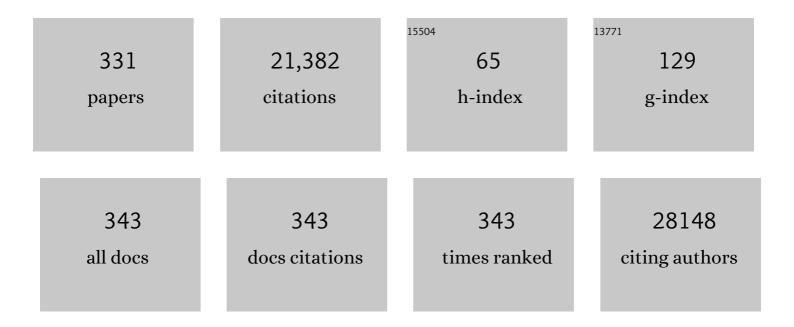
List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8489216/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Complete nitrification by Nitrospira bacteria. Nature, 2015, 528, 504-509.	27.8	1,878
2	Sex Differences in the Gut Microbiome Drive Hormone-Dependent Regulation of Autoimmunity. Science, 2013, 339, 1084-1088.	12.6	1,565
3	Assembly of Ï,, protein into Alzheimer paired helical filaments depends on a local sequence motif () Tj ETQq1 1 0. Sciences of the United States of America, 2000, 97, 5129-5134.	784314 rg 7.1	BT /Overlock 909
4	Mutations of Tau Protein in Frontotemporal Dementia Promote Aggregation of Paired Helical Filaments by Enhancing Local β-Structure. Journal of Biological Chemistry, 2001, 276, 48165-48174.	3.4	501
5	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. Gut, 2013, 62, 1591-1601.	12.1	488
6	Global Hairpin Folding of Tau in Solution. Biochemistry, 2006, 45, 2283-2293.	2.5	350
7	A nucleated assembly mechanism of Alzheimer paired helical filaments. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 15712-15717.	7.1	328
8	Tau aggregation is driven by a transition from random coil to beta sheet structure. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2005, 1739, 158-166.	3.8	321
9	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. Gut, 2016, 65, 225-237.	12.1	317
10	Anthraquinones Inhibit Tau Aggregation and Dissolve Alzheimer's Paired Helical Filaments in Vitro and in Cells. Journal of Biological Chemistry, 2005, 280, 3628-3635.	3.4	305
11	Inducible Expression of Tau Repeat Domain in Cell Models of Tauopathy. Journal of Biological Chemistry, 2006, 281, 1205-1214.	3.4	302
12	Soil Fungal:Bacterial Ratios Are Linked to Altered Carbon Cycling. Frontiers in Microbiology, 2016, 7, 1247.	3.5	292
13	Sites of Tau Important for Aggregation Populate β-Structure and Bind to Microtubules and Polyanions. Journal of Biological Chemistry, 2005, 280, 24978-24986.	3.4	275
14	Functional metaproteome analysis of protein extracts from contaminated soil and groundwater. ISME Journal, 2007, 1, 224-234.	9.8	267
15	Membrane Vesicle Formation as a Multiple-Stress Response Mechanism Enhances Pseudomonas putida DOT-T1E Cell Surface Hydrophobicity and Biofilm Formation. Applied and Environmental Microbiology, 2012, 78, 6217-6224.	3.1	235
16	Cyanate as an energy source for nitrifiers. Nature, 2015, 524, 105-108.	27.8	231
17	The Natively Unfolded Character of Tau and Its Aggregation to Alzheimer-like Paired Helical Filaments. Biochemistry, 2008, 47, 10526-10539.	2.5	224
18	Structural Principles of Tau and the Paired Helical Filaments of Alzheimer's Disease. Brain Pathology, 2007, 17, 83-90.	4.1	221

#	Article	IF	CITATIONS
19	Highly Populated Turn Conformations in Natively Unfolded Tau Protein Identified from Residual Dipolar Couplings and Molecular Simulation. Journal of the American Chemical Society, 2007, 129, 5235-5243.	13.7	208
20	Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure. Environmental Microbiology, 2013, 15, 211-226.	3.8	206
21	Combined Proteomic and Metabolomic Profiling of Serum Reveals Association of the Complement System with Obesity and Identifies Novel Markers of Body Fat Mass Changes. Journal of Proteome Research, 2011, 10, 4769-4788.	3.7	201
22	MiR-130a, miR-203 and miR-205 jointly repress key oncogenic pathways and are downregulated in prostate carcinoma. Oncogene, 2013, 32, 277-285.	5.9	198
23	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	3.5	188
24	Diverse sulfate-reducing bacteria of the <i>Desulfosarcina/Desulfococcus</i> clade are the key alkane degraders at marine seeps. ISME Journal, 2014, 8, 2029-2044.	9.8	182
25	Rational design of a microbial consortium of mucosal sugar utilizers reduces Clostridiodes difficile colonization. Nature Communications, 2020, 11, 5104.	12.8	177
26	Maternal and newborn vitamin D status and its impact on food allergy development in the German LINA cohort study. Allergy: European Journal of Allergy and Clinical Immunology, 2013, 68, 220-228.	5.7	170
27	The "Jaws―of the Tau-Microtubule Interaction. Journal of Biological Chemistry, 2007, 282, 12230-12239.	3.4	167
28	Higher plasma levels of lysophosphatidylcholine 18:0 are related to a lower risk of common cancers in a prospective metabolomics study. BMC Medicine, 2016, 14, 13.	5.5	163
29	The gut bacterium <i>Extibacter muris</i> produces secondary bile acids and influences liver physiology in gnotobiotic mice. Gut Microbes, 2021, 13, 1-21.	9.8	161
30	Adipose tissue derived bacteria are associated with inflammation in obesity and type 2 diabetes. Gut, 2020, 69, 1796-1806.	12.1	149
31	Characterization of Alzheimer's-like Paired Helical Filaments from the Core Domain of Tau Protein Using Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 5922-5928.	13.7	147
32	Prospects and challenges of multi-omics data integration in toxicology. Archives of Toxicology, 2020, 94, 371-388.	4.2	142
33	Maternal and cord blood miR-223 expression associates with prenatal tobacco smoke exposure and low regulatory T-cell numbers. Journal of Allergy and Clinical Immunology, 2014, 133, 543-550.e4.	2.9	137
34	Structure of tau protein and assembly into paired helical filaments. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2000, 1502, 122-132.	3.8	130
35	The Core of Tau-Paired Helical Filaments Studied by Scanning Transmission Electron Microscopy and Limited Proteolysis. Biochemistry, 2006, 45, 6446-6457.	2.5	130
36	MicroRNA-21 targets tumor suppressor genes ANP32A and SMARCA4. Oncogene, 2011, 30, 2975-2985.	5.9	129

