

Thomas O Metz

List of Publications by Year in descending order

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129
papers

11,074
citations

31902

53
h-index

34900

98
g-index

143
all docs

143
docs citations

143
times ranked

18396
citing authors

#	ARTICLE	IF	CITATIONS
1	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	9.4	2,802
2	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	13.5	701
3	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. <i>PLoS Pathogens</i> , 2010, 6, e1000719.	2.1	361
4	Dengue Virus Infection Perturbs Lipid Homeostasis in Infected Mosquito Cells. <i>PLoS Pathogens</i> , 2012, 8, e1002584.	2.1	290
5	Effect of Genetic Diagnosis on Patients with Previously Undiagnosed Disease. <i>New England Journal of Medicine</i> , 2018, 379, 2131-2139.	13.9	261
6	Mechanisms of Severe Acute Respiratory Syndrome Coronavirus-Induced Acute Lung Injury. <i>MBio</i> , 2013, 4, .	1.8	251
7	Pathogenic Influenza Viruses and Coronaviruses Utilize Similar and Contrasting Approaches To Control Interferon-Stimulated Gene Responses. <i>MBio</i> , 2014, 5, e01174-14.	1.8	246
8	Review, Evaluation, and Discussion of the Challenges of Missing Value Imputation for Mass Spectrometry-Based Label-Free Global Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 1993-2001.	1.8	217
9	Uncovering biologically significant lipid isomers with liquid chromatography, ion mobility spectrometry and mass spectrometry. <i>Analyst</i> , The, 2016, 141, 1649-1659.	1.7	196
10	MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. <i>MSystems</i> , 2016, 1, .	1.7	166
11	A statistical framework for protein quantitation in bottom-up MS-based proteomics. <i>Bioinformatics</i> , 2009, 25, 2028-2034.	1.8	149
12	Enrichment and Analysis of Nonenzymatically Glycated Peptides: A Boronate Affinity Chromatography Coupled with Electron-Transfer Dissociation Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2323-2330.	1.8	147
13	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. <i>Molecular Systems Biology</i> , 2012, 8, 558.	3.2	142
14	The Undiagnosed Diseases Network: Accelerating Discovery about Health and Disease. <i>American Journal of Human Genetics</i> , 2017, 100, 185-192.	2.6	142
15	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1012-E1021.	3.3	142
16	Release of Severe Acute Respiratory Syndrome Coronavirus Nuclear Import Block Enhances Host Transcription in Human Lung Cells. <i>Journal of Virology</i> , 2013, 87, 3885-3902.	1.5	140
17	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , 2017, 2, 16221.	5.9	138
18	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. <i>Bioinformatics</i> , 2013, 29, 2900-2908.	1.8	122

