Michael Witting

List of Publications by Year
in descending order

93	3,283	159585 30	182427 51
papers	citations	h-index	g-index

98	98	98	5494
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	High-confidence structural annotation of metabolites absent from spectral libraries. Nature Biotechnology, 2022, 40, 411-421.	17.5	100
2	Current state-of-the-art of separation methods used in LC-MS based metabolomics and lipidomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2022, 1188, 123069.	2.3	44
3	Impaired phosphocreatine metabolism in white adipocytes promotes inflammation. Nature Metabolism, 2022, 4, 190-202.	11.9	21
4	A Modular and Expandable Ecosystem for Metabolomics Data Annotation in R. Metabolites, 2022, 12, 173.	2.9	43
5	DIAMetAlyzer allows automated false-discovery rate-controlled analysis for data-independent acquisition in metabolomics. Nature Communications, 2022, 13, 1347.	12.8	11
6	Genome-Wide Association Study of Alzheimerâ€™s Disease Brain Imaging Biomarkers and Neuropsychological Phenotypes in the European Medical Information Framework for Alzheimerâ€™s Disease Multimodal Biomarker Discovery Dataset. Frontiers in Aging Neuroscience, 2022, 14, 840651.	3.4	20
7	Networks and Graphs Discovery in Metabolomics Data Analysis and Interpretation. Frontiers in Molecular Biosciences, 2022, 9, 841373.	3.5	35
8	UBTF::ATXN7L3 gene fusion defines novel B cell precursor ALL subtype with CDX2 expression and need for intensified treatment. Leukemia, 2022, 36, 1676-1680.	7.2	12
9	N-Alkylpyridinium sulfonates for retention time indexing in reversed-phase-liquid chromatography-mass spectrometryâ€“based metabolomics. Analytical and Bioanalytical Chemistry, 2022, 414, 7387-7398.	3.7	9
10	Genetic Associations and Differential mRNA Expression Levels of Host Genes Suggest a Viral Trigger for Endemic Pemphigus Foliaceus. Viruses, 2022, 14, 879.	3.3	4
11	High-throughput method for the hybridisation-based targeted enrichment of long genomic fragments for PacBio third-generation sequencing. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	7
12	MobilityTransformR: an R package for effective mobility transformation of CE-MS data. Bioinformatics, 2022, 38, 4044-4045.	4.1	4
13	Genetic variability of immuneâ€related lncRNAs: polymorphisms in LINCâ€PINT and LY86â€AS1 are associated with pemphigus foliaceus susceptibility. Experimental Dermatology, 2021, 30, 831-840.	2.9	11
14	Reduced peroxisomal import triggers peroxisomal retrograde signaling. Cell Reports, 2021, 34, 108653.	6.4	9
15	Comparison of lipidome profiles of Caenorhabditis elegansâ€”results from an inter-laboratory ring trial. Metabolomics, 2021, 17, 25.	3.0	3
16	UHPLC-IM-Q-ToFMS analysis of maradolipids, found exclusively in Caenorhabditis elegans dauer larvae. Analytical and Bioanalytical Chemistry, 2021, 413, 2091-2102.	3.7	6
17	IL-17 controls central nervous system autoimmunity through the intestinal microbiome. Science Immunology, 2021, 6, .	11.9	67
18	HLHâ€30â€dependent rewiring of metabolism during starvation in C. elegans. Aging Cell, 2021, 20, e13342.	6.7	6

