 30-38.	8.8	59
41	Tracking active groundwater microbes with D ₂ O labelling to understand their ecosystem function. <i>Environmental Microbiology</i> , 2018, 20, 369-384.	3.8	57
42	Metabolic Adaptation of Methanogens in Anaerobic Digesters Upon Trace Element Limitation. <i>Frontiers in Microbiology</i> , 2018, 9, 405.	3.5	52
43	Using proteins to study how microbes contribute to soil ecosystem services: The current state and future perspectives of soil metaproteomics. <i>Journal of Proteomics</i> , 2019, 198, 50-58.	2.4	52
44	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylotroph. <i>Environmental Microbiology</i> , 2015, 17, 4007-4018.	3.8	51
45	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. <i>Environmental Microbiology</i> , 2017, 19, 2246-2257.	3.8	50
46	Proteome profile and proteogenomics of the organohalide-respiring bacterium <i>Dehalococcoides mccartyi</i> strain CBDB1 grown on hexachlorobenzene as electron acceptor. <i>Journal of Proteomics</i> , 2014, 98, 59-64.	2.4	49
47	Proteomics of the organohalide-respiring Epsilonproteobacterium <i>Sulfurospirillum multivorans</i> adapted to tetrachloroethene and other energy substrates. <i>Scientific Reports</i> , 2015, 5, 13794.	3.3	48
48	Elucidating MTBE degradation in a mixed consortium using a multidisciplinary approach. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	2.7	47
49	Proteomic analysis of oropharyngeal carcinomas reveals novel HPVâ€”associated biological pathways. <i>International Journal of Cancer</i> , 2013, 132, 568-579.	5.1	47
50	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
51	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. <i>Proteomics</i> , 2013, 13, 2786-2804.	2.2	46
52	The effects of struvite and sewage sludge on plant yield and the microbial community of a semiarid Mediterranean soil. <i>Geoderma</i> , 2019, 337, 1051-1057.	5.1	46
53	Biochemical and molecular genetic characterisation of a novel laccase produced by the aquatic ascomycete <i>Phoma</i> sp. UHH 5-1-03. <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 1095-1105.	3.6	45
54	An integrative overview of genomic, transcriptomic and proteomic analyses in organohalide respiration research. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	45

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55	When drought meets forest management: Effects on the soil microbial community of a Holm oak forest ecosystem. <i>Science of the Total Environment</i> , 2019, 662, 276-286.	8.0	45
56	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 575-584.	3.6	44
57	Insight into the modulation of intestinal proteome of juvenile common carp (<i>Cyprinus carpio</i> L.) after dietary exposure to ZnO nanoparticles. <i>Science of the Total Environment</i> , 2018, 613-614, 62-71.	8.0	44
58	Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM). <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 283-291.	3.7	41
59	Decarboxylating and Nondecarboxylating Glutaryl-Coenzyme A Dehydrogenases in the Aromatic Metabolism of Obligately Anaerobic Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 4401-4409.	2.2	40
60	Time resolved protein ¹⁵ N-based stable isotope probing (Protein ¹⁵ NIP) analysis allows quantification of induced proteins in substrate shift experiments. <i>Proteomics</i> , 2011, 11, 2265-2274.	2.2	40
61	The Wood Rot Ascomycete <i>Xylaria polymorpha</i> Produces a Novel GH78 Glycoside Hydrolase That Exhibits \pm -L-Rhamnosidase and Feruloyl Esterase Activities and Releases Hydroxycinnamic Acids from Lignocelluloses. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4893-4901.	3.1	40
62	Gastric bypass surgery in a rat model alters the community structure and functional composition of the intestinal microbiota independently of weight loss. <i>Microbiome</i> , 2020, 8, 13.	11.1	40