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19	The impact of proinflammatory cytokines on the β -cell regulatory landscape provides insights into the genetics of type 1 diabetes. <i>Nature Genetics</i> , 2019, 51, 1588-1595.	9.4	117
20	Tutorial: best practices and considerations for mass-spectrometry-based protein biomarker discovery and validation. <i>Nature Protocols</i> , 2021, 16, 3737-3760.	5.5	110
21	LIQUID: an open source software for identifying lipids in LC-MS/MS-based lipidomics data. <i>Bioinformatics</i> , 2017, 33, 1744-1746.	1.8	108
22	Diel metabolomics analysis of a hot spring chlorophototrophic microbial mat leads to new hypotheses of community member metabolisms. <i>Frontiers in Microbiology</i> , 2015, 6, 209.	1.5	104
23	Phototrophic biofilm assembly in microbial-mat-derived unicyanobacterial consortia: model systems for the study of autotroph-heterotroph interactions. <i>Frontiers in Microbiology</i> , 2014, 5, 109.	1.5	97
24	Decreased abundance of type III secretion system-inducing signals in <i>Arabidopsis mkp1</i> enhances resistance against <i>Pseudomonas syringae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6846-6851.	3.3	97
25	Separation and Classification of Lipids Using Differential Ion Mobility Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1146-55.	1.2	96
26	Combined Statistical Analyses of Peptide Intensities and Peptide Occurrences Improves Identification of Significant Peptides from MS-Based Proteomics Data. <i>Journal of Proteome Research</i> , 2010, 9, 5748-5756.	1.8	93
27	Serum proteomics reveals systemic dysregulation of innate immunity in type 1 diabetes. <i>Journal of Experimental Medicine</i> , 2013, 210, 191-203.	4.2	91
28	Improved quality control processing of peptide-centric LC-MS proteomics data. <i>Bioinformatics</i> , 2011, 27, 2866-2872.	1.8	88
29	Multi-platform â^{TM} Omics Analysis of Human Ebola Virus Disease Pathogenesis. <i>Cell Host and Microbe</i> , 2017, 22, 817-829.e8.	5.1	88
30	An integrated multi-omics approach identifies the landscape of interferon- β -mediated responses of human pancreatic beta cells. <i>Nature Communications</i> , 2020, 11, 2584.	5.8	87
31	A reversed-phase capillary ultra-performance liquid chromatography-mass spectrometry (UPLC-MS) method for comprehensive top-down/bottom-up lipid profiling. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 2923-2933.	1.9	86
32	A Multi-Omic View of Host-Pathogen-Commensal Interplay in Salmonella-Mediated Intestinal Infection. <i>PLoS ONE</i> , 2013, 8, e67155.	1.1	81
33	Proteomic Analysis of the Site Specificity of Glycation and Carboxymethylation of Ribonuclease. <i>Journal of Proteome Research</i> , 2003, 2, 506-513.	1.8	78
34	Future of liquid chromatography-mass spectrometry in metabolic profiling and metabolomic studies for biomarker discovery. <i>Biomarkers in Medicine</i> , 2007, 1, 159-185.	0.6	78
35	Comprehensive Proteomics Analysis of Stressed Human Islets Identifies GDF15 as a Target for Type 1 Diabetes Intervention. <i>Cell Metabolism</i> , 2020, 31, 363-374.e6.	7.2	78
36	Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	9.4	78

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37	SLIM Ultrahigh Resolution Ion Mobility Spectrometry Separations of Isotopologues and Isotopomers Reveal Mobility Shifts due to Mass Distribution Changes. <i>Analytical Chemistry</i> , 2019, 91, 11952-11962.	3.2	76
38	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. <i>Cell Host and Microbe</i> , 2016, 19, 254-266.	5.1	75
39	Elucidation of roles for vitamin B ₁₂ in regulation of folate, ubiquinone, and methionine metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1205-E1214.	3.3	75
40	A comparative analysis of computational approaches to relative protein quantification using peptide peak intensities in label-free LC-MS proteomics experiments. <i>Proteomics</i> , 2013, 13, 493-503.	1.3	74
41	ISICLE: A Quantum Chemistry Pipeline for Establishing in Silico Collision Cross Section Libraries. <i>Analytical Chemistry</i> , 2019, 91, 4346-4356.	3.2	74
42	Ion mobility spectrometry and the omics: Distinguishing isomers, molecular classes and contaminant ions in complex samples. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 116, 292-299.	5.8	71
43	A Network Integration Approach to Predict Conserved Regulators Related to Pathogenicity of Influenza and SARS-CoV Respiratory Viruses. <i>PLoS ONE</i> , 2013, 8, e69374.	1.1	68
44	New mass spectrometry technologies contributing towards comprehensive and high throughput omics analyses of single cells. <i>Analyst</i> , 2019, 144, 794-807.	1.7	67
45	Lipidomics reveals dramatic lipid compositional changes in the maturing postnatal lung. <i>Scientific Reports</i> , 2017, 7, 40555.	1.6	67
46	The succinated proteome. <i>Mass Spectrometry Reviews</i> , 2014, 33, 98-109.	2.8	66
47	Integrating ion mobility spectrometry into mass spectrometry-based exposome measurements: what can it add and how far can it go?. <i>Bioanalysis</i> , 2017, 9, 81-98.	0.6	66
48	SPE-IMS-MS: An automated platform for sub-sixty second surveillance of endogenous metabolites and xenobiotics in biofluids. <i>Clinical Mass Spectrometry</i> , 2016, 2, 1-10.	1.9	63
49	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	2.4	62
50	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . <i>BMC Genomics</i> , 2016, 17, 138.	1.2	62
51	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. <i>American Journal of Human Genetics</i> , 2018, 102, 494-504.	2.6	59
52	Characterization of the Human Pancreatic Islet Proteome by Two-Dimensional LC/MS/MS. <i>Journal of Proteome Research</i> , 2006, 5, 3345-3354.	1.8	58
53	<i>In silico</i> identification software (ISIS): a machine learning approach to tandem mass spectral identification of lipids. <i>Bioinformatics</i> , 2012, 28, 1705-1713.	1.8	58
54	Temporospatial shifts in the human gut microbiome and metabolome after gastric bypass surgery. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 12.	2.9	57