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19	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. Gut, 2021, 70, 1538-1549.	12.1	21
20	Quo Vadis Caenorhabditis elegans Metabolomicsâ€"A Review of Current Methods and Applications to Explore Metabolism in the Nematode. Metabolites, 2021, 11, 284.	2.9	20
21	Identification of two novel bullous pemphigoid- associated alleles, HLA-DQA1*05:05 and -DRB1*07:01, in Germans. Orphanet Journal of Rare Diseases, 2021, 16, 228.	2.7	16
22	TMEM106B and CPOX are genetic determinants of cerebrospinal fluid Alzheimer's disease biomarker levels. Alzheimer's and Dementia, 2021, 17, 1628-1640.	0.8	23
23	Identifying genetic modifiers of age-associated penetrance in X-linked dystonia-parkinsonism. Nature Communications, 2021, 12, 3216.	12.8	34
24	Genetic association and differential expression of HLA Complex Group lncRNAs in pemphigus. Journal of Autoimmunity, 2021, 123, 102705.	6.5	8
25	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. Nature Genetics, 2021, 53, 147-155.	21.4	101
26	Validity and Prognostic Value of a Polygenic Risk Score for Parkinsonâ€™s Disease. Genes, 2021, 12, 1859.	2.4	15
27	Novel Extraction Method for Combined Lipid and Metal Speciation From Caenorhabditis elegans With Focus on Iron Redox Status and Lipid Profiling. Frontiers in Chemistry, 2021, 9, 788094.	3.6	4
28	Wholeâ€exome and HLA sequencing in Febrile infectionâ€related epilepsy syndrome. Annals of Clinical and Translational Neurology, 2020, 7, 1429-1435.	3.7	15
29	Metabolomic adjustments in the orchid mycorrhizal fungus Tulasnella calospora during symbiosis with Serapias vomeracea. New Phytologist, 2020, 228, 1939-1952.	7.3	21
30	Genome-wide association study of Alzheimerâ€™s disease CSF biomarkers in the EMIF-AD Multimodal Biomarker Discovery dataset. Translational Psychiatry, 2020, 10, 403.	4.8	42
31	Comprehensive Vitamer Profiling of Folate Mono- and Polyglutamates in Bakerâ€™s Yeast (Saccharomyces) Tj ETQq1 1 0.784314 rgBT	2.9	9
32	Feature-based molecular networking in the GNPS analysis environment. Nature Methods, 2020, 17, 905-908.	19.0	650
33	Current status of retention time prediction in metabolite identification. Journal of Separation Science, 2020, 43, 1746-1754.	2.5	71
34	Autophagy compensates for defects in mitochondrial dynamics. PLoS Genetics, 2020, 16, e1008638.	3.5	22
35	iTAG-RNA Isolates Cell-Specific Transcriptional Responses to Environmental Stimuli and Identifies an RNA-Based Endocrine Axis. Cell Reports, 2020, 30, 3183-3194.e4.	6.4	6
36	In Silico Guided Discovery of Novel Class I and II Trypanosoma cruzi Epitopes Recognized by T Cells from Chagasâ€™ Disease Patients. Journal of Immunology, 2020, 204, 1571-1581.	0.8	10

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37	Suggestions for Standardized Identifiers for Fatty Acyl Compounds in Genome Scale Metabolic Models and Their Application to the WormJam Caenorhabditis elegans Model. Metabolites, 2020, 10, 130.	2.9	3
38	Using Genome-Scale Metabolic Networks for Analysis, Visualization, and Integration of Targeted Metabolomics Data. Methods in Molecular Biology, 2020, 2104, 361-386.	0.9	2
39	Autophagy compensates for defects in mitochondrial dynamics. , 2020, 16, e1008638.		0
40	Autophagy compensates for defects in mitochondrial dynamics. , 2020, 16, e1008638.		0
41	Autophagy compensates for defects in mitochondrial dynamics. , 2020, 16, e1008638.		0
42	Autophagy compensates for defects in mitochondrial dynamics. , 2020, 16, e1008638.		0
43	The metaRbolomics Toolbox in Bioconductor and beyond. Metabolites, 2019, 9, 200.	2.9	64
44	The sphingolipidome of the model organism Caenorhabditis elegans. Chemistry and Physics of Lipids, 2019, 222, 15-22.	3.2	17
45	Development and application of a HILIC UHPLC-MS method for polar fecal metabolome profiling. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2019, 1109, 142-148.	2.3	26
46	Complement Receptor 1 (CR1, CD35) Polymorphisms and Soluble CR1: A Proposed Anti-inflammatory Role to Quench the Fire of â€œFogo Selvagemâ€•Pemphigus Foliaceus. Frontiers in Immunology, 2019, 10, 2585.	4.8	12
47	Construction and benchmarking of a multi-ethnic reference panel for the imputation of HLA class I and II alleles. Human Molecular Genetics, 2019, 28, 2078-2092.	2.9	48
48	Metformin impacts cecal bile acid profiles in mice. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1083, 35-43.	2.3	8
49	Bio- and Chemoinformatics Approaches for Metabolomics Data Analysis. Methods in Molecular Biology, 2018, 1738, 41-61.	0.9	3
50	Mycorrhiza-Triggered Transcriptomic and Metabolomic Networks Impinge on Herbivore Fitness. Plant Physiology, 2018, 176, 2639-2656.	4.8	75
51	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. Nature Communications, 2018, 9, 1569.	12.8	67
52	Tandem HILICâ€RP liquid chromatography for increased polarity coverage in food analysis. Electrophoresis, 2018, 39, 1645-1653.	2.4	12
53	Modeling Meets Metabolomicsâ€"The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism Caenorhabditis elegans. Frontiers in Molecular Biosciences, 2018, 5, 96.	3.5	40
54	Pharmacometabolic response to pirfenidone in pulmonary fibrosis detected by MALDI-FTICR-MSI. European Respiratory Journal, 2018, 52, 1702314.	6.7	26

