

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	Functional soil mycobiome across ecosystems. <i>Journal of Proteomics</i> , 2022, 252, 104428.	2.4	15
2	Oxygen and nitrogen production by an ammonia-oxidizing archaeon. <i>Science</i> , 2022, 375, 97-100.	12.6	91
3	Deconstructing <i>Methanosarcina acetivorans</i> into an acetogenic archaeon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
4	Bolstering fitness via CO ₂ fixation and organic carbon uptake: mixotrophs in modern groundwater. <i>ISME Journal</i> , 2022, 16, 1153-1162.	9.8	21
5	Genes and enzymes involved in the biodegradation of the quaternary carbon compound pivalate in the denitrifying <i>Thauera humireducens</i> strain PIV-1. <i>Environmental Microbiology</i> , 2022, , .	3.8	0
6	Effects of Different Formulations of Glyphosate on Rumen Microbial Metabolism and Bacterial Community Composition in the Rumen Simulation Technique System. <i>Frontiers in Microbiology</i> , 2022, 13, 873101.	3.5	0
7	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
8	Microbial community functioning during plant litter decomposition. <i>Scientific Reports</i> , 2022, 12, 7451.	3.3	12
9	Insight Into the Molecular Mechanisms Underpinning the Mycoremediation of Multiple Metals by Proteomic Technique. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	8
10	Novel Unspecific Peroxygenase from <i>Truncatella angustata</i> Catalyzes the Synthesis of Bioactive Lipid Mediators. <i>Microorganisms</i> , 2022, 10, 1267.	3.6	2
11	Bacterial Necromass Is Rapidly Metabolized by Heterotrophic Bacteria and Supports Multiple Trophic Levels of the Groundwater Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	5
12	HumanMetagenomeDB: a public repository of curated and standardized metadata for human metagenomes. <i>Nucleic Acids Research</i> , 2021, 49, D743-D750.	14.5	37
13	Protein stable isotope probing with H ₂ ¹⁸ O differentiated cold stress response at permissive temperatures from general growth at optimal conditions in <i>Escherichia coli</i> K12. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e8941.	1.5	2
14	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
15	Explorative Meta-Analysis of 417 Extant Archaeal Genomes to Predict Their Contribution to the Total Microbiome Functionality. <i>Microorganisms</i> , 2021, 9, 381.	3.6	2
16	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. <i>Microbiome</i> , 2021, 9, 55.	11.1	24
17	The structure and function of soil archaea across biomes. <i>Journal of Proteomics</i> , 2021, 237, 104147.	2.4	10
18	A workflow to identify novel proteins based on the direct mapping of peptide-spectrum-matches to genomic locations. <i>BMC Bioinformatics</i> , 2021, 22, 277.	2.6	4

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19	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). <i>Microorganisms</i> , 2021, 9, 1368.	3.6	2
20	First Dye-Decolorizing Peroxidase from an Ascomycetous Fungus Secreted by <i>Xylaria grammica</i> . <i>Biomolecules</i> , 2021, 11, 1391.	4.0	6
21	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
22	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
23	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
24	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
25	Mucosal-associated invariant T-Cell (MAIT) activation is altered by chlorpyrifos- and glyphosate-treated commensal gut bacteria. <i>Journal of Immunotoxicology</i> , 2020, 17, 10-20.	1.7	22
26	Enrichment and identification of small proteins in a simplified human gut microbiome. <i>Journal of Proteomics</i> , 2020, 213, 103604.	2.4	32
27	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
28	The total microbiome functions in bacteria and fungi. <i>Journal of Proteomics</i> , 2020, 213, 103623.	2.4	16
29	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
30	Environmentally Relevant Concentration of Bisphenol S Shows Slight Effects on SIHUMlx. <i>Microorganisms</i> , 2020, 8, 1436.	3.6	10
31	The glyphosate formulation Roundup® LB plus influences the global metabolome of pig gut microbiota in vitro. <i>Science of the Total Environment</i> , 2020, 745, 140932.	8.0	22
32	Synergistic biodegradation of aromatic-aliphatic copolyester plastic by a marine microbial consortium. <i>Nature Communications</i> , 2020, 11, 5790.	12.8	122
33	Channeling C1 Metabolism toward S-Adenosylmethionine-Dependent Conversion of Estrogens to Androgens in Estrogen-Degrading Bacteria. <i>MBio</i> , 2020, 11, .	4.1	8
34	Seasonal Patterns of Dominant Microbes Involved in Central Nutrient Cycles in the Subsurface. <i>Microorganisms</i> , 2020, 8, 1694.	3.6	13
35	The Activation of Mucosal-Associated Invariant T (MAIT) Cells Is Affected by Microbial Diversity and Riboflavin Utilization in vitro. <i>Frontiers in Microbiology</i> , 2020, 11, 755.	3.5	14
36	Benzylsuccinate Synthase is Post-Transcriptionally Regulated in the Toluene-Degrading Denitrifier <i>Magnetospirillum</i> sp. Strain 15-1. <i>Microorganisms</i> , 2020, 8, 681.	3.6	6