#	Article	IF	CITATIONS
37	Protein-based stable isotope probing (Protein-SIP) reveals active species within anoxic mixed cultures. ISME Journal, 2008, 2, 1122-1133.	9.8	126
38	Metaproteogenomic insights beyond bacterial response to naphthalene exposure and bio-stimulation. ISME Journal, 2013, 7, 122-136.	9.8	124
39	Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. ISME Journal, 2012, 6, 2291-2301.	9.8	109
40	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. ISME Journal, 2013, 7, 1877-1885.	9.8	107
41	Identification of a multiâ€protein reductive dehalogenase complex in <scp><i>D</i></scp> <i>ehalococcoides mccartyi</i> strain <scp>CBDB</scp> 1 suggests a proteinâ€dependent respiratory electron transport chain obviating quinone involvement. Environmental Microbiology, 2016, 18, 3044-3056.	3.8	106
42	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. Molecular Metabolism, 2019, 22, 96-109.	6.5	102
43	Combined Genomic and Proteomic Approaches Identify Gene Clusters Involved in Anaerobic 2-Methylnaphthalene Degradation in the Sulfate-Reducing Enrichment Culture N47. Journal of Bacteriology, 2010, 192, 295-306.	2.2	101
44	Identification of spore allergens from the indoor mould <i>Aspergillus versicolor</i> . Allergy: European Journal of Allergy and Clinical Immunology, 2008, 63, 454-460.	5.7	98
45	Expression cartography of human tissues using self organizing maps. BMC Bioinformatics, 2011, 12, 306.	2.6	98
46	Protein-based stable isotope probing. Nature Protocols, 2010, 5, 1957-1966.	12.0	97
47	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. Journal of Allergy and Clinical Immunology, 2018, 141, 741-753.	2.9	92
48	Microbial minorities modulate methane consumption through niche partitioning. ISME Journal, 2013, 7, 2214-2228.	9.8	91
49	Improving protein extraction and separation methods for investigating the metaproteome of anaerobic benzene communities within sediments. Biodegradation, 2009, 20, 737-750.	3.0	86
50	Reversible Biological Birch Reduction at an Extremely Low Redox Potential. Journal of the American Chemical Society, 2010, 132, 9850-9856.	13.7	85
51	Discrimination of different species from the genus Drosophila by intact protein profiling using matrix-assisted laser desorption ionization mass spectrometry. BMC Evolutionary Biology, 2010, 10, 95.	3.2	83
52	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus "Candidatus Sulfobium― Applied and Environmental Microbiology, 2018, 84, .	3.1	83
53	Screening for Inhibitors of Tau Polymerization. Current Alzheimer Research, 2005, 2, 219-226.	1.4	81
54	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. Gut Microbes, 2013, 4, 306-315.	9.8	81

4

#	Article	IF	CITATIONS
55	<i>In situ</i> â€ <scp>p</scp> roteinâ€ <scp>SIP</scp> highlights <i>Burkholderiaceae</i> as key players degrading toluene by para ring hydroxylation in a constructed wetland model. Environmental Microbiology, 2016, 18, 1176-1186.	3.8	81
56	Incorporation of carbon and nitrogen atoms into proteins measured by proteinâ€based stable isotope probing (Protein‣IP). Rapid Communications in Mass Spectrometry, 2008, 22, 2889-2897.	1.5	77
57	Maternal paraben exposure triggers childhood overweight development. Nature Communications, 2020, 11, 561.	12.8	77
58	Human fibroblasts support the expansion of IL-17–producing T cells via up-regulation of IL-23 production by dendritic cells. Blood, 2010, 116, 1715-1725.	1.4	76
59	Phenol Degradation in the Strictly Anaerobic Iron-Reducing Bacterium <i>Geobacter metallireducens</i> GS-15. Applied and Environmental Microbiology, 2009, 75, 3912-3919.	3.1	74
60	Metabolomic biomarkers correlating with hepatic lipidosis in dairy cows. BMC Veterinary Research, 2014, 10, 122.	1.9	74
61	The effect of the degree of sulfation of glycosaminoglycans on osteoclast function and signaling pathways. Biomaterials, 2012, 33, 8418-8429.	11.4	73
62	Relationship between sources and patterns of VOCs in indoor air. Atmospheric Pollution Research, 2014, 5, 129-137.	3.8	73
63	Interactions between bile salts, gut microbiota, and hepatic innate immunity. Immunological Reviews, 2017, 279, 23-35.	6.0	73
64	Identification of T helper (Th)1- and Th2-associated antigens of Cryptococcus neoformans in a murine model of pulmonary infection. Scientific Reports, 2018, 8, 2681.	3.3	73
65	Mining SOM expression portraits: feature selection and integrating concepts of molecular function. BioData Mining, 2012, 5, 18.	4.0	70
66	The Venomics of <i>Bothrops alternatus</i> is a Pool of Acidic Proteins with Predominant Hemorrhagic and Coagulopathic Activities. Journal of Proteome Research, 2010, 9, 2422-2437.	3.7	69
67	Elucidation of in situ polycyclic aromatic hydrocarbon degradation by functional metaproteomics (proteinâ€SIP). Proteomics, 2013, 13, 2910-2920.	2.2	69
68	Anaerobic naphthalene degradation by sulfate-reducing Desulfobacteraceae from various anoxic aquifers. FEMS Microbiology Ecology, 2015, 91, .	2.7	67
69	Random Survival Forest in practice: a method for modelling complex metabolomics data in time to event analysis. International Journal of Epidemiology, 2016, 45, 1406-1420.	1.9	67
70	Protein-SIP in environmental studies. Current Opinion in Biotechnology, 2016, 41, 26-33.	6.6	67
71	The Acclimation of Phaeodactylum tricornutum to Blue and Red Light Does Not Influence the Photosynthetic Light Reaction but Strongly Disturbs the Carbon Allocation Pattern. PLoS ONE, 2014, 9, e99727.	2.5	67
72	Comparative Analysis of the Venom Proteomes of <i>Vipera ammodytes ammodytes</i> and <i>Vipera ammodytes meridionalis</i> . Journal of Proteome Research, 2008, 7, 866-886.	3.7	66

#	Article	IF	CITATIONS
73	Snake venomics of the Siamese Russell's viper (Daboia russelli siamensis) — Relation to pharmacological activities. Journal of Proteomics, 2009, 72, 256-269.	2.4	66
74	The aromatic volatile organic compounds toluene, benzene and styrene induce COX-2 and prostaglandins in human lung epithelial cells via oxidative stress and p38 MAPK activation. Toxicology, 2011, 289, 28-37.	4.2	66
75	Structure, Stability, and Aggregation of Paired Helical Filaments from Tau Protein and FTDP-17 Mutants Probed by Tryptophan Scanning Mutagenesis. Journal of Biological Chemistry, 2002, 277, 41390-41400.	3.4	65
76	Structural and Microtubule Binding Properties of Tau Mutants of Frontotemporal Dementiasâ€. Biochemistry, 2007, 46, 2574-2582.	2.5	65
77	Microbiome manipulation modifies sex-specific risk for autoimmunity. Gut Microbes, 2014, 5, 485-493.	9.8	65
78	Effects of chronic dietary exposure of zinc oxide nanoparticles on the serum protein profile of juvenile common carp (Cyprinus carpio L.). Science of the Total Environment, 2017, 579, 1504-1511.	8.0	65
79	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. Journal of Proteome Research, 2015, 14, 619-627.	3.7	64
80	Metaproteome Analysis and Molecular Genetics of Rat Intestinal Microbiota Reveals Section and Localization Resolved Species Distribution and Enzymatic Functionalities. Journal of Proteome Research, 2012, 11, 5406-5417.	3.7	63
81	Serum metabolites and risk of myocardial infarction and ischemic stroke: a targeted metabolomic approach in two German prospective cohorts. European Journal of Epidemiology, 2018, 33, 55-66.	5.7	63
82	Sulfated Hyaluronan Containing Collagen Matrices Enhance Cell-Matrix-Interaction, Endocytosis, and Osteogenic Differentiation of Human Mesenchymal Stromal Cells. Journal of Proteome Research, 2013, 12, 378-389.	3.7	62
83	Dehalococcoides mccartyi Strain DCMB5 Respires a Broad Spectrum of Chlorinated Aromatic Compounds. Applied and Environmental Microbiology, 2015, 81, 587-596.	3.1	62
84	Enhancing metaproteomics—The value of models and defined environmental microbial systems. Proteomics, 2016, 16, 783-798.	2.2	62
85	Proteinâ€based stable isotope probing (proteinâ€SIP) in functional metaproteomics. Mass Spectrometry Reviews, 2012, 31, 683-697.	5.4	61
86	An unusual strategy for the anoxic biodegradation of phthalate. ISME Journal, 2017, 11, 224-236.	9.8	61
87	Di-(2-Ethylhexyl)-Phthalate (DEHP) Causes Impaired Adipocyte Function and Alters Serum Metabolites. PLoS ONE, 2015, 10, e0143190.	2.5	61
88	Snake Venomic of <i>Crotalus durissus terrificus</i> —Correlation with Pharmacological Activities. Journal of Proteome Research, 2010, 9, 2302-2316.	3.7	60
89	Volatile Organic Compounds Enhance Allergic Airway Inflammation in an Experimental Mouse Model. PLoS ONE, 2012, 7, e39817.	2.5	60
90	Bacteria dominate the short-term assimilation of plant-derived N in soil. Soil Biology and Biochemistry, 2016, 96, 30-38.	8.8	59