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55	Metabotype variation in a field population of tansy plants influences aphid host selection. Plant, Cell and Environment, 2018, 41, 2791-2805.	5.7	30
56	Usage of FT-ICR-MS Metabolomics for Characterizing the Chemical Signatures of Barrel-Aged Whisky. Frontiers in Chemistry, 2018, 6, 29.	3.6	42
57	High-Resolution HLA-Typing by Next-Generation Sequencing of Randomly Fragmented Target DNA. Methods in Molecular Biology, 2018, 1802, 63-88.	0.9	4
58	Pharmacometabolic effect of pirfenidone treatment in IPF detected by high resolution MALDI-FTICR imaging. , 2018, , .		0
59	Amniotic Fluid and Maternal Serum Metabolic Signatures in the Second Trimester Associated with Preterm Delivery. Journal of Proteome Research, 2017, 16, 898-910.	3.7	48
60	Identification of a High-Affinity Pyruvate Receptor in Escherichia coli. Scientific Reports, 2017, 7, 1388.	3.3	36
61	Metabolic profile of human coelomic fluid. Bioanalysis, 2017, 9, 37-51.	1.5	7
62	New Investigator Award: announcing our finalists!. Bioanalysis, 2017, 9, 969-973.	1.5	0
63	Identification of molecules from non-targeted analysis. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1071, 1-2.	2.3	2
64	QSRR Modeling for Metabolite Standards Analyzed by Two Different Chromatographic Columns Using Multiple Linear Regression. Metabolites, 2017, 7, 7.	2.9	19
65	Comparative analysis of LytS/LytTR-type histidine kinase/response regulator systems in Î³-proteobacteria. PLoS ONE, 2017, 12, e0182993.	2.5	18
66	LipidFrag: Improving reliability of in silico fragmentation of lipids and application to the Caenorhabditis elegans lipidome. PLoS ONE, 2017, 12, e0172311.	2.5	21
67	A post-GWAS analysis of predicted regulatory variants and tuberculosis susceptibility. PLoS ONE, 2017, 12, e0174738.	2.5	19
68	The Role of Dafachronic Acid Signaling in Development and Longevity in Caenorhabditis elegans: Digging Deeper Using Cutting-Edge Analytical Chemistry. Frontiers in Endocrinology, 2016, 7, 12.	3.5	30
69	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. BMC Medical Genetics, 2016, 17, 26.	2.1	14
70	Natural oxygenation of Champagne wine during ageing on lees: A metabolomics picture of hormesis. Food Chemistry, 2016, 203, 207-215.	8.2	35
71	The Caenorhabditis elegans lipidome. Archives of Biochemistry and Biophysics, 2016, 589, 27-37.	3.0	41
72	Evidence for the recent origin of a bacterial protein-coding, overlapping orphan gene by evolutionary overprinting. BMC Evolutionary Biology, 2015, 15, 283.	3.2	43