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37	Actinobacterial Degradation of 2-Hydroxyisobutyric Acid Proceeds via Acetone and Formyl-CoA by Employing a Thiamine-Dependent Lyase Reaction. <i>Frontiers in Microbiology</i> , 2020, 11, 691.	3.5	6
38	Soil protein as a potential antimicrobial agent against methicillin-resistant <i>Staphylococcus aureus</i> . <i>Environmental Research</i> , 2020, 188, 109320.	7.5	4
39	Function is what counts: how microbial community complexity affects species, proteome and pathway coverage in metaproteomics. <i>Expert Review of Proteomics</i> , 2020, 17, 163-173.	3.0	17
40	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
41	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
42	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
43	Microbial metaproteome data from decayed beech dead wood. <i>Data in Brief</i> , 2020, 29, 105285.	1.0	2
44	Quantification of glyphosate and aminomethylphosphonic acid from microbiome reactor fluids. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8668.	1.5	10
45	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
46	Tracing incorporation of heavy water into proteins for species-specific metabolic activity in complex communities. <i>Journal of Proteomics</i> , 2020, 222, 103791.	2.4	7
47	Protein-Based Stable Isotope Probing (Protein-SIP): Applications for Studying Aromatic Hydrocarbon Degradation in Microbial Communities. , 2020, , 277-284.		1
48	Thermal proteome profiling allows quantitative assessment of interactions between tetrachloroethene reductive dehalogenase and trichloroethene. <i>Journal of Proteomics</i> , 2019, 192, 10-17.	2.4	25
49	Global ecological predictors of the soil priming effect. <i>Nature Communications</i> , 2019, 10, 3481.	12.8	148
50	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
51	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
52	<i>Pseudomonas</i> spp. are key players in agricultural biogas substrate degradation. <i>Scientific Reports</i> , 2019, 9, 12871.	3.3	28
53	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
54	Enzymes involved in phthalate degradation in sulphate-reducing bacteria. <i>Environmental Microbiology</i> , 2019, 21, 3601-3612.	3.8	22

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55	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
56	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
57	Incomplete cell disruption of resistant microbes. <i>Scientific Reports</i> , 2019, 9, 5618.	3.3	22
58	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
59	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
60	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
61	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
62	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
63	Protein-Based Stable Isotope Probing (Protein-SIP): Applications for Studying Aromatic Hydrocarbon Degradation in Microbial Communities. , 2019, , 1-8.		0
64	Active site alanine preceding catalytic cysteine determines unique substrate specificity in bacterial CoA-acylating prenal dehydrogenase. <i>FEBS Letters</i> , 2018, 592, 1150-1160.	2.8	6
65	Gut microbial functional maturation and succession during human early life. <i>Environmental Microbiology</i> , 2018, 20, 2160-2177.	3.8	30
66	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
67	An integrative overview of genomic, transcriptomic and proteomic analyses in organohalide respiration research. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	45
68	The extracellular metaproteome of soils under semiarid climate: A methodological comparison of extraction buffers. <i>Science of the Total Environment</i> , 2018, 619-620, 707-711.	8.0	18
69	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
70	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
71	Sulfur-34S and 36S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34/36) of Proteome Analyses. <i>Methods in Molecular Biology</i> , 2018, 1841, 163-174.	0.9	0
72	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47

