Thomas O Metz

List of Publications by Year
in descending order

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	GDF15: a potential therapeutic target for type 1 diabetes. Expert Opinion on Therapeutic Targets, 2022, 26, 57-67.	1.5	12
2	DEIMoS: An Open-Source Tool for Processing High-Dimensional Mass Spectrometry Data. Analytical Chemistry, 2022, 94, 6130-6138.	3.2	14
3	Integration of Infant Metabolite, Genetic, and Islet Autoimmunity Signatures to Predict Type 1 Diabetes by Age 6 Years. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2329-2338.	1.8	10
4	A global lipid map reveals host dependency factors conserved across SARS-CoV-2 variants. Nature Communications, 2022, 13, .	5.8	22
5	Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. Nature Biotechnology, 2021, 39, 169-173.	9.4	78
6	Supernatants of intestinal luminal contents from mice fed high–fat diet impair intestinal motility by injuring enteric neurons and smooth muscle cells. Neurogastroenterology and Motility, 2021, 33, e13990.	1.6	2
7	Prediction of the development of islet autoantibodies through integration of environmental, genetic, and metabolic markers. Journal of Diabetes, 2021, 13, 143-153.	0.8	25
8	Exploring the Impacts of Conformer Selection Methods on Ion Mobility Collision Cross Section Predictions. Analytical Chemistry, 2021, 93, 3830-3838.	3.2	8
9	Xanthohumol Microbiome and Signature in Healthy Adults (the XMaS Trial): Safety and Tolerability Results of a Phase I Triple–Masked, Placebo–Controlled Clinical Trial. Molecular Nutrition and Food Research, 2021, 65, e2001170.	1.5	18
10	A resource of lipidomics and metabolomics data from individuals with undiagnosed diseases. Scientific Data, 2021, 8, 114.	2.4	12
11	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. MSystems, 2021, 6, e0105820.	1.7	5
12	Quantum Chemistry Calculations for Metabolomics. Chemical Reviews, 2021, 121, 5633-5670.	23.0	47
13	AutoCCS: automated collision cross-section calculation software for ion mobility spectrometry–mass spectrometry. Bioinformatics, 2021, 37, 4193-4201.	1.8	13
14	Tutorial: best practices and considerations for mass-spectrometry-based protein biomarker discovery and validation. Nature Protocols, 2021, 16, 3737-3760.	5.5	110
15	Unfolded Protein Response Inhibition Reduces Middle East Respiratory Syndrome Coronavirus-Induced Acute Lung Injury. MBio, 2021, 12, e0157221.	1.8	16
16	Bridging the Gap between Analytical and Microbial Sciences in Microbiome Research. MSystems, 2021, 6, e0058521.	1.7	4
17	Deoxyhypusine synthase promotes a pro-inflammatory macrophage phenotype. Cell Metabolism, 2021, 33, 1883-1893.e7.	7.2	24
18	Ceramide synthase 2 deletion decreases the infectivity of HIV-1. Journal of Biological Chemistry, 2021, 296, 100340.	1.6	15