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55	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	56
56	Genetic and metabolic links between the murine microbiome and memory. <i>Microbiome</i> , 2020, 8, 53.	4.9	56
57	Untargeted metabolomic profiling of <i>Sphagnum fallax</i> reveals novel antimicrobial metabolites. <i>Plant Direct</i> , 2019, 3, e00179.	0.8	55
58	Comprehensive Metabolomic, Lipidomic and Microscopic Profiling of <i>Yarrowia lipolytica</i> during Lipid Accumulation Identifies Targets for Increased Lipogenesis. <i>PLoS ONE</i> , 2015, 10, e0123188.	1.1	54
59	Silymarin Suppresses Cellular Inflammation By Inducing Reparative Stress Signaling. <i>Journal of Natural Products</i> , 2015, 78, 1990-2000.	1.5	53
60	A global lipid map defines a network essential for Zika virus replication. <i>Nature Communications</i> , 2020, 11, 3652.	5.8	50
61	Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes. <i>Molecular BioSystems</i> , 2013, 9, 1522.	2.9	49
62	Systems Virology Identifies a Mitochondrial Fatty Acid Oxidation Enzyme, Dodecenoyl Coenzyme A Delta Isomerase, Required for Hepatitis C Virus Replication and Likely Pathogenesis. <i>Journal of Virology</i> , 2011, 85, 11646-11654.	1.5	48
63	Quantum Chemistry Calculations for Metabolomics. <i>Chemical Reviews</i> , 2021, 121, 5633-5670.	23.0	47
64	Effects of ingested nanocellulose on intestinal microbiota and homeostasis in Wistar Han rats. <i>NanoImpact</i> , 2020, 18, 100216.	2.4	44
65	MPLEx: a method for simultaneous pathogen inactivation and extraction of samples for multi-omics profiling. <i>Analyst</i> , The, 2017, 142, 442-448.	1.7	43
66	High-resolution separations and improved ion production and transmission in metabolomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2008, 27, 205-214.	5.8	41
67	Sexual dimorphism in the fetal cardiac response to maternal nutrient restriction. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 108, 181-193.	0.9	41
68	Perturbations in the lipid profile of individuals with newly diagnosed type 1 diabetes mellitus: Lipidomics analysis of a Diabetes Antibody Standardization Program sample subset. <i>Clinical Biochemistry</i> , 2010, 43, 948-956.	0.8	38
69	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3639-3646.	2.5	38
70	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	1.8	38
71	An automated framework for NMR chemical shift calculations of small organic molecules. <i>Journal of Cheminformatics</i> , 2018, 10, 52.	2.8	37
72	A multi-omic systems approach to elucidating <i>Yersinia</i> virulence mechanisms. <i>Molecular BioSystems</i> , 2013, 9, 44-54.	2.9	29