63	Quantitative analysis of the intra ² and inter ² subject variability of the whole salivary proteome. <i>Journal of Periodontal Research</i> , 2013, 48, 392-403.	2.7	37
64	Disease Development Is Accompanied by Changes in Bacterial Protein Abundance and Functions in a Refined Model of Dextran Sulfate Sodium (DSS)-Induced Colitis. <i>Journal of Proteome Research</i> , 2019, 18, 1774-1786.	3.7	37
65	HumanMetagenomeDB: a public repository of curated and standardized metadata for human metagenomes. <i>Nucleic Acids Research</i> , 2021, 49, D743-D750.	14.5	37
66	Candidate Brocadiales dominates C, N and S cycling in anoxic groundwater of a pristine limestone-fracture aquifer. <i>Journal of Proteomics</i> , 2017, 152, 153-160.	2.4	36
67	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
68	ATP-Dependent C ¹⁸ F Bond Cleavage Allows the Complete Degradation of 4-Fluoroaromatics without Oxygen. <i>MBio</i> , 2016, 7, .	4.1	35
69	Comparative performance evaluation of multi-metal resistant fungal strains for simultaneous removal of multiple hazardous metals. <i>Journal of Hazardous Materials</i> , 2016, 318, 679-685.	12.4	35
70	The Simplified Human Intestinal Microbiota (SIHUMix) Shows High Structural and Functional Resistance against Changing Transit Times in In Vitro Bioreactors. <i>Microorganisms</i> , 2019, 7, 641.	3.6	35
71	Ecological and functional adaptations to water management in a semiarid agroecosystem: a soil metaproteomics approach. <i>Scientific Reports</i> , 2017, 7, 10221.	3.3	34
72	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34

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73	Phylogenetic and proteomic analysis of an anaerobic toluene-degrading community. <i>Journal of Applied Microbiology</i> , 2010, 109, 1937-1945.	3.1	33
74	The secretome of <i>Trametes versicolor</i> grown on tomato juice medium and purification of the secreted oxidoreductases including a versatile peroxidase. <i>Journal of Biotechnology</i> , 2013, 168, 15-23.	3.8	32
75	Enrichment and identification of small proteins in a simplified human gut microbiome. <i>Journal of Proteomics</i> , 2020, 213, 103604.	2.4	32
76	Following the community development of SIHUMix – a new intestinal <i>in vitro</i> model for bioreactor use. <i>Gut Microbes</i> , 2020, 11, 1116-1129.	9.8	32
77	Aromatizing Cyclohexa-1,5-diene-1-carbonyl-Coenzyme A Oxidase. <i>Journal of Biological Chemistry</i> , 2008, 283, 20713-20721.	3.4	30
78	Characterization of the microbial community in biological soil crusts dominated by <i>Fulgensia desertorum</i> (Tomlin) Poelt and <i>Squamarina cartilaginea</i> (With.) P. James and in the underlying soil. <i>Soil Biology and Biochemistry</i> , 2014, 76, 70-79.	8.8	30
79	Maximization of cell viability rather than biocatalyst activity improves whole-cell C_60 functionalization performance. <i>Biotechnology and Bioengineering</i> , 2017, 114, 874-884.	3.3	30
80	Gut microbial functional maturation and succession during human early life. <i>Environmental Microbiology</i> , 2018, 20, 2160-2177.	3.8	30
81	Pulsed $^{13}\text{C}_2$ -Acetate Protein-SIP Unveils Epsilonproteobacteria as Dominant Acetate Utilizers in a Sulfate-Reducing Microbial Community Mineralizing Benzene. <i>Microbial Ecology</i> , 2016, 71, 901-911.	2.8	29
82	Comparison of methods for simultaneous identification of bacterial species and determination of metabolic activity by protein-based stable isotope probing (Protein-SIP) experiments. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1871-1878.	1.5	28
83	Impaired HDL function in obese adolescents: Impact of lifestyle intervention and bariatric surgery. <i>Obesity</i> , 2013, 21, E687-95.	3.0	28