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73	<i>Desulfitobacterium</i> contributes to the microbial transformation of 2,4,5-TP by methanogenic enrichment cultures from a Vietnamese active landfill. <i>Microbial Biotechnology</i> , 2018, 11, 1137-1156.	4.2	12
74	<i>Delftia</i> sp. LCW, a strain isolated from a constructed wetland shows novel properties for dimethylphenol isomers degradation. <i>BMC Microbiology</i> , 2018, 18, 108.	3.3	17
75	Land use driven change in soil pH affects microbial carbon cycling processes. <i>Nature Communications</i> , 2018, 9, 3591.	12.8	380
76	Climate shapes the protein abundance of dominant soil bacteria. <i>Science of the Total Environment</i> , 2018, 640-641, 18-21.	8.0	12
77	Metabolic Adaptation of Methanogens in Anaerobic Digesters Upon Trace Element Limitation. <i>Frontiers in Microbiology</i> , 2018, 9, 405.	3.5	52
78	An unusual strategy for the anoxic biodegradation of phthalate. <i>ISME Journal</i> , 2017, 11, 224-236.	9.8	61
79	A Peroxygenase from <i>Chaetomium globosum</i> Catalyzes the Selective Oxygenation of Testosterone. <i>ChemBioChem</i> , 2017, 18, 563-569.	2.6	63
80	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. <i>Environmental Microbiology</i> , 2017, 19, 2246-2257.	3.8	50
81	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
82	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
83	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
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	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
86	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	3.8	107
87	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
88	Maximization of cell viability rather than biocatalyst activity improves whole-cell γ -oxyfunctionalization performance. <i>Biotechnology and Bioengineering</i> , 2017, 114, 874-884.	3.3	30
89	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
90	Soil Fungal:Bacterial Ratios Are Linked to Altered Carbon Cycling. <i>Frontiers in Microbiology</i> , 2016, 7, 1247.	3.5	292

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91	Enhancing metaproteomicsâ€”The value of models and defined environmental microbial systems. <i>Proteomics</i> , 2016, 16, 783-798.	2.2	62
92	<i>In situ</i> â€¦â€¦roteinâ€¦SIP highlights <i>Burkholderiaceae</i> 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
93	ATP-Dependent C=C Bond Cleavage Allows the Complete Degradation of 4-Fluoroaromatics without Oxygen. <i>MBio</i> , 2016, 7, .	4.1	35
94	Proteome data on the microbial microbiome of grasshopper feces. <i>Data in Brief</i> , 2016, 9, 1147-1154.	1.0	2
95	Proteomic interrogation of the gut microbiota: potential clinical impact. <i>Expert Review of Proteomics</i> , 2016, 13, 535-537.	3.0	17
96	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
97	Proteome profiles of HDL particles of patients with chronic heart failure are associated with immune response and also include bacteria proteins. <i>Clinica Chimica Acta</i> , 2016, 453, 114-122.	1.1	24
98	Aerobic Toluene Degraders in the Rhizosphere of a Constructed Wetland Model Show Diurnal Polyhydroxyalkanoate Metabolism. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4126-4132.	3.1	23
99	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
100	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
101	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
102	Proteomic data set of the organohalide-respiring Epsilonproteobacterium <i>Sulfurospirillum multivorans</i> adapted to tetrachloroethene and other energy substrates. <i>Data in Brief</i> , 2016, 8, 637-642.	1.0	7
103	Proteome data of whole saliva which are associated with development of oral mucositis in head and neck cancer patients undergoing radiotherapy. <i>Data in Brief</i> , 2016, 8, 501-505.	1.0	6
104	Protocol for Performing Protein Stable Isotope Probing (Protein-SIP) Experiments. <i>Springer Protocols</i> , 2016, , 199-214.	0.3	1
105	25-Hydroxyvitamin ₃ Synthesis by Enzymatic Steroid Side-Chain Hydroxylation with Water. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 1881-1884.	13.8	20
106	Protein-SIP in environmental studies. <i>Current Opinion in Biotechnology</i> , 2016, 41, 26-33.	6.6	67
107	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
108	Pulsed ¹³ 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