#	Article	IF	CITATIONS
91	Metaproteomics and metabolomics analyses of chronically petroleumâ€polluted sites reveal the importance of general anaerobic processes uncoupled with degradation. Proteomics, 2015, 15, 3508-3520.	2.2	58
92	Fatty Acid Oxidation Compensates for Lipopolysaccharide-Induced Warburg Effect in Glucose-Deprived Monocytes. Frontiers in Immunology, 2017, 8, 609.	4.8	58
93	Spectroscopic Approaches to the Conformation of Tau Protein in Solution and in Paired Helical Filaments. Neurodegenerative Diseases, 2006, 3, 197-206.	1.4	57
94	Tracking active groundwater microbes with D ₂ O labelling to understand their ecosystem function. Environmental Microbiology, 2018, 20, 369-384.	3.8	57
95	Vitellogenin cleavage products as indicators for toxic stress in zebra fish embryos: A proteomic approach. Proteomics, 2007, 7, 4541-4554.	2.2	56
96	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. Scientific Reports, 2016, 6, 28616.	3.3	55
97	Prenatal VOC exposure and redecoration are related to wheezing in early infancy. Environment International, 2014, 73, 393-401.	10.0	54
98	Identification and characterization of 2â€naphthoylâ€coenzyme A reductase, the prototype of a novel class of dearomatizing reductases. Molecular Microbiology, 2013, 88, 1032-1039.	2.5	52
99	A metabolomics approach to characterize phenotypes of metabolic transition from late pregnancy to early lactation in dairy cows. Metabolomics, 2016, 12, 1.	3.0	52
100	Structural characterization of β-sheeted oligomers formed on the pathway of oxidative prion protein aggregation in vitro. Journal of Structural Biology, 2007, 157, 308-320.	2.8	51
101	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylotroph. Environmental Microbiology, 2015, 17, 4007-4018.	3.8	51
102	Bidirectional Role of NLRP3 During Acute and Chronic Cholestatic Liver Injury. Hepatology, 2021, 73, 1836-1854.	7.3	51
103	Mechanistic Insights Into the Global Response to Phenol in the Phenol-biodegrading Strain <i>Pseudomonas</i> sp. M1 Revealed by Quantitative Proteomics. OMICS A Journal of Integrative Biology, 2007, 11, 233-251.	2.0	50
104	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. Environmental Microbiology, 2017, 19, 2246-2257.	3.8	50
105	Proteome profile and proteogenomics of the organohalide-respiring bacterium Dehalococcoides mccartyi strain CBDB1 grown on hexachlorobenzene as electron acceptor. Journal of Proteomics, 2014, 98, 59-64.	2.4	49
106	Analysis of structure, function, and activity of a benzene-degrading microbial community. FEMS Microbiology Ecology, 2013, 85, 14-26.	2.7	48
107	Proteomics of the organohalide-respiring Epsilonproteobacterium Sulfurospirillum multivorans adapted to tetrachloroethene and other energy substrates. Scientific Reports, 2015, 5, 13794.	3.3	48
108	Characterization of a multianalyte GC-MS/MS procedure for detecting and quantifying polycyclic aromatic hydrocarbons (PAHs) and PAH derivatives from air particulate matter for an improved risk assessment. Environmental Pollution, 2019, 255, 112967.	7.5	48

#	Article	IF	CITATIONS
109	Elucidating MTBE degradation in a mixed consortium using a multidisciplinary approach. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	47
110	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. Proteomics, 2013, 13, 2786-2804.	2.2	46
111	Biochemical and molecular genetic characterisation of a novel laccase produced by the aquatic ascomycete Phoma sp. UHH 5-1-03. Applied Microbiology and Biotechnology, 2009, 84, 1095-1105.	3.6	45
112	An integrative overview of genomic, transcriptomic and proteomic analyses in organohalide respiration research. FEMS Microbiology Ecology, 2018, 94, .	2.7	45
113	Identification of harmless and pathogenic algae of the genus <i>Prototheca</i> by MALDIâ€MS. Proteomics - Clinical Applications, 2009, 3, 774-784.	1.6	44
114	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. Applied Microbiology and Biotechnology, 2010, 88, 575-584.	3.6	44
115	Osteoblast-released Matrix Vesicles, Regulation of Activity and Composition by Sulfated and Non-sulfated Glycosaminoglycans. Molecular and Cellular Proteomics, 2016, 15, 558-572.	3.8	44
116	Insight into the modulation of intestinal proteome of juvenile common carp (Cyprinus carpio L.) after dietary exposure to ZnO nanoparticles. Science of the Total Environment, 2018, 613-614, 62-71.	8.0	44
117	Styrene induces an inflammatory response in human lung epithelial cells via oxidative stress and NF-κB activation. Toxicology and Applied Pharmacology, 2008, 231, 241-247.	2.8	43
118	Optimization of parameters for coverage of low molecular weight proteins. Analytical and Bioanalytical Chemistry, 2010, 398, 2867-2881.	3.7	43
119	Concentration–response concept in ecotoxicoproteomics: Effects of different phenanthrene concentrations to the zebrafish (Danio rerio) embryo proteome. Ecotoxicology and Environmental Safety, 2012, 76, 11-22.	6.0	41
120	Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM). Analytical and Bioanalytical Chemistry, 2014, 406, 283-291.	3.7	41
121	Decarboxylating and Nondecarboxylating Glutaryl-Coenzyme A Dehydrogenases in the Aromatic Metabolism of Obligately Anaerobic Bacteria. Journal of Bacteriology, 2009, 191, 4401-4409.	2.2	40
122	Time resolved proteinâ€based stable isotope probing (Proteinâ€SIP) analysis allows quantification of induced proteins in substrate shift experiments. Proteomics, 2011, 11, 2265-2274.	2.2	40
123	Gastric bypass surgery in a rat model alters the community structure and functional composition of the intestinal microbiota independently of weight loss. Microbiome, 2020, 8, 13.	11.1	40
124	Enzymes involved in the anaerobic degradation of <i>meta</i> â€substituted halobenzoates. Molecular Microbiology, 2011, 82, 758-769.	2.5	39
125	Identification of new protein coding sequences and signal peptidase cleavage sites of Helicobacter pylori strain 26695 by proteogenomics. Journal of Proteomics, 2013, 86, 27-42.	2.4	37
126	Biochemical Foundations of Health and Energy Conservation in Hibernating Free-ranging Subadult Brown Bear Ursus arctos. Journal of Biological Chemistry, 2016, 291, 22509-22523.	3.4	37