84	A patchwork pathway for oxygenase-independent degradation of side chain containing steroids. <i>Environmental Microbiology</i> , 2017, 19, 4684-4699.	3.8	28
85	Communal metabolism by <i>Methylococcaceae</i> and <i>Methylophilaceae</i> is driving rapid aerobic methane oxidation in sediments of a shallow seep near Elba, Italy. <i>Environmental Microbiology</i> , 2019, 21, 3780-3795.	3.8	28
86	<i>Pseudomonas</i> spp. are key players in agricultural biogas substrate degradation. <i>Scientific Reports</i> , 2019, 9, 12871.	3.3	28
87	Mechanistic insight to mycoremediation potential of a metal resistant fungal strain for removal of hazardous metals from multimetal pesticide matrix. <i>Environmental Pollution</i> , 2020, 262, 114255.	7.5	28
88	Deforestation fosters bacterial diversity and the cyanobacterial community responsible for carbon fixation processes under semiarid climate: a metaproteomics study. <i>Applied Soil Ecology</i> , 2015, 93, 65-67.	4.3	27
89	Interspecies metabolite transfer and aggregate formation in a co-culture of <i>Dehalococcoides</i> and <i>Sulfurospirillum</i> dehalogenating tetrachloroethene to ethene. <i>ISME Journal</i> , 2021, 15, 1794-1809.	9.8	27
90	Metabolic in Vivo Labeling Highlights Differences of Metabolically Active Microbes from the Mucosal Gastrointestinal Microbiome between High-Fat and Normal Chow Diet. <i>Journal of Proteome Research</i> , 2017, 16, 1593-1604.	3.7	26

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91	Purification and Characterization of Active-Site Components of the Putative <i>p</i> -Cresol Methylhydroxylase Membrane Complex from <i>Geobacter metallireducens</i> . Journal of Bacteriology, 2008, 190, 6493-6500.	2.2	25
92	Thermal proteome profiling allows quantitative assessment of interactions between tetrachloroethene reductive dehalogenase and trichloroethene. Journal of Proteomics, 2019, 192, 10-17.	2.4	25
93	In-depth proteomic analysis of the human cerumen – A potential novel diagnostically relevant biofluid. Journal of Proteomics, 2013, 83, 119-129.	2.4	24
94	A peptide resource for the analysis of Staphylococcus aureus in host-pathogen interaction studies. Proteomics, 2015, 15, 3648-3661.	2.2	24
95	Proteome profiles of HDL particles of patients with chronic heart failure are associated with immune response and also include bacteria proteins. Clinica Chimica Acta, 2016, 453, 114-122.	1.1	24
96	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. Microbiome, 2021, 9, 55.	11.1	24
97	Aerobic Toluene Degradation in the Rhizosphere of a Constructed Wetland Model Show Diurnal Polyhydroxyalkanoate Metabolism. Applied and Environmental Microbiology, 2016, 82, 4126-4132.	3.1	23
98	Enzymes involved in phthalate degradation in sulphate-reducing bacteria. Environmental Microbiology, 2019, 21, 3601-3612.	3.8	22
99	Incomplete cell disruption of resistant microbes. Scientific Reports, 2019, 9, 5618.	3.3	22
100	Mucosal-associated invariant T-Cell (MAIT) activation is altered by chlorpyrifos- and glyphosate-treated commensal gut bacteria. Journal of Immunotoxicology, 2020, 17, 10-20.	1.7	22
101	The glyphosate formulation Roundup® LB plus influences the global metabolome of pig gut microbiota in vitro. Science of the Total Environment, 2020, 745, 140932.	8.0	22
102	Differences in the whole saliva baseline proteome profile associated with development of oral mucositis in head and neck cancer patients undergoing radiotherapy. Journal of Proteomics, 2015, 125, 98-103.	2.4	21
103	Bolstering fitness via CO ₂ fixation and organic carbon uptake: mixotrophs in modern groundwater. ISME Journal, 2022, 16, 1153-1162.	9.8	21