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109	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
110	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
111	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
112	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methyloph. <i>Environmental Microbiology</i> , 2015, 17, 4007-4018.	3.8	51
113	A peptide resource for the analysis of <i>Staphylococcus aureus</i> in host-pathogen interaction studies. <i>Proteomics</i> , 2015, 15, 3648-3661.	2.2	24
114	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
115	Differences in the whole saliva baseline proteome profile associated with development of oral mucositis in head and neck cancer patients undergoing radiotherapy. <i>Journal of Proteomics</i> , 2015, 125, 98-103.	2.4	21
116	<i>Dehalococcoides mccartyi</i> Strain DCMB5 Respires a Broad Spectrum of Chlorinated Aromatic Compounds. <i>Applied and Environmental Microbiology</i> , 2015, 81, 587-596.	3.1	62
117	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015, 524, 105-108.	27.8	231
118	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
119	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
120	Anaerobic naphthalene degradation by sulfate-reducing <i>Desulfobacteraceae</i> from various anoxic aquifers. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	67
121	Complete nitrification by <i>Nitospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	27.8	1,878
122	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
123	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. <i>Microbiology (United Kingdom)</i> , 2015, 161, 2204-2219.	1.8	13
124	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
125	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
126	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. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 140-150.	1.5	13

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127	A global proteome approach in uric acid stimulated human aortic endothelial cells revealed regulation of multiple major cellular pathways. <i>International Journal of Cardiology</i> , 2014, 176, 746-752.	1.7	17
128	Differences in the secretion pattern of oxidoreductases from <i>Bjerkandera adusta</i> induced by a phenolic olive mill extract. <i>Fungal Genetics and Biology</i> , 2014, 72, 99-105.	2.1	15
129	Altered immune proteome of <i>Staphylococcus aureus</i> under iron-restricted growth conditions. <i>Proteomics</i> , 2014, 14, 1857-1867.	2.2	13
130	Characterization of the microbial community in biological soil crusts dominated by <i>Fulgensia desertorum</i> (Tomin) Poelt and <i>Squamaria cartilaginea</i> (With.) P. James and in the underlying soil. <i>Soil Biology and Biochemistry</i> , 2014, 76, 70-79.	8.8	30
131	Comparative evaluation of peptide desalting methods for salivary proteome analysis. <i>Clinica Chimica Acta</i> , 2014, 434, 16-20.	1.1	15
132	Proteomic analysis of oropharyngeal carcinomas reveals novel HPV-associated biological pathways. <i>International Journal of Cancer</i> , 2013, 132, 568-579.	5.1	47
133	In-depth proteomic analysis of the human cerumen – A potential novel diagnostically relevant biofluid. <i>Journal of Proteomics</i> , 2013, 83, 119-129.	2.4	24
134	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
135	Quantitative analysis of the intra- and inter-subject variability of the whole salivary proteome. <i>Journal of Periodontal Research</i> , 2013, 48, 392-403.	2.7	37
136	Comparative evaluation of saliva collection methods for proteome analysis. <i>Clinica Chimica Acta</i> , 2013, 419, 42-46.	1.1	85
137	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
138	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. <i>ISME Journal</i> , 2013, 7, 1877-1885.	9.8	107
139	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
140	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
141	Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in <i>Pseudomonas fluorescens</i> during Naphthalene Degradation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2060-2069.	3.8	17
142	Impaired HDL function in obese adolescents: Impact of lifestyle intervention and bariatric surgery. <i>Obesity</i> , 2013, 21, E687-95.	3.0	28
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