#	Article	IF	CITATIONS
127	Disease Development Is Accompanied by Changes in Bacterial Protein Abundance and Functions in a Refined Model of Dextran Sulfate Sodium (DSS)-Induced Colitis. Journal of Proteome Research, 2019, 18, 1774-1786.	3.7	37
128	Combined Serum Proteomic and Metabonomic Profiling After Laparoscopic Sleeve Gastrectomy in Children and Adolescents. Journal of Laparoendoscopic and Advanced Surgical Techniques - Part A, 2012, 22, 184-188.	1.0	36
129	Candidate Brocadiales dominates C, N and S cycling in anoxic groundwater of a pristine limestone-fracture aquifer. Journal of Proteomics, 2017, 152, 153-160.	2.4	36
130	Subpopulation-proteomics in prokaryotic populations. Current Opinion in Biotechnology, 2013, 24, 79-87.	6.6	35
131	Attenuation of Postoperative Acute Liver Failure by Mesenchymal Stem Cell Treatment Due to Metabolic Implications. Annals of Surgery, 2016, 263, 546-556.	4.2	35
132	ATP-Dependent C–F Bond Cleavage Allows the Complete Degradation of 4-Fluoroaromatics without Oxygen. MBio, 2016, 7, .	4.1	35
133	Comparative performance evaluation of multi-metal resistant fungal strains for simultaneous removal of multiple hazardous metals. Journal of Hazardous Materials, 2016, 318, 679-685.	12.4	35
134	The ABCG2 Efflux Transporter in the Mammary Gland Mediates Veterinary Drug Secretion across the Blood-Milk Barrier into Milk of Dairy Cows. Drug Metabolism and Disposition, 2016, 44, 700-708.	3.3	35
135	The Simplified Human Intestinal Microbiota (SIHUMIx) Shows High Structural and Functional Resistance against Changing Transit Times in In Vitro Bioreactors. Microorganisms, 2019, 7, 641.	3.6	35
136	The effect of green Mediterranean diet on cardiometabolic risk; a randomised controlled trial. Heart, 2021, 107, 1054-1061.	2.9	35
137	<i>Pseudechis australis</i> Venomics: Adaptation for a Defense against Microbial Pathogens and Recruitment of Body Transferrin. Journal of Proteome Research, 2011, 10, 2440-2464.	3.7	34
138	Pathway and Time-Resolved Benzo[<i>a</i>]pyrene Toxicity on Hepa1c1c7 Cells at Toxic and Subtoxic Exposure. Journal of Proteome Research, 2015, 14, 164-182.	3.7	34
139	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	12.8	34
140	Phylogenetic and proteomic analysis of an anaerobic toluene-degrading community. Journal of Applied Microbiology, 2010, 109, 1937-1945.	3.1	33
141	Impact of Vitamin B ₁₂ on Formation of the Tetrachloroethene Reductive Dehalogenase in Desulfitobacterium hafniense Strain Y51. Applied and Environmental Microbiology, 2012, 78, 8025-8032.	3.1	33
142	Microbial interactions during residual oil and <i>n</i> â€fatty acid metabolism by a methanogenic consortium. Environmental Microbiology Reports, 2012, 4, 297-306.	2.4	33
143	Chlorinated Benzenes Cause Concomitantly Oxidative Stress and Induction of Apoptotic Markers in Lung Epithelial Cells (A549) at Nonacute Toxic Concentrations. Journal of Proteome Research, 2011, 10, 363-378.	3.7	32
144	The <scp>LINA</scp> cohort: indoor chemical exposure, circulating eosinophil/basophil (<scp>E</scp> o/ <scp>B</scp>) progenitors and early life skin manifestations. Clinical and Experimental Allergy, 2012, 42, 1337-1346.	2.9	32

#	Article	IF	CITATIONS
145	Common and phylogenetically widespread coding for peptides by bacterial small RNAs. BMC Genomics, 2017, 18, 553.	2.8	32
146	One-megadalton metalloenzyme complex in <i>Geobacter metallireducens</i> involved in benzene ring reduction beyond the biological redox window. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2259-2264.	7.1	32
147	Enrichment and identification of small proteins in a simplified human gut microbiome. Journal of Proteomics, 2020, 213, 103604.	2.4	32
148	Following the community development of SIHUMIx – a new intestinal <i>in vitro</i> model for bioreactor use. Gut Microbes, 2020, 11, 1116-1129.	9.8	32
149	Exploring the limits of robust detection of incorporation of 13C by mass spectrometry in protein-based stable isotope probing (protein-SIP). Analytical and Bioanalytical Chemistry, 2011, 401, 1975-1982.	3.7	31
150	Metaproteogenomic analysis of a sulfate-reducing enrichment culture reveals genomic organization of key enzymes in the m-xylene degradation pathway and metabolic activity of proteobacteria. Systematic and Applied Microbiology, 2014, 37, 488-501.	2.8	31
151	Context-specific metabolic network reconstruction of a naphthalene-degrading bacterial community guided by metaproteomic data. Bioinformatics, 2015, 31, 1771-1779.	4.1	31
152	Structural and functional insights into the interaction of sulfated glycosaminoglycans with tissue inhibitor of metalloproteinase-3 – A possible regulatory role on extracellular matrix homeostasis. Acta Biomaterialia, 2016, 45, 143-154.	8.3	31
153	Prenatal phthalate exposure associates with low regulatory T-cell numbers and atopic dermatitis in early childhood: Results from the LINA mother-child study. Journal of Allergy and Clinical Immunology, 2017, 139, 1376-1379.e8.	2.9	31
154	Aromatizing Cyclohexa-1,5-diene-1-carbonyl-Coenzyme A Oxidase. Journal of Biological Chemistry, 2008, 283, 20713-20721.	3.4	30
155	MALDI-typing of infectious algae of the genus Prototheca using SOM portraits. Journal of Microbiological Methods, 2012, 88, 83-97.	1.6	30
156	Characterization of the microbial community in biological soil crusts dominated by Fulgensia desertorum (Tomin) Poelt and Squamarina cartilaginea (With.) P. James and in the underlying soil. Soil Biology and Biochemistry, 2014, 76, 70-79.	8.8	30
157	Genomic, Proteomic, and Metabolite Characterization of Gemfibrozil-Degrading Organism <i>Bacillus</i> sp. GeD10. Environmental Science & Technology, 2016, 50, 744-755.	10.0	30
158	Maximization of cell viability rather than biocatalyst activity improves wholeâ€cell ωâ€oxyfunctionalization performance. Biotechnology and Bioengineering, 2017, 114, 874-884.	3.3	30
159	Gut microbial functional maturation and succession during human early life. Environmental Microbiology, 2018, 20, 2160-2177.	3.8	30
160	Validation of a multi-analyte HPLC-DAD method for determination of uric acid, creatinine, homovanillic acid, niacinamide, hippuric acid, indole-3-acetic acid and 2-methylhippuric acid in human urine. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2015, 998-999, 40-44.	2.3	29
161	Pulsed 13C2-Acetate Protein-SIP Unveils Epsilonproteobacteria as Dominant Acetate Utilizers in a Sulfate-Reducing Microbial Community Mineralizing Benzene. Microbial Ecology, 2016, 71, 901-911.	2.8	29
162	Comparison of methods for simultaneous identification of bacterial species and determination of metabolic activity by proteinâ€based stable isotope probing (Proteinâ€SIP) experiments. Rapid Communications in Mass Spectrometry, 2009, 23, 1871-1878.	1.5	28