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19	Mass Spectrometry Adduct Calculator. Journal of Chemical Information and Modeling, 2021, 61, 5721-5725.	2.5	7
20	Comprehensive Proteomics Analysis of Stressed Human Islets Identifies GDF15 as a Target for Type 1 Diabetes Intervention. Cell Metabolism, 2020, 31, 363-374.e6.	7.2	78
21	Statistically Driven Metabolite and Lipid Profiling of Patients from the Undiagnosed Diseases Network. Analytical Chemistry, 2020, 92, 1796-1803.	3.2	7
22	Soil microbial EPS resiliency is influenced by carbon source accessibility. Soil Biology and Biochemistry, 2020, 151, 108037.	4.2	17
23	A global lipid map defines a network essential for Zika virus replication. Nature Communications, 2020, 11, 3652.	5.8	50
24	Who Is Metabolizing What? Discovering Novel Biomolecules in the Microbiome and the Organisms Who Make Them. Frontiers in Cellular and Infection Microbiology, 2020, 10, 388.	1.8	6
25	Xanthohumol microbiome and signature in healthy adults (the XMaS trial): a phase I triple-masked, placebo-controlled clinical trial. Trials, 2020, 21, 835.	0.7	10
26	Chespa: Streamlining Expansive Chemical Space Evaluation of Molecular Sets. Journal of Chemical Information and Modeling, 2020, 60, 6251-6257.	2.5	2
27	yippee like 3Â(ypel3) is a novel gene required for myelinating and perineurial glia development. PLoS Genetics, 2020, 16, e1008841.	1.5	11
28	Temporospatial shifts in the human gut microbiome and metabolome after gastric bypass surgery. Npj Biofilms and Microbiomes, 2020, 6, 12.	2.9	57
29	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. Scientific Reports, 2020, 10, 10882.	1.6	9
30	Effects of ingested nanocellulose on intestinal microbiota and homeostasis in Wistar Han rats. NanoImpact, 2020, 18, 100216.	2.4	44
31	Genetic and metabolic links between the murine microbiome and memory. Microbiome, 2020, 8, 53.	4.9	56
32	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. Methods in Molecular Biology, 2020, 2099, 173-194.	0.4	15
33	An integrated multi-omics approach identifies the landscape of interferon-Î±-mediated responses of human pancreatic beta cells. Nature Communications, 2020, 11, 2584.	5.8	87
34	Probing islet stress in type 1 diabetes. Aging, 2020, 12, 18795-18796.	1.4	0
35	Probing islet stress in type 1 diabetes. Aging, 2020, 12, 18795-18796.	1.4	0
36	Extending Classification Algorithms to Case-Control Studies. Biomedical Engineering and Computational Biology, 2019, 10, 117759721985895.	0.8	12

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37	Evaluation of *In Silico* Multifeature Libraries for Providing Evidence for the Presence of Small Molecules in Synthetic Blinded Samples. Journal of Chemical Information and Modeling, 2019, 59, 4052-4060.	2.5	13
38	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. Frontiers in Molecular Biosciences, 2019, 6, 108.	1.6	26
39	The impact of proinflammatory cytokines on the β-cell regulatory landscape provides insights into the genetics of type 1 diabetes. Nature Genetics, 2019, 51, 1588-1595.	9.4	117
40	SLIM Ultrahigh Resolution Ion Mobility Spectrometry Separations of Isotopologues and Isotopomers Reveal Mobility Shifts due to Mass Distribution Changes. Analytical Chemistry, 2019, 91, 11952-11962.	3.2	76
41	P-Mart: Interactive Analysis of Ion Abundance Global Proteomics Data. Journal of Proteome Research, 2019, 18, 1426-1432.	1.8	3
42	New mass spectrometry technologies contributing towards comprehensive and high throughput omics analyses of single cells. Analyst, The, 2019, 144, 794-807.	1.7	67
43	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. ISME Journal, 2019, 13, 2690-2700.	4.4	18
44	The role of proteomics in assessing beta-cell dysfunction and death in type 1 diabetes. Expert Review of Proteomics, 2019, 16, 569-582.	1.3	8
45	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. Cell, 2019, 177, 1600-1618.e17.	13.5	701
46	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. MSystems, 2019, 4, .	1.7	56
47	Ion mobility spectrometry and the omics: Distinguishing isomers, molecular classes and contaminant ions in complex samples. TrAC - Trends in Analytical Chemistry, 2019, 116, 292-299.	5.8	71
48	ISiCLE: A Quantum Chemistry Pipeline for Establishing in Silico Collision Cross Section Libraries. Analytical Chemistry, 2019, 91, 4346-4356.	3.2	74
49	Untargeted metabolomic profiling of *Sphagnum fallax* reveals novel antimicrobial metabolites. Plant Direct, 2019, 3, e00179.	0.8	55
50	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. Journal of Proteome Research, 2019, 18, 694-699.	1.8	11
51	Salmonella-Mediated Inflammation Eliminates Competitors for Fructose-Asparagine in the Gut. Infection and Immunity, 2018, 86, .	1.0	12
52	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. American Journal of Human Genetics, 2018, 102, 494-504.	2.6	59
53	Quality Control Analysis in Real-time (QC-ART): A Tool for Real-time Quality Control Assessment of Mass Spectrometry-based Proteomics Data. Molecular and Cellular Proteomics, 2018, 17, 1824-1836.	2.5	25
54	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1012-E1021.	3.3	142