104	Sulfur- ³⁶ S stable isotope labeling of amino acids for quantification (SULAQ). Proteomics, 2012, 12, 37-42.	2.2	20
105	25-Hydroxyvitamin D ₃ Synthesis by Enzymatic Steroid Side-Chain Hydroxylation with Water. Angewandte Chemie - International Edition, 2016, 55, 1881-1884.	13.8	20
106	Decimal Place Slope, A Fast and Precise Method for Quantifying ¹³ C Incorporation Levels for Detecting the Metabolic Activity of Microbial Species. Molecular and Cellular Proteomics, 2010, 9, 1221-1227.	3.8	19
107	Molecular Fingerprint of High Fat Diet Induced Urinary Bladder Metabolic Dysfunction in a Rat Model. PLoS ONE, 2013, 8, e66636.	2.5	18
108	The extracellular metaproteome of soils under semiarid climate: A methodological comparison of extraction buffers. Science of the Total Environment, 2018, 619-620, 707-711.	8.0	18

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109	Deconstructing <i>Methanosarcina acetivorans</i> into an acetogenic archaeon. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	18
110	Detection, quantification and identification of fungal extracellular laccases using polyclonal antibody and mass spectrometry. Enzyme and Microbial Technology, 2007, 41, 694-701.	3.2	17
111	Purification and biochemical characterization of a laccase from the aquatic fungus <i>Myrioconium</i> sp. UHH 1-13-18-4 and molecular analysis of the laccase-encoding gene. Applied Microbiology and Biotechnology, 2007, 77, 613-624.	3.6	17
112	Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in <i>Pseudomonas fluorescens</i> during Naphthalene Degradation. Molecular and Cellular Proteomics, 2013, 12, 2060-2069.	3.8	17
113	A global proteome approach in uric acid stimulated human aortic endothelial cells revealed regulation of multiple major cellular pathways. International Journal of Cardiology, 2014, 176, 746-752.	1.7	17
114	Proteomic interrogation of the gut microbiota: potential clinical impact. Expert Review of Proteomics, 2016, 13, 535-537.	3.0	17
115	<i>Delftia</i> sp. LCW, a strain isolated from a constructed wetland shows novel properties for dimethylphenol isomers degradation. BMC Microbiology, 2018, 18, 108.	3.3	17
116	Function is what counts: how microbial community complexity affects species, proteome and pathway coverage in metaproteomics. Expert Review of Proteomics, 2020, 17, 163-173.	3.0	17
117	The total microbiome functions in bacteria and fungi. Journal of Proteomics, 2020, 213, 103623.	2.4	16
118	Differences in the secretion pattern of oxidoreductases from <i>Bjerkandera adusta</i> induced by a phenolic olive mill extract. Fungal Genetics and Biology, 2014, 72, 99-105.	2.1	15
119	Comparative evaluation of peptide desalting methods for salivary proteome analysis. Clinica Chimica Acta, 2014, 434, 16-20.	1.1	15
120	Functional soil mycobiome across ecosystems. Journal of Proteomics, 2022, 252, 104428.	2.4	15
121	Declining Capacity of Starving <i>Delftia acidovorans</i> MC1 to Degrade Phenoxypyronate Herbicides Correlates with Oxidative Modification of the Initial Enzyme. Environmental Science & Technology, 2010, 44, 3793-3799.	10.0	14
122	The Activation of Mucosal-Associated Invariant T (MAIT) Cells Is Affected by Microbial Diversity and Riboflavin Utilization in vitro. Frontiers in Microbiology, 2020, 11, 755.	3.5	14
123	Labeling of the pathogenic bacterium <i>Staphylococcus aureus</i> with gold or ferric oxide core nanoparticles highlights new capabilities for investigation of host-pathogen interactions. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 140-150.	1.5	13
124	Altered immune proteome of <i>Staphylococcus aureus</i> under iron-restricted growth conditions. Proteomics, 2014, 14, 1857-1867.	2.2	13