#	Article	IF	CITATIONS
163	Transcriptional signatures of regulatory and toxic responses to benzo-[a]-pyrene exposure. BMC Genomics, 2011, 12, 502.	2.8	28
164	Identification and Characterization of a <i>Re</i> -Citrate Synthase in Dehalococcoides Strain CBDB1. Journal of Bacteriology, 2011, 193, 5171-5178.	2.2	28
165	Optimization of metabolomics of defined in vitro gut microbial ecosystems. International Journal of Medical Microbiology, 2016, 306, 280-289.	3.6	28
166	A patchwork pathway for oxygenaseâ€independent degradation of side chain containing steroids. Environmental Microbiology, 2017, 19, 4684-4699.	3.8	28
167	A H ₂ â€oxidizing, 1,2,3â€trichlorobenzeneâ€reducing multienzyme complex isolated from the obligately organohalideâ€respiring bacterium <i>Dehalococcoides mccartyi</i> strain CBDB1. Environmental Microbiology Reports, 2017, 9, 618-625.	2.4	28
168	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. Environmental Microbiology, 2019, 21, 3780-3795.	3.8	28
169	Sulfated hyaluronic acid and dexamethasone possess a synergistic potential in the differentiation of osteoblasts from human bone marrow stromal cells. Journal of Cellular Biochemistry, 2019, 120, 8706-8722.	2.6	28
170	Mechanistic insight to mycoremediation potential of a metal resistant fungal strain for removal of hazardous metals from multimetal pesticide matrix. Environmental Pollution, 2020, 262, 114255.	7.5	28
171	Cyclohexanecarboxyl-Coenzyme A (CoA) and Cyclohex-1-ene-1-Carboxyl-CoA Dehydrogenases, Two Enzymes Involved in the Fermentation of Benzoate and Crotonate in Syntrophus aciditrophicus. Journal of Bacteriology, 2013, 195, 3193-3200.	2.2	27
172	Deforestation fosters bacterial diversity and the cyanobacterial community responsible for carbon fixation processes under semiarid climate: a metaproteomics study. Applied Soil Ecology, 2015, 93, 65-67.	4.3	27
173	Characterization of chemical-induced sterile inflammation in vitro: application of the model compound ketoconazole in a human hepatic co-culture system. Archives of Toxicology, 2017, 91, 799-810.	4.2	27
174	Accumulation of distinct persistent organic pollutants is associated with adipose tissue inflammation. Science of the Total Environment, 2020, 748, 142458.	8.0	27
175	Interspecies metabolite transfer and aggregate formation in a co-culture of <i>Dehalococcoides</i> and <i>Sulfurospirillum</i> dehalogenating tetrachloroethene to ethene. ISME Journal, 2021, 15, 1794-1809.	9.8	27
176	Comparison and optimization of methods for the simultaneous extraction of DNA, RNA, proteins, and metabolites. Analytical Biochemistry, 2016, 508, 25-33.	2.4	26
177	Metabolic in Vivo Labeling Highlights Differences of Metabolically Active Microbes from the Mucosal Gastrointestinal Microbiome between High-Fat and Normal Chow Diet. Journal of Proteome Research, 2017, 16, 1593-1604.	3.7	26
178	Mono(2â€ethylhexyl) phthalate (MEHP) and mono(2â€ethylâ€5â€oxohexyl) phthalate (MEOHP) but not di(2â€ethylhexyl) phthalate (DEHP) bind productively to the peroxisome proliferatorâ€activated receptor γ. Rapid Communications in Mass Spectrometry, 2019, 33, 75-85.	1.5	26
179	An in-depth multi-omics analysis in RLE-6TN rat alveolar epithelial cells allows for nanomaterial categorization. Particle and Fibre Toxicology, 2019, 16, 38.	6.2	26
180	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

#	Article	IF	CITATIONS
181	Identification and Characterization of a Succinyl-Coenzyme A (CoA):Benzoate CoA Transferase in Geobacter metallireducens. Journal of Bacteriology, 2012, 194, 2501-2508.	2.2	25
182	Thermal proteome profiling allows quantitative assessment of interactions between tetrachloroethene reductive dehalogenase and trichloroethene. Journal of Proteomics, 2019, 192, 10-17.	2.4	25
183	Physiology of Geobacter metallireducens under excess and limitation of electron donors. Part II. Mimicking environmental conditions during cultivation in retentostats. Systematic and Applied Microbiology, 2014, 37, 287-295.	2.8	24
184	Stable Isotope Probing Approaches to Study Anaerobic Hydrocarbon Degradation and Degraders. Journal of Molecular Microbiology and Biotechnology, 2016, 26, 195-210.	1.0	24
185	A multi-omics approach reveals mechanisms of nanomaterial toxicity and structure–activity relationships in alveolar macrophages. Nanotoxicology, 2020, 14, 181-195.	3.0	24
186	Disturbed gut microbiota and bile homeostasis in <i>Giardia</i> -infected mice contributes to metabolic dysregulation and growth impairment. Science Translational Medicine, 2020, 12, .	12.4	24
187	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. Microbiome, 2021, 9, 55.	11.1	24
188	Prediction of flocculation ability of brewing yeast inoculates by flow cytometry, proteome analysis, and mRNA profiling. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 140-147.	1.5	23
189	Aerobic Toluene Degraders in the Rhizosphere of a Constructed Wetland Model Show Diurnal Polyhydroxyalkanoate Metabolism. Applied and Environmental Microbiology, 2016, 82, 4126-4132.	3.1	23
190	Alternatives for the worse: Molecular insights into adverse effects of bisphenol a and substitutes during human adipocyte differentiation. Environment International, 2021, 156, 106730.	10.0	23
191	Stable Isotope Peptide Mass Spectrometry To Decipher Amino Acid Metabolism in Dehalococcoides Strain CBDB1. Journal of Bacteriology, 2012, 194, 4169-4177.	2.2	22
192	Combination of Metabolomics with Cellular Assays Reveals New Biomarkers and Mechanistic Insights on Xenoestrogenic Exposures in MCF-7 Cells. Chemical Research in Toxicology, 2017, 30, 883-892.	3.3	22
193	Enzymes involved in phthalate degradation in sulphateâ€reducing bacteria. Environmental Microbiology, 2019, 21, 3601-3612.	3.8	22
194	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
195	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
196	Proteomics and Metabolomics for <i>In Situ</i> Monitoring of Wound Healing. BioMed Research International, 2014, 2014, 1-12.	1.9	21
197	Structural analysis of the interleukin-8/glycosaminoglycan interactions by amide hydrogen/deuterium exchange mass spectrometry. Methods, 2015, 89, 45-53.	3.8	21
198	Early-onset childhood atopic dermatitis is related to NLRP2 repression. Journal of Allergy and Clinical Immunology, 2018, 141, 1482-1485.e16.	2.9	21

#	Article	IF	CITATIONS
199	Glucocorticoid Treatment Leads to Aberrant Ion and Macromolecular Transport in Regenerating Zebrafish Fins. Frontiers in Endocrinology, 2019, 10, 674.	3.5	21
200	Bolstering fitness via CO2 fixation and organic carbon uptake: mixotrophs in modern groundwater. ISME Journal, 2022, 16, 1153-1162.	9.8	21
201	Assimilation of benzene carbon through multiple trophic levels traced by different stable isotope probing methodologies. FEMS Microbiology Ecology, 2011, 77, 357-369.	2.7	20
202	Sulfurâ€ ³⁶ S stable isotope labeling of amino acids for quantification (SULAQ). Proteomics, 2012, 12, 37-42.	2.2	20
203	Functional analysis of an anaerobic m-xylene-degrading enrichment culture using protein-based stable isotope probing. FEMS Microbiology Ecology, 2012, 81, 134-144.	2.7	20
204	Endogenous metabolites and inflammasome activity in early childhood and links to respiratory diseases. Journal of Allergy and Clinical Immunology, 2015, 136, 495-497.	2.9	20
205	Rearrangement of the Extracellular Domain/Extracellular Loop 1 Interface Is Critical for Thyrotropin Receptor Activation. Journal of Biological Chemistry, 2016, 291, 14095-14108.	3.4	20
206	25â€Hydroxyvitaminâ€D ₃ Synthesis by Enzymatic Steroid Sideâ€Chain Hydroxylation with Water. Angewandte Chemie - International Edition, 2016, 55, 1881-1884.	13.8	20
207	Proteomic definition of human mucosalâ€associated invariant TÂcells determines their unique molecular effector phenotype. European Journal of Immunology, 2018, 48, 1336-1349.	2.9	20
208	Non-Genomic AhR-Signaling Modulates the Immune Response in Endotoxin-Activated Macrophages After Activation by the Environmental Stressor BaP. Frontiers in Immunology, 2021, 12, 620270.	4.8	20
209	Roux-en-Y gastric bypass contributes to weight loss-independent improvement in hypothalamic inflammation and leptin sensitivity through gut-microglia-neuron-crosstalk. Molecular Metabolism, 2021, 48, 101214.	6.5	20
210	Proteome changes in human bronchoalveolar cells following styrene exposure indicate involvement of oxidative stress in the molecularâ€response mechanism. Proteomics, 2009, 9, 4920-4933.	2.2	19
211	Decimal Place Slope, A Fast and Precise Method for Quantifying 13C Incorporation Levels for Detecting the Metabolic Activity of Microbial Species. Molecular and Cellular Proteomics, 2010, 9, 1221-1227.	3.8	19
212	Identification of Lipidomic Biomarkers for Coexposure to Subtoxic Doses of Benzo[<i>a</i>]pyrene and Cadmium: The Toxicological Cascade Biomarker Approach. Environmental Science & Technology, 2014, 48, 10423-10431.	10.0	19
213	Physiology of Geobacter metallireducens under excess and limitation of electron donors. Part I. Batch cultivation with excess of carbon sources. Systematic and Applied Microbiology, 2014, 37, 277-286.	2.8	19
214	Differential cellular metabolite alterations in HaCaT cells caused by exposure to the aryl hydrocarbon receptor-binding polycyclic aromatic hydrocarbons chrysene, benzo[a]pyrene and dibenzo[a,l]pyrene. Toxicology Reports, 2016, 3, 763-773.	3.3	19
215	Proteomics analysis of dendritic cell activation by contact allergens reveals possible biomarkers regulated by Nrf2. Toxicology and Applied Pharmacology, 2016, 313, 170-179.	2.8	19
216	Maternal cytokine status may prime the metabolic profile and increase risk of obesity in children. International Journal of Obesity, 2017, 41, 1440-1446.	3.4	19