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55	Temporal dynamics of CO2 and CH4 loss potentials in response to rapid hydrological shifts in tidal freshwater wetland soils. Ecological Engineering, 2018, 114, 104-114.	1.6	13
56	Measurement of Fructoseâ€"Asparagine Concentrations in Human and Animal Foods. Journal of Agricultural and Food Chemistry, 2018, 66, 212-217.	2.4	15
57	Effect of Genetic Diagnosis on Patients with Previously Undiagnosed Disease. New England Journal of Medicine, 2018, 379, 2131-2139.	13.9	261
58	An automated framework for NMR chemical shift calculations of small organic molecules. Journal of Cheminformatics, 2018, 10, 52.	2.8	37
59	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. Journal of Visualized Experiments, 2018, , .	0.2	19
60	Time-resolved proteome profiling of normal lung development. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L11-L24.	1.3	25
61	Salinivirga fredricksonii gen. nov., sp. nov., a heterotrophic halophile isolated from a photosynthetic mat, a member of a novel lineage (Salinarimonadaceae fam. nov.) within the order Rhizobiales, and reclassification of the genus Salinarimonas Liu et al. 2010 into Salinarimonadaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1591-1598.	0.8	25
62	MPLEx: a method for simultaneous pathogen inactivation and extraction of samples for multi-omics profiling. Analyst, The, 2017, 142, 442-448.	1.7	43
63	The Undiagnosed Diseases Network: Accelerating Discovery about Health and Disease. American Journal of Human Genetics, 2017, 100, 185-192.	2.6	142
64	Elucidation of roles for vitamin B$_{12}$ in regulation of folate, ubiquinone, and methionine metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1205-E1214.	3.3	75
65	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in *Yarrowia lipolytica*. MBio, 2017, 8, .	1.8	38
66	PIXiE: an algorithm for automated ion mobility arrival time extraction and collision cross section calculation using global data association. Bioinformatics, 2017, 33, 2715-2722.	1.8	10
67	LIQUID: an-open source software for identifying lipids in LC-MS/MS-based lipidomics data. Bioinformatics, 2017, 33, 1744-1746.	1.8	108
68	Characterizing the lipid and metabolite changes associated with placental function and pregnancy complications using ion mobility spectrometry-mass spectrometry and mass spectrometry imaging. Placenta, 2017, 60, S67-S72.	0.7	20
69	Integrating ion mobility spectrometry into mass spectrometry-based exposome measurements: what can it add and how far can it go?. Bioanalysis, 2017, 9, 81-98.	0.6	66
70	Bayesian Posterior Integration for Classification of Mass Spectrometry Data. , 2017, , 203-211.		1
71	Multi-platform â€™Omics Analysis of Human Ebola Virus Disease Pathogenesis. Cell Host and Microbe, 2017, 22, 817-829.e8.	5.1	88
72	Sexual dimorphism in the fetal cardiac response to maternal nutrient restriction. Journal of Molecular and Cellular Cardiology, 2017, 108, 181-193.	0.9	41