125	Seasonal Patterns of Dominant Microbes Involved in Central Nutrient Cycles in the Subsurface. Microorganisms, 2020, 8, 1694.	3.6	13
126	Heterologous complementation studies in <i>Escherichia coli</i> with the Hyp accessory protein machinery from <i>Chloroflexi</i> provide insight into [NiFe]-hydrogenase large subunit recognition by the HypC protein family. Microbiology (United Kingdom), 2015, 161, 2204-2219.	1.8	13

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127	A Retentive Memory of Tetrachloroethene Respiration in <i>Sulfurospirillum halorespirans</i> - involved Proteins and a possible link to Acetylation of a Two-Component Regulatory System. <i>Journal of Proteomics</i> , 2018, 181, 36-46.	2.4	12
128	<i>Desulfitobacterium</i> contributes to the microbial transformation of 2,4,5-TCF by methanogenic enrichment cultures from a Vietnamese active landfill. <i>Microbial Biotechnology</i> , 2018, 11, 1137-1156.	4.2	12
129	Climate shapes the protein abundance of dominant soil bacteria. <i>Science of the Total Environment</i> , 2018, 640-641, 18-21.	8.0	12
130	Microbial community functioning during plant litter decomposition. <i>Scientific Reports</i> , 2022, 12, 7451.	3.3	12
131	Genome and secretome of <i>Chondrostereum purpureum</i> correspond to saprotrophic and phytopathogenic life styles. <i>PLoS ONE</i> , 2019, 14, e0212769.	2.5	11
132	Comparative Proteomics of <i>Marinobacter</i> sp. TT1 Reveals Corexit Impacts on Hydrocarbon Metabolism, Chemotactic Motility, and Biofilm Formation. <i>Microorganisms</i> , 2021, 9, 3.	3.6	11
133	Proteomic dataset of the organohalide-respiring bacterium <i>Dehalococcoides mccartyi</i> strain CBDB1 grown on hexachlorobenzene as electron acceptor. <i>Data in Brief</i> , 2016, 7, 253-256.	1.0	10
134	The class II benzoyl-coenzyme A reductase complex from the sulfate-reducing <i>Desulfosarcina cetonica</i> . <i>Environmental Microbiology</i> , 2019, 21, 4241-4252.	3.8	10
135	Environmentally Relevant Concentration of Bisphenol S Shows Slight Effects on SIHUMlx. <i>Microorganisms</i> , 2020, 8, 1436.	3.6	10
136	Quantification of glyphosate and aminomethylphosphonic acid from microbiome reactor fluids. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8668.	1.5	10
137	The structure and function of soil archaea across biomes. <i>Journal of Proteomics</i> , 2021, 237, 104147.	2.4	10
138	Identification of novel substrates of <i>Shigella</i> T3SA through analysis of its virulence plasmid-encoded secretome. <i>PLoS ONE</i> , 2017, 12, e0186920.	2.5	10
139	Selenocysteine-independent suppression of UGA codons in the archaeon <i>Methanococcus maripaludis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015, 1850, 2385-2392.	2.4	9
140	In vitro elucidation of suppression effects of composts to soil-borne pathogen <i>Phytophthora nicotianae</i> on pepper plants using 16S amplicon sequencing and metaproteomics. <i>Renewable Agriculture and Food Systems</i> , 2020, 35, 206-214.	1.8	9
141	Emission of CO ₂ and CH ₄ From 13 Deadwood Tree Species Is Linked to Tree Species Identity and Management Intensity in Forest and Grassland Habitats. <i>Global Biogeochemical Cycles</i> , 2022, 36, .	4.9	9
142	Channeling C1 Metabolism toward S-Adenosylmethionine-Dependent Conversion of Estrogens to Androgens in Estrogen-Degrading Bacteria. <i>MBio</i> , 2020, 11, .	4.1	8
143	Explorative Meta-Analysis of 377 Extant Fungal Genomes Predicted a Total Mycobiome Functionality of 42.4 Million KEGG Functions. <i>Frontiers in Microbiology</i> , 2020, 11, 143.	3.5	8
144	Insight Into the Molecular Mechanisms Underpinning the Mycoremediation of Multiple Metals by Proteomic Technique. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	8

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