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73	A statistical analysis of the effects of urease pre-treatment on the measurement of the urinary metabolome by gas chromatography–mass spectrometry. <i>Metabolomics</i> , 2014, 10, 897-908.	1.4	28
74	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 717-727.	2.5	26
75	Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. <i>Journal of Proteome Research</i> , 2015, 14, 3123-3135.	1.8	26
76	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 108.	1.6	26
77	Quality Control Analysis in Real-time (QC-ART): A Tool for Real-time Quality Control Assessment of Mass Spectrometry-based Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1824-1836.	2.5	25
78	Time-resolved proteome profiling of normal lung development. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L11-L24.	1.3	25
79	Prediction of the development of islet autoantibodies through integration of environmental, genetic, and metabolic markers. <i>Journal of Diabetes</i> , 2021, 13, 143-153.	0.8	25
80	<i>Salinivirga fredricksonii</i> gen. nov., sp. nov., a heterotrophic halophile isolated from a photosynthetic mat, a member of a novel lineage (<i>Salinarimonadaceae</i> fam. nov.) within the order Rhizobiales, and reclassification of the genus <i>Salinarimonas</i> Liu et al. 2010 into <i>Salinarimonadaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1591-1598.	0.8	25
81	MultiAlign: a multiple LC-MS analysis tool for targeted omics analysis. <i>BMC Bioinformatics</i> , 2013, 14, 49.	1.2	24
82	Deoxyhypusine synthase promotes a pro-inflammatory macrophage phenotype. <i>Cell Metabolism</i> , 2021, 33, 1883-1893.e7.	7.2	24
83	A global lipid map reveals host dependency factors conserved across SARS-CoV-2 variants. <i>Nature Communications</i> , 2022, 13, .	5.8	22
84	The fungus gardens of leaf-cutter ants undergo a distinct physiological transition during biomass degradation. <i>Environmental Microbiology Reports</i> , 2014, 6, 389-395.	1.0	21
85	Specific mutations in H5N1 mainly impact the magnitude and velocity of the host response in mice. <i>BMC Systems Biology</i> , 2013, 7, 69.	3.0	20
86	Characterizing the lipid and metabolite changes associated with placental function and pregnancy complications using ion mobility spectrometry-mass spectrometry and mass spectrometry imaging. <i>Placenta</i> , 2017, 60, S67-S72.	0.7	20
87	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	19
88	Technologies and Approaches to Elucidate and Model the Virulence Program of Salmonella. <i>Frontiers in Microbiology</i> , 2011, 2, 121.	1.5	18
89	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019, 13, 2690-2700.	4.4	18
90	Xanthohumol Microbiome and Signature in Healthy Adults (the XMaS Trial): Safety and Tolerability Results of a Phase I Triple-Masked, Placebo-Controlled Clinical Trial. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001170.	1.5	18

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91	Soil microbial EPS resiliency is influenced by carbon source accessibility. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108037.	4.2	17
92	Unfolded Protein Response Inhibition Reduces Middle East Respiratory Syndrome Coronavirus-Induced Acute Lung Injury. <i>MBio</i> , 2021, 12, e0157221.	1.8	16
93	Measurement of Fructose-Asparagine Concentrations in Human and Animal Foods. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 212-217.	2.4	15
94	Ceramide synthase 2 deletion decreases the infectivity of HIV-1. <i>Journal of Biological Chemistry</i> , 2021, 296, 100340.	1.6	15
95	Metabolite, Protein, and Lipid Extraction (MPLEx): A Method that Simultaneously Inactivates Middle East Respiratory Syndrome Coronavirus and Allows Analysis of Multiple Host Cell Components Following Infection. <i>Methods in Molecular Biology</i> , 2020, 2099, 173-194.	0.4	15
96	Formation of dehydroalanine from mimosine and cysteine: artifacts in gas chromatography/mass spectrometry based metabolomics. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 2561-2564.	0.7	14
97	Effects of delayed NSAID administration after experimental eccentric contraction injury – A cellular and proteomics study. <i>PLoS ONE</i> , 2017, 12, e0172486.	1.1	14
98	DEIMoS: An Open-Source Tool for Processing High-Dimensional Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2022, 94, 6130-6138.	3.2	14
99	Sequential projection pursuit principal component analysis – dealing with missing data associated with new -omics technologies. <i>BioTechniques</i> , 2013, 54, 165-168.	0.8	13
100	Temporal dynamics of CO ₂ and CH ₄ loss potentials in response to rapid hydrological shifts in tidal freshwater wetland soils. <i>Ecological Engineering</i> , 2018, 114, 104-114.	1.6	13
101	Evaluation of <i>In Silico</i> Multifeature Libraries for Providing Evidence for the Presence of Small Molecules in Synthetic Blinded Samples. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4052-4060.	2.5	13
102	AutoCCS: automated collision cross-section calculation software for ion mobility spectrometry–mass spectrometry. <i>Bioinformatics</i> , 2021, 37, 4193-4201.	1.8	13
103	Salmonella-Mediated Inflammation Eliminates Competitors for Fructose-Asparagine in the Gut. <i>Infection and Immunity</i> , 2018, 86, .	1.0	12
104	Extending Classification Algorithms to Case-Control Studies. <i>Biomedical Engineering and Computational Biology</i> , 2019, 10, 117959721985895.	0.8	12
105	A resource of lipidomics and metabolomics data from individuals with undiagnosed diseases. <i>Scientific Data</i> , 2021, 8, 114.	2.4	12
106	GDF15: a potential therapeutic target for type 1 diabetes. <i>Expert Opinion on Therapeutic Targets</i> , 2022, 26, 57-67.	1.5	12
107	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. <i>Journal of Proteome Research</i> , 2019, 18, 694-699.	1.8	11
108	yippee like 3 (ypel3) is a novel gene required for myelinating and perineurial glia development. <i>PLoS Genetics</i> , 2020, 16, e1008841.	1.5	11