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73	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. Nature Microbiology, 2017, 2, 16221.	5.9	138
74	Effects of delayed NSAID administration after experimental eccentric contraction injury â€" A cellular and proteomics study. PLoS ONE, 2017, 12, e0172486.	1.1	14
75	Lipidomics reveals dramatic lipid compositional changes in the maturing postnatal lung. Scientific Reports, 2017, 7, 40555.	1.6	67
76	MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. MSystems, 2016, 1, .	1.7	166
77	ROFI - The Use of Repeated Optimization for Feature Interpretation. , 2016, , .		3
78	SPE-IMS-MS: An automated platform for sub-sixty second surveillance of endogenous metabolites and xenobiotics in biofluids. Clinical Mass Spectrometry, 2016, 2, 1-10.	1.9	63
79	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	9.4	2,802
80	Multi-omics analysis reveals regulators of the response to nitrogen limitation in Yarrowia lipolytica. BMC Genomics, 2016, 17, 138.	1.2	62
81	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. Cell Host and Microbe, 2016, 19, 254-266.	5.1	75
82	Uncovering biologically significant lipid isomers with liquid chromatography, ion mobility spectrometry and mass spectrometry. Analyst, The, 2016, 141, 1649-1659.	1.7	196
83	Proteomic analysis reveals down-regulation of surfactant protein B in murine type II pneumocytes infected with influenza A virus. Virology, 2015, 483, 96-107.	1.1	7
84	Silymarin Suppresses Cellular Inflammation By Inducing Reparative Stress Signaling. Journal of Natural Products, 2015, 78, 1990-2000.	1.5	53
85	Diel metabolomics analysis of a hot spring chlorophototrophic microbial mat leads to new hypotheses of community member metabolisms. Frontiers in Microbiology, 2015, 6, 209.	1.5	104
86	Review, Evaluation, and Discussion of the Challenges of Missing Value Imputation for Mass Spectrometry-Based Label-Free Global Proteomics. Journal of Proteome Research, 2015, 14, 1993-2001.	1.8	217
87	Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. Journal of Proteome Research, 2015, 14, 3123-3135.	1.8	26
88	Diacyltransferase Activity and Chain Length Specificity ofMycobacterium tuberculosisPapA5 in the Synthesis of Alkyl Î²-Diol Lipids. Biochemistry, 2015, 54, 5457-5468.	1.2	9
89	Comprehensive Metabolomic, Lipidomic and Microscopic Profiling of Yarrowia lipolytica during Lipid Accumulation Identifies Targets for Increased Lipogenesis. PLoS ONE, 2015, 10, e0123188.	1.1	54
90	Phototrophic biofilm assembly in microbial-mat-derived unicyanobacterial consortia: model systems for the study of autotroph-heterotroph interactions. Frontiers in Microbiology, 2014, 5, 109.	1.5	97

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91	Pathogenic Influenza Viruses and Coronaviruses Utilize Similar and Contrasting Approaches To Control Interferon-Stimulated Gene Responses. MBio, 2014, 5, e01174-14.	1.8	246
92	A comprehensive collection of systems biology data characterizing the host response to viral infection. Scientific Data, 2014, 1, 140033.	2.4	62
93	The fungus gardens of leaf€cutter ants undergo a distinct physiological transition during biomass degradation. Environmental Microbiology Reports, 2014, 6, 389-395.	1.0	21
94	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. Molecular and Cellular Proteomics, 2014, 13, 3639-3646.	2.5	38
95	A statistical analysis of the effects of urease pre-treatment on the measurement of the urinary metabolome by gas chromatography€"mass spectrometry. Metabolomics, 2014, 10, 897-908.	1.4	28
96	Decreased abundance of type III secretion system-inducing signals in *Arabidopsis mkp1* enhances resistance against *Pseudomonas syringae*. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6846-6851.	3.3	97
97	The succinated proteome. Mass Spectrometry Reviews, 2014, 33, 98-109.	2.8	66
98	MultiAlign: a multiple LC-MS analysis tool for targeted omics analysis. BMC Bioinformatics, 2013, 14, 49.	1.2	24
99	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. Bioinformatics, 2013, 29, 2900-2908.	1.8	122
100	Specific mutations in H5N1 mainly impact the magnitude and velocity of the host response in mice. BMC Systems Biology, 2013, 7, 69.	3.0	20
101	A comparative analysis of computational approaches to relative protein quantification using peptide peak intensities in label€free LC€MS proteomics experiments. Proteomics, 2013, 13, 493-503.	1.3	74
102	A multi-omic systems approach to elucidating Yersinia virulence mechanisms. Molecular BioSystems, 2013, 9, 44-54.	2.9	29
103	Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes. Molecular BioSystems, 2013, 9, 1522.	2.9	49
104	Sequential projection pursuit principal component analysis €" dealing with missing data associated with new -omics technologies. BioTechniques, 2013, 54, 165-168.	0.8	13
105	Mechanisms of Severe Acute Respiratory Syndrome Coronavirus-Induced Acute Lung Injury. MBio, 2013, 4, .	1.8	251
106	Serum proteomics reveals systemic dysregulation of innate immunity in type 1 diabetes. Journal of Experimental Medicine, 2013, 210, 191-203.	4.2	91
107	Release of Severe Acute Respiratory Syndrome Coronavirus Nuclear Import Block Enhances Host Transcription in Human Lung Cells. Journal of Virology, 2013, 87, 3885-3902.	1.5	140
108	A Multi-Omic View of Host-Pathogen-Commensal Interplay in Salmonella-Mediated Intestinal Infection. PLoS ONE, 2013, 8, e67155.	1.1	81