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73	Acute physical exercise improves shifting in adolescents at school: evidence for a dopaminergic contribution. Frontiers in Behavioral Neuroscience, 2015, 9, 196.	2.0	26
74	Development of a high-resolution NGS-based HLA-typing and analysis pipeline. Nucleic Acids Research, 2015, 43, e70-e70.	14.5	77
75	Integrating analytical resolutions in non-targeted wine metabolomics. Tetrahedron, 2015, 71, 2983-2990.	1.9	45
76	Combined Nontargeted Analytical Methodologies for the Characterization of the Chemical Evolution of Bottled Wines. ACS Symposium Series, 2015, , 13-27.	0.5	0
77	Fast separation and quantification of steroid hormones Î”4- and Î”7-dafachronic acid in Caenorhabditis elegans. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2015, 978-979, 118-121.	2.3	4
78	DI-ICR-FT-MS-based high-throughput deep metabotyping: a case study of the Caenorhabditis elegansâ€“Pseudomonas aeruginosa infection model. Analytical and Bioanalytical Chemistry, 2015, 407, 1059-1073.	3.7	26
79	Computational analysis and ratiometric comparison approaches aimed to assist column selection in hydrophilic interaction liquid chromatographyâ€“tandem mass spectrometry targeted metabolomics. Journal of Chromatography A, 2015, 1406, 145-155.	3.7	22
80	Chemical messages in 170-year-old champagne bottles from the Baltic Sea: Revealing tastes from the past. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5893-5898.	7.1	47
81	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080.	2.9	61
82	Transcriptome and Metabolome Data Integrationâ€”Technical Perquisites for Successful Data Fusion and Visualization. Comprehensive Analytical Chemistry, 2014, 63, 421-442.	1.3	6
83	Highâ€resolution metabolite imaging of light and dark treated retina using <scp>MALDI</scp>â€<scp>FTICR</scp> mass spectrometry. Proteomics, 2014, 14, 913-923.	2.2	40
84	Phenotype ofhtgA(mbiA), a recently evolved orphan gene ofEscherichia coliandShigella, completely overlapping in antisense toyaaW. FEMS Microbiology Letters, 2014, 350, 57-64.	1.8	44
85	Optimizing a ultrahigh pressure liquid chromatography-time of flight-mass spectrometry approach using a novel sub-2Î¼m coreâ€“shell particle for in depth lipidomic profiling of Caenorhabditis elegans. Journal of Chromatography A, 2014, 1359, 91-99.	3.7	51
86	Steroid hormone signalling links reproduction to lifespan in dietary-restricted Caenorhabditis elegans. Nature Communications, 2014, 5, 4879.	12.8	65
87	Ultrahigh resolution mass spectrometry-based metabolic characterization reveals cerebellum as a disturbed region in two animal models. Talanta, 2014, 118, 45-53.	5.5	31
88	Distinct signatures of hostâ€“microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. ISME Journal, 2014, 8, 2380-2396.	9.8	106
89	Molecular and structural characterization of dissolved organic matter during and post cyanobacterial bloom in Taihu by combination of NMR spectroscopy and FTICR mass spectrometry. Water Research, 2014, 57, 280-294.	11.3	87
90	High precision mass measurements for wine metabolomics. Frontiers in Chemistry, 2014, 2, 102.	3.6	71

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91	Ultrahigh Resolution Mass Spectrometry Based Non-targeted Microbial Metabolomics. , 2012, , 57-71.		0
92	MassTRIX Reloaded: Combined Analysis and Visualization of Transcriptome and Metabolome Data. PLoS ONE, 2012, 7, e39860.	2.5	82
93	ITag-RNA Allows in Vivo Cell-Type Specific Transcriptional Characterization and Tracking of Circulating Transcripts. SSRN Electronic Journal, 0, , .	0.4	0