

# Mingxun Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1267593/publications.pdf>

Version: 2024-02-01

49  
papers

20,652  
citations

159358

30  
h-index

197535

49  
g-index

79  
all docs

79  
docs citations

79  
times ranked

24623  
citing authors

#	ARTICLE	IF	CITATIONS
1	GNPS Dashboard: collaborative exploration of mass spectrometry data in the web browser. <i>Nature Methods</i> , 2022, 19, 134-136.	9.0	35
2	Tandem Mass Spectrometry Molecular Networking as a Powerful and Efficient Tool for Drug Metabolism Studies. <i>Analytical Chemistry</i> , 2022, 94, 1456-1464.	3.2	17
3	foodMASST a mass spectrometry search tool for foods and beverages. <i>Npj Science of Food</i> , 2022, 6, 22.	2.5	9
4	SIMILE enables alignment of tandem mass spectra with statistical significance. <i>Nature Communications</i> , 2022, 13, 2510.	5.8	16
5	TIMSCONVERT: a workflow to convert trapped ion mobility data to open data formats. <i>Bioinformatics</i> , 2022, 38, 4046-4047.	1.8	1
6	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	9.4	25
7	Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	9.4	78
8	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	3.9	73
9	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
10	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	3.9	81
11	Non-targeted tandem mass spectrometry enables the visualization of organic matter chemotype shifts in coastal seawater. <i>Chemosphere</i> , 2021, 271, 129450.	4.2	33
12	Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. <i>Nature Communications</i> , 2021, 12, 3832.	5.8	119
13	Quick-start infrastructure for untargeted metabolomics analysis in GNPS. <i>Nature Metabolism</i> , 2021, 3, 880-882.	5.1	11
14	Chemical Gradients of Plant Substrates in an <i>Atta texana</i> Fungus Garden. <i>MSystems</i> , 2021, 6, e0060121.	1.7	2
15	Chemical Proportionality within Molecular Networks. <i>Analytical Chemistry</i> , 2021, 93, 12833-12839.	3.2	22
16	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	5.8	45
17	NPClassifier: A Deep Neural Network-Based Structural Classification Tool for Natural Products. <i>Journal of Natural Products</i> , 2021, 84, 2795-2807.	1.5	131
18	Mass spectrometry searches using MASST. <i>Nature Biotechnology</i> , 2020, 38, 23-26.	9.4	160

#	ARTICLE	IF	CITATIONS
19	Fungal-bacterial interaction selects for quorum sensing mutants with increased production of natural antifungal compounds. <i>Communications Biology</i> , 2020, 3, 670.	2.0	12
20	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	9.0	650
21	ReDU: a framework to find and reanalyze public mass spectrometry data. <i>Nature Methods</i> , 2020, 17, 901-904.	9.0	79
22	Reproducible molecular networking of untargeted mass spectrometry data using GNPS. <i>Nature Protocols</i> , 2020, 15, 1954-1991.	5.5	344
23	Global chemical effects of the microbiome include new bile-acid conjugations. <i>Nature</i> , 2020, 579, 123-129.	13.7	316
24	A Convolutional Neural Network-Based Approach for the Rapid Annotation of Molecularly Diverse Natural Products. <i>Journal of the American Chemical Society</i> , 2020, 142, 4114-4120.	6.6	114
25	Protocol for community-created public MS/MS reference spectra within the Global Natural Products Social Molecular Networking infrastructure. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8725.	0.7	14
26	MolNetEnhancer: Enhanced Molecular Networks by Integrating Metabolome Mining and Annotation Tools. <i>Metabolites</i> , 2019, 9, 144.	1.3	245
27	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
28	Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	9.0	184
29	The Natural Products Atlas: An Open Access Knowledge Base for Microbial Natural Products Discovery. <i>ACS Central Science</i> , 2019, 5, 1824-1833.	5.3	258
30	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019, 4, .	1.7	23
31	Initial Development toward Non-Invasive Drug Monitoring via Untargeted Mass Spectrometric Analysis of Human Skin. <i>Analytical Chemistry</i> , 2019, 91, 8062-8069.	3.2	17
32	Whole Cell MALDI Fingerprinting Is a Robust Tool for Differential Profiling of Two-Component Mammalian Cell Mixtures. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 344-354.	1.2	11
33	Bioactivity-Based Molecular Networking for the Discovery of Drug Leads in Natural Product Bioassay-Guided Fractionation. <i>Journal of Natural Products</i> , 2018, 81, 758-767.	1.5	237
34	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
35	Assembling the Community-Scale Discoverable Human Proteome. <i>Cell Systems</i> , 2018, 7, 412-421.e5.	2.9	136
36	Propagating annotations of molecular networks using in silico fragmentation. <i>PLoS Computational Biology</i> , 2018, 14, e1006089.	1.5	242

#	ARTICLE	IF	CITATIONS
37	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
38	Three-Dimensional Microbiome and Metabolome Cartography of a Diseased Human Lung. <i>Cell Host and Microbe</i> , 2017, 22, 705-716.e4.	5.1	111
39	Significance estimation for large scale metabolomics annotations by spectral matching. <i>Nature Communications</i> , 2017, 8, 1494.	5.8	128
40	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	860
41	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. <i>ELife</i> , 2017, 6, .	2.8	33
42	SweetNET: A Bioinformatics Workflow for Glycopeptide MS/MS Spectral Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 2826-2840.	1.8	49
43	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
44	Lifestyle chemistries from phones for individual profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7645-E7654.	3.3	55
45	SPLASH, a hashed identifier for mass spectra. <i>Nature Biotechnology</i> , 2016, 34, 1099-1101.	9.4	61
46	Molecular Networking and Pattern-Based Genome Mining Improves Discovery of Biosynthetic Gene Clusters and their Products from <i>Salinispora</i> Species. <i>Chemistry and Biology</i> , 2015, 22, 460-471.	6.2	150
47	Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.	1.6	133
48	Spectral Library Generating Function for Assessing Spectrum-Spectrum Match Significance. <i>Journal of Proteome Research</i> , 2013, 12, 3944-3951.	1.8	23
49	Three Dimensional Cartography of Microbiome and Metabolome Data onto Radiological Images of the Human Lung. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0