#	Article	IF	CITATIONS
217	Mitochondrial Transfer by Human Mesenchymal Stromal Cells Ameliorates Hepatocyte Lipid Load in a Mouse Model of NASH. Biomedicines, 2020, 8, 350.	3.2	19
218	Di-(2-ethylhexyl) phthalate substitutes accelerate human adipogenesis through PPARγ activation and cause oxidative stress and impaired metabolic homeostasis in mature adipocytes. Environment International, 2022, 164, 107279.	10.0	19
219	Benzo[a]pyrene affects Jurkat T cells in the activated state via the antioxidant response element dependent Nrf2 pathway leading to decreased IL-2 secretion and redirecting glutamine metabolism. Toxicology and Applied Pharmacology, 2013, 269, 307-316.	2.8	18
220	High metabolic in vivo stability and bioavailability of a palmitoylated ghrelin receptor ligand assessed by mass spectrometry. Bioorganic and Medicinal Chemistry, 2015, 23, 3925-3932.	3.0	18
221	Metabolomics reveals effects of maternal smoking on endogenous metabolites from lipid metabolism in cord blood of newborns. Metabolomics, 2016, 12, 76.	3.0	18
222	The Emerging Plasticizer Alternative DINCH and Its Metabolite MINCH Induce Oxidative Stress and Enhance Inflammatory Responses in Human THP-1 Macrophages. Cells, 2021, 10, 2367.	4.1	18
223	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
224	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
225	Growth of <i>Aquincola tertiaricarbonis</i> L108 on <i>tert</i> â€Butyl Alcohol Leads to the Induction of a Phthalate Dioxygenaseâ€related Protein and its Associated Oxidoreductase Subunit. Engineering in Life Sciences, 2007, 7, 512-519.	3.6	17
226	Purification and biochemical characterization of a laccase from the aquatic fungus Myrioconium 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
227	DIGE-Based Protein Expression Analysis of B[a]P-Exposed Hepatoma Cells Reveals a Complex Stress Response Including Alterations in Oxidative Stress, Cell Cycle Control, and Cytoskeleton Motility at Toxic and Subacute Concentrations. Journal of Proteome Research, 2011, 10, 379-393.	3.7	17
228	Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in Pseudomonas fluorescens during Naphthalene Degradation. Molecular and Cellular Proteomics, 2013, 12, 2060-2069.	3.8	17
229	Stable isotope labeling by amino acids in cell culture based proteomics reveals differences in protein abundances between spiral and coccoid forms of the gastric pathogen Helicobacter pylori. Journal of Proteomics, 2015, 126, 34-45.	2.4	17
230	Microdialysis Sampling from Wound Fluids Enables Quantitative Assessment of Cytokines, Proteins, and Metabolites Reveals Bone Defect-Specific Molecular Profiles. PLoS ONE, 2016, 11, e0159580.	2.5	17
231	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
232	Occupational IgE-Mediated Softwood Allergy: Characterization of the Causative Allergen. International Archives of Allergy and Immunology, 2012, 157, 202-208.	2.1	16
233	The LINA cohort: Cord blood eosinophil/basophil progenitors predict respiratory outcomes in early infancy. Clinical Immunology, 2014, 152, 68-76.	3.2	16
234	Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in Pseudomonas putida KT2440. AMB Express, 2014, 4, 71.	3.0	16

#	Article	IF	CITATIONS
235	A glycosyl hydrolase family 16 gene is responsible for the endogenous production of β-1,3-glucanases within decapod crustaceans. Gene, 2015, 569, 203-217.	2.2	16
236	Elevated Gestational IL-13 During Fetal Development Is Associated With Hyperactivity and Inattention in Eight-Year-Old Children. Frontiers in Immunology, 2019, 10, 1658.	4.8	16
237	Autoproteolytic stability of a trypsin from the marine crab Cancer pagurus. Biochemical and Biophysical Research Communications, 2008, 370, 566-571.	2.1	15
238	Quantitative proteomics reveals novel functions of osteoclast-associated receptor in STAT signaling and cell adhesion in human endothelial cells. Journal of Molecular and Cellular Cardiology, 2012, 53, 829-837.	1.9	15
239	Subtoxic and toxic concentrations of benzene and toluene induce Nrf2-mediated antioxidative stress response and affect the central carbon metabolism in lung epithelial cells A549. Proteomics, 2013, 13, 3211-3221.	2.2	15
240	Comparison of quantitation methods in proteomics to define relevant toxicological information on AhR activation of HepG2 cells by BaP. Toxicology, 2021, 448, 152652.	4.2	15
241	Nanomaterials induce different levels of oxidative stress, depending on the used model system: Comparison of in vitro and in vivo effects. Science of the Total Environment, 2021, 801, 149538.	8.0	15
242	Danger signal extracellular calcium initiates differentiation of monocytes into SPP1/osteopontin-producing macrophages. Cell Death and Disease, 2022, 13, 53.	6.3	15
243	Declining Capacity of Starving <i>Delftia acidovorans</i> MC1 to Degrade Phenoxypropionate Herbicides Correlates with Oxidative Modification of the Initial Enzyme. Environmental Science & Technology, 2010, 44, 3793-3799.	10.0	14
244	Species determination of Culicoides biting midges via peptide profiling using matrix-assisted laser desorption ionization mass spectrometry. Parasites and Vectors, 2014, 7, 392.	2.5	14
245	Monitoring of drug intake during pregnancy by questionnaires and LCâ€MS/MS drug urine screening: evaluation of both monitoring methods. Drug Testing and Analysis, 2015, 7, 695-702.	2.6	14
246	Systematic Review of Multi-Omics Approaches to Investigate Toxicological Effects in Macrophages. International Journal of Molecular Sciences, 2020, 21, 9371.	4.1	14
247	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
248	Quantitative proteomics reveals altered expression of extracellular matrix related proteins of human primary dermal fibroblasts in response to sulfated hyaluronan and collagen applied as artificial extracellular matrix. Journal of Materials Science: Materials in Medicine, 2012, 23, 3053-3065.	3.6	13
249	Limitations in detection of 15N incorporation by mass spectrometry in protein-based stable isotope probing (protein-SIP). Analytical and Bioanalytical Chemistry, 2013, 405, 3989-3996.	3.7	13
250	Two-dimensional proteome reference map of <i>Prototheca zopfii</i> revealed reduced metabolism and enhanced signal transduction as adaptation to an infectious life style. Proteomics, 2013, 13, 2664-2669.	2.2	13
251	Seasonal Patterns of Dominant Microbes Involved in Central Nutrient Cycles in the Subsurface. Microorganisms, 2020, 8, 1694.	3.6	13
252	A Multi-Omics Analysis of Mucosal-Associated-Invariant T Cells Reveals Key Drivers of Distinct Modes of Activation. Frontiers in Immunology, 2021, 12, 616967.	4.8	13