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109	PIXiE: an algorithm for automated ion mobility arrival time extraction and collision cross section calculation using global data association. <i>Bioinformatics</i> , 2017, 33, 2715-2722.	1.8	10
110	Xanthohumol microbiome and signature in healthy adults (the XMaS trial): a phase I triple-masked, placebo-controlled clinical trial. <i>Trials</i> , 2020, 21, 835.	0.7	10
111	Integration of Infant Metabolite, Genetic, and Islet Autoimmunity Signatures to Predict Type 1 Diabetes by Age 6 Years. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 2329-2338.	1.8	10
112	Diacyltransferase Activity and Chain Length Specificity of <i>Mycobacterium tuberculosis</i> PapA5 in the Synthesis of Alkyl $\hat{1}^2$ -Diol Lipids. <i>Biochemistry</i> , 2015, 54, 5457-5468.	1.2	9
113	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. <i>Scientific Reports</i> , 2020, 10, 10882.	1.6	9
114	The role of proteomics in assessing beta-cell dysfunction and death in type 1 diabetes. <i>Expert Review of Proteomics</i> , 2019, 16, 569-582.	1.3	8
115	Exploring the Impacts of Conformer Selection Methods on Ion Mobility Collision Cross Section Predictions. <i>Analytical Chemistry</i> , 2021, 93, 3830-3838.	3.2	8
116	Proteomic analysis reveals down-regulation of surfactant protein B in murine type II pneumocytes infected with influenza A virus. <i>Virology</i> , 2015, 483, 96-107.	1.1	7
117	Statistically Driven Metabolite and Lipid Profiling of Patients from the Undiagnosed Diseases Network. <i>Analytical Chemistry</i> , 2020, 92, 1796-1803.	3.2	7
118	Mass Spectrometry Adduct Calculator. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5721-5725.	2.5	7
119	Who Is Metabolizing What? Discovering Novel Biomolecules in the Microbiome and the Organisms Who Make Them. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 388.	1.8	6
120	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. <i>MSystems</i> , 2021, 6, e0105820.	1.7	5
121	Simulated Night- Shift Schedule Disrupts the Plasma Lipidome and Reveals Early Markers of Cardiovascular Disease Risk. <i>Nature and Science of Sleep</i> , 0, Volume 14, 981-994.	1.4	5
122	Bridging the Gap between Analytical and Microbial Sciences in Microbiome Research. <i>MSystems</i> , 2021, 6, e0058521.	1.7	4
123	ROFI - The Use of Repeated Optimization for Feature Interpretation. , 2016, , .		3
124	P-Mart: Interactive Analysis of Ion Abundance Global Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 1426-1432.	1.8	3
125	Chespa: Streamlining Expansive Chemical Space Evaluation of Molecular Sets. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6251-6257.	2.5	2
126	Supernatants of intestinal luminal contents from mice fed high-fat diet impair intestinal motility by injuring enteric neurons and smooth muscle cells. <i>Neurogastroenterology and Motility</i> , 2021, 33, e13990.	1.6	2

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127	Bayesian Posterior Integration for Classification of Mass Spectrometry Data. , 2017, , 203-211.		1
128	Probing islet stress in type 1 diabetes. Aging, 2020, 12, 18795-18796.	1.4	0
129	Probing islet stress in type 1 diabetes. Aging, 2020, 12, 18795-18796.	1.4	0