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109	A Network Integration Approach to Predict Conserved Regulators Related to Pathogenicity of Influenza and SARS-CoV Respiratory Viruses. PLoS ONE, 2013, 8, e69374.	1.1	68
110	Dengue Virus Infection Perturbs Lipid Homeostasis in Infected Mosquito Cells. PLoS Pathogens, 2012, 8, e1002584.	2.1	290
111	*In silico* identification software (ISIS): a machine learning approach to tandem mass spectral identification of lipids. Bioinformatics, 2012, 28, 1705-1713.	1.8	58
112	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. Molecular Systems Biology, 2012, 8, 558.	3.2	142
113	A reversed-phase capillary ultra-performance liquid chromatography–mass spectrometry (UPLC-MS) method for comprehensive top-down/bottom-up lipid profiling. Analytical and Bioanalytical Chemistry, 2012, 402, 2923-2933.	1.9	86
114	Technologies and Approaches to Elucidate and Model the Virulence Program of Salmonella. Frontiers in Microbiology, 2011, 2, 121.	1.5	18
115	Separation and Classification of Lipids Using Differential Ion Mobility Spectrometry. Journal of the American Society for Mass Spectrometry, 2011, 22, 1146-55.	1.2	96
116	Formation of dehydroalanine from mimosine and cysteine: artifacts in gas chromatography/mass spectrometry based metabolomics. Rapid Communications in Mass Spectrometry, 2011, 25, 2561-2564.	0.7	14
117	Systems Virology Identifies a Mitochondrial Fatty Acid Oxidation Enzyme, Dodecenoyl Coenzyme A Delta Isomerase, Required for Hepatitis C Virus Replication and Likely Pathogenesis. Journal of Virology, 2011, 85, 11646-11654.	1.5	48
118	Improved quality control processing of peptide-centric LC-MS proteomics data. Bioinformatics, 2011, 27, 2866-2872.	1.8	88
119	Perturbations in the lipid profile of individuals with newly diagnosed type 1 diabetes mellitus: Lipidomics analysis of a Diabetes Antibody Standardization Program sample subset. Clinical Biochemistry, 2010, 43, 948-956.	0.8	38
120	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. PLoS Pathogens, 2010, 6, e1000719.	2.1	361
121	Combined Statistical Analyses of Peptide Intensities and Peptide Occurrences Improves Identification of Significant Peptides from MS-Based Proteomics Data. Journal of Proteome Research, 2010, 9, 5748-5756.	1.8	93
122	A statistical framework for protein quantitation in bottom-up MS-based proteomics. Bioinformatics, 2009, 25, 2028-2034.	1.8	149
123	High-resolution separations and improved ion production and transmission in metabolomics. TrAC - Trends in Analytical Chemistry, 2008, 27, 205-214.	5.8	41
124	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. Molecular and Cellular Proteomics, 2007, 6, 717-727.	2.5	26
125	Enrichment and Analysis of Nonenzymatically Glycated Peptides:Â Boronate Affinity Chromatography Coupled with Electron-Transfer Dissociation Mass Spectrometry. Journal of Proteome Research, 2007, 6, 2323-2330.	1.8	147
126	Future of liquid chromatography–mass spectrometry in metabolic profiling and metabolomic studies for biomarker discovery. Biomarkers in Medicine, 2007, 1, 159-185.	0.6	78

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127	Characterization of the Human Pancreatic Islet Proteome by Two-Dimensional LC/MS/MS. Journal of Proteome Research, 2006, 5, 3345-3354.	1.8	58
128	Proteomic Analysis of the Site Specificity of Glycation and Carboxymethylation of Ribonuclease. Journal of Proteome Research, 2003, 2, 506-513.	1.8	78
129	Simulated Night- Shift Schedule Disrupts the Plasma Lipidome and Reveals Early Markers of Cardiovascular Disease Risk. Nature and Science of Sleep, 0, Volume 14, 981-994.	1.4	5