#	Article	IF	CITATIONS
253	Prenatal paraben exposure and atopic dermatitisâ€related outcomes among children. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 3122-3132.	5.7	13
254	Intrinsic Fluorescent Detection of Tau Conformation and Aggregation. , 2005, 299, 175-184.		12
255	Interactions of recombinant prions with compounds of therapeutical significance. Biochemical and Biophysical Research Communications, 2006, 344, 463-470.	2.1	12
256	DIGE Proteome Analysis Reveals Suitability of Ischemic Cardiac In Vitro Model for Studying Cellular Response to Acute Ischemia and Regeneration. PLoS ONE, 2012, 7, e31669.	2.5	12
257	Evaluation of the tolerability and immunogenicity of ultraviolet Câ€irradiated autologous platelets in a dog model. Transfusion, 2012, 52, 2414-2426.	1.6	12
258	Effects of ceftiofur treatment on the susceptibility of commensal porcine E.coli – comparison between treated and untreated animals housed in the same stable. BMC Veterinary Research, 2015, 11, 265.	1.9	12
259	A Retentive Memory of Tetrachloroethene Respiration in Sulfurospirillum halorespirans - involved Proteins and a possible link to Acetylation of a Two-Component Regulatory System. Journal of Proteomics, 2018, 181, 36-46.	2.4	12
260	<i>Desulfitobacterium</i> contributes to the microbial transformation of 2,4,5â€T by methanogenic enrichment cultures from a Vietnamese active landfill. Microbial Biotechnology, 2018, 11, 1137-1156.	4.2	12
261	Multiomics reveal unique signatures of human epiploic adipose tissue related to systemic insulin resistance. Gut, 2022, 71, 2179-2193.	12.1	12
262	Microbial community functioning during plant litter decomposition. Scientific Reports, 2022, 12, 7451.	3.3	12
263	Establishing a Reliable Multiple Reaction Monitoring-Based Method for the Quantification of Obesity-Associated Comorbidities in Serum and Adipose Tissue Requires Intensive Clinical Validation. Journal of Proteome Research, 2014, 13, 5784-5800.	3.7	11
264	A cleavable cytolysin–neuropeptide Y bioconjugate enables specific drug delivery and demonstrates intracellular mode of action. Journal of Controlled Release, 2015, 209, 170-178.	9.9	11
265	Effects of exposure to single and multiple parabens on asthma development in an experimental mouse model and a prospective cohort study. Science of the Total Environment, 2022, 814, 152676.	8.0	11
266	Autophagopathies: from autophagy gene polymorphisms to precision medicine for human diseases. Autophagy, 2022, 18, 2519-2536.	9.1	11
267	Analysis of the STAT3 interactome using in-situ biotinylation and SILAC. Journal of Proteomics, 2013, 94, 370-386.	2.4	10
268	Integration of conventional quantitative and phosphoâ€proteomics reveals new elements in activated Jurkat Tâ€cell receptor pathway maintenance. Proteomics, 2015, 15, 25-33.	2.2	10
269	Proteomic dataset of the organohalide-respiring bacterium Dehalococcoides mccartyi strain CBDB1 grown on hexachlorobenzene as electron acceptor. Data in Brief, 2016, 7, 253-256.	1.0	10
270	Mesenchymal stem cells correct haemodynamic dysfunction associated with liver injury after extended resection in a pig model. Scientific Reports, 2017, 7, 2617.	3.3	10

#	Article	IF	CITATIONS
271	Pilot Study on Mass Spectrometry–Based Analysis of the Proteome of CD34+CD123+ Progenitor Cells for the Identification of Potential Targets for Immunotherapy in Acute Myeloid Leukemia. Proteomes, 2018, 6, 11.	3.5	10
272	The class II benzoylâ€coenzyme A reductase complex from the sulfateâ€reducing <i>Desulfosarcina cetonica</i> . Environmental Microbiology, 2019, 21, 4241-4252.	3.8	10
273	Environmentally Relevant Concentration of Bisphenol S Shows Slight Effects on SIHUMIx. Microorganisms, 2020, 8, 1436.	3.6	10
274	Quantification of glyphosate and aminomethylphosphonic acid from microbiome reactor fluids. Rapid Communications in Mass Spectrometry, 2020, 34, e8668.	1.5	10
275	Differences in cortical contractile properties between healthy epithelial and cancerous mesenchymal breast cells. New Journal of Physics, 2021, 23, 103020.	2.9	10
276	Identification of novel substrates of Shigella T3SA through analysis of its virulence plasmid-encoded secretome. PLoS ONE, 2017, 12, e0186920.	2.5	10
277	Selenocysteine-independent suppression of UGA codons in the archaeon Methanococcus maripaludis. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 2385-2392.	2.4	9
278	Allergen-Induced IL-6 Regulates IL-9/IL-17A Balance in CD4+ T Cells in Allergic Airway Inflammation. Journal of Immunology, 2016, 197, 2653-2664.	0.8	9
279	Comparison of metabolite networks from four German population-based studies. International Journal of Epidemiology, 2018, 47, 2070-2081.	1.9	9
280	An MRM-Based Multiplexed Quantification Assay for Human Adipokines and Apolipoproteins. Molecules, 2020, 25, 775.	3.8	9
281	The Contact Allergen NiSO4 Triggers a Distinct Molecular Response in Primary Human Dendritic Cells Compared to Bacterial LPS. Frontiers in Immunology, 2021, 12, 644700.	4.8	9
282	Channeling C1 Metabolism toward S -Adenosylmethionine-Dependent Conversion of Estrogens to Androgens in Estrogen-Degrading Bacteria. MBio, 2020, 11, .	4.1	8
283	In Depth Quantitative Proteomic and Transcriptomic Characterization of Human Adipocyte Differentiation using the SGBS Cell Line. Proteomics, 2020, 20, e1900405.	2.2	8
284	Insight Into the Molecular Mechanisms Underpinning the Mycoremediation of Multiple Metals by Proteomic Technique. Frontiers in Microbiology, 2022, 13, .	3.5	8
285	Peptide NMHRYPNQ of the Cellular Prion Protein (PrPC) Inhibits Aggregation and Is a Potential Key for Understanding Prion–Prion Interactions. Journal of Molecular Biology, 2009, 392, 198-207.	4.2	7
286	Calculation of partial isotope incorporation into peptides measured by mass spectrometry. BMC Research Notes, 2010, 3, 178.	1.4	7
287	Proteomic data set of the organohalide-respiring Epsilonproteobacterium Sulfurospirillum multivorans adapted to tetrachloroethene and other energy substrates. Data in Brief, 2016, 8, 637-642.	1.0	7
288	Resistance towards monensin is proposed to be acquired in a <i>Toxoplasma gondii</i> model by reduced invasion and egress activities, in addition to increased intracellular replication. Parasitology, 2018, 145, 313-325.	1.5	7

#	Article	IF	CITATIONS
289	Effects of Five Substances with Different Modes of Action on Cathepsin H, C and L Activities in Zebrafish Embryos. International Journal of Environmental Research and Public Health, 2019, 16, 3956.	2.6	7
290	Tracing incorporation of heavy water into proteins for species-specific metabolic activity in complex communities. Journal of Proteomics, 2020, 222, 103791.	2.4	7
291	Wood emissions and asthma development: Results from an experimental mouse model and a prospective cohort study. Environment International, 2021, 151, 106449.	10.0	7
292	Mesenchymal stromal cells mitigate liver damage after extended resection in the pig by modulating thrombospondin-1/TGF-β. Npj Regenerative Medicine, 2021, 6, 84.	5.2	7
293	The EU chemicals strategy for sustainability: an opportunity to develop new approaches for hazard and risk assessment. Archives of Toxicology, 2022, 96, 2381-2386.	4.2	7
294	The lasting effect of limonene-induced particle formation on air quality in a genuine indoor environment. Environmental Science and Pollution Research, 2015, 22, 14209-14219.	5.3	6
295	Identification of pesticide exposure-induced metabolic changes in mosquito larvae. Science of the Total Environment, 2018, 643, 1533-1541.	8.0	6
296	Benzylsuccinate Synthase is Post-Transcriptionally Regulated in the Toluene-Degrading Denitrifier Magnetospirillum sp. Strain 15-1. Microorganisms, 2020, 8, 681.	3.6	6
297	Comparison of preservation methods for bacterial cells in cytomics and proteomics. Journal of Integrated OMICS, 2013, 3, .	0.5	5
298	Compartment resolved reference proteome map from highly purified naÃ ⁻ ve, activated, effector, and memory CD8+ murine immune cells. Proteomics, 2015, 15, 1808-1812.	2.2	5
299	The LINA Study: Higher Sensitivity of Infant Compared to Maternal Eosinophil/Basophil Progenitors to Indoor Chemical Exposures. Journal of Environmental and Public Health, 2016, 2016, 1-10.	0.9	5
300	Hepatic co-cultures in vitro reveal suitable to detect Nrf2-mediated oxidative stress responses on the bladder carcinogen o -anisidine. Toxicology in Vitro, 2017, 40, 153-160.	2.4	5
301	Changes of the Proteome and Acetylome during Transition into the Stationary Phase in the Organohalide-Respiring Dehalococcoides mccartyi Strain CBDB1. Microorganisms, 2021, 9, 365.	3.6	5
302	An environmental ecocorona influences the formation and evolution of the biological corona on the surface of single-walled carbon nanotubes. NanoImpact, 2021, 22, 100315.	4.5	5
303	Identification of intracellular glycosaminoglycan-interacting proteins by affinity purification mass spectrometry. Biological Chemistry, 2021, 402, 1427-1440.	2.5	5
304	Proteomic Characterization of the Cellular Effects of AhR Activation by Microbial Tryptophan Catabolites in Endotoxin-Activated Human Macrophages. International Journal of Environmental Research and Public Health, 2021, 18, 10336.	2.6	5
305	Bacterial Necromass Is Rapidly Metabolized by Heterotrophic Bacteria and Supports Multiple Trophic Levels of the Groundwater Microbiome. Microbiology Spectrum, 2022, 10, .	3.0	5
306	Mid- and long-term correlations of plasma metabolite concentrations measured by a targeted metabolomics approach. Metabolomics, 2016, 12, 1.	3.0	4

#	Article	IF	CITATIONS
307	Serum Amino Acid Concentrations in Infants from Malawi are Associated with Linear Growth. Current Developments in Nutrition, 2019, 3, nzz100.	0.3	4
308	Ethnomedicinal survey and in vitro confirmation of anti-inflammatory and antispasmodic properties of the termite strain Macrotermes bellicosus used in traditional medicine in the Republic of Benin Journal of Ethnopharmacology, 2020, 254, 112705.	4.1	4
309	Proteomics reveals sex-specific heat shock response of Baikal amphipod Eulimnogammarus cyaneus. Science of the Total Environment, 2021, 763, 143008.	8.0	4
310	A workflow to identify novel proteins based on the direct mapping of peptide-spectrum-matches to genomic locations. BMC Bioinformatics, 2021, 22, 277.	2.6	4
311	Posttranslational oxidative modification of (<i><scp>R</scp></i>)â€2â€(2,4â€dichlorophenoxy)propionate/αâ€ketoglutarateâ€dependent dioxygenases (R leads to improved degradation of 2,4â€dichlorophenoxyacetate (2,4â€D). Engineering in Life Sciences, 2013, 13. 278-291.	dgA)	3
312	Biomonitoring of prenatal analgesic intake and correlation with infantile anti-aeroallergens IgE. Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 901-906.	5.7	3
313	Long-term indoor VOC concentrations assessment a trend analysis of distribution, disposition, and personal exposure in cohort study samples. Air Quality, Atmosphere and Health, 2016, 9, 941-950.	3.3	3
314	Influence of formic acid treatment on the proteome of the ectoparasite Varroa destructor. PLoS ONE, 2021, 16, e0258845.	2.5	3
315	Molecular phenotypic portraits - Exploring the 'OMES' with individual resolution. , 2011, , .		2
316	Proteome data on the microbial microbiome of grasshopper feces. Data in Brief, 2016, 9, 1147-1154.	1.0	2
317	Assessment of maternal drug intake by urinary bio monitoring during pregnancy and postpartally until the third perinatal year. Pharmacoepidemiology and Drug Safety, 2016, 25, 431-437.	1.9	2
318	The benzene metabolite 1,4-benzoquinone reduces regulatory T-cell function: AÂpotential mechanism for tobacco smoke–associated atopic dermatitis. Journal of Allergy and Clinical Immunology, 2017, 140, 603-605.	2.9	2
319	Protein stable isotope probing with H ₂ ¹⁸ O differentiated cold stress response at permissive temperatures from general growth at optimal conditions in <scp><i>Escherichia coli</i></scp> K12. Rapid Communications in Mass Spectrometry, 2021, 35, e8941.	1.5	2
320	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). Microorganisms, 2021, 9, 1368.	3.6	2
321	Requirements and Perspectives for Integrating Metabolomics with other Omics Data. Current Metabolomics, 2012, 1, 15-27.	0.5	1
322	Protocol for Performing Protein Stable Isotope Probing (Protein-SIP) Experiments. Springer Protocols, 2016, , 199-214.	0.3	1
323	Protein-Based Stable Isotope Probing (Protein-SIP): Applications for Studying Aromatic Hydrocarbon Degradation in Microbial Communities. , 2020, , 277-284.		1
324	Interactions of Ginkgolides A and B with a Recombinant Human Prion Protein. Protein and Peptide Letters, 2010, 17, 399-404.	0.9	0

#	Article	IF	CITATIONS
325	Subtoxic concentrations of benzo[a]pyrene induce metabolic changes and oxidative stress in non-activated and affect the mTOR pathway in activated Jurkat T cells. Journal of Integrated OMICS, 2014, 4, .	0.5	0
326	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. BioMed Research International, 2016, 2016, 1-13.	1.9	0
327	Sulfur-34S and 36S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34/36) of Proteome Analyses. Methods in Molecular Biology, 2018, 1841, 163-174.	0.9	0
328	Protein Stable Isotope Probing. , 0, , 73-95.		0
329	Protein-Based Stable Isotope Probing (Protein-SIP): Applications for Studying Aromatic Hydrocarbon Degradation in Microbial Communities. , 2019, , 1-8.		0
330	Genes and enzymes involved in the biodegradation of the quaternary carbon compound pivalate in the denitrifying <i>Thauera humireducens</i> strain <scp>PIV</scp> â€1. Environmental Microbiology, 2022, ,	3.8	0
331	Effects of Different Formulations of Glyphosate on Rumen Microbial Metabolism and Bacterial Community Composition in the Rumen Simulation Technique System. Frontiers in Microbiology, 2022, 13, 873101.	3.5	0