Mingxun Wang

List of Publications by Year
in descending order

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	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
2	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
3	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. Nucleic Acids Research, 2017, 45, D1100-D1106.	6.5	860
4	Feature-based molecular networking in the GNPS analysis environment. Nature Methods, 2020, 17, 905-908.	9.0	650
5	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	9.0	459
6	Reproducible molecular networking of untargeted mass spectrometry data using GNPS. Nature Protocols, 2020, 15, 1954-1991.	5.5	344
7	Global chemical effects of the microbiome include new bile-acid conjugations. Nature, 2020, 579, 123-129.	13.7	316
8	The Natural Products Atlas: An Open Access Knowledge Base for Microbial Natural Products Discovery. ACS Central Science, 2019, 5, 1824-1833.	5.3	258
9	MolNetEnhancer: Enhanced Molecular Networks by Integrating Metabolome Mining and Annotation Tools. Metabolites, 2019, 9, 144.	1.3	245
10	Propagating annotations of molecular networks using in silico fragmentation. PLoS Computational Biology, 2018, 14, e1006089.	1.5	242
11	Bioactivity-Based Molecular Networking for the Discovery of Drug Leads in Natural Product Bioassay-Guided Fractionation. Journal of Natural Products, 2018, 81, 758-767.	1.5	237
12	Learning representations of microbeâ€“metabolite interactions. Nature Methods, 2019, 16, 1306-1314.	9.0	184
13	Mass spectrometry searches using MASST. Nature Biotechnology, 2020, 38, 23-26.	9.4	160
14	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
15	Molecular Networking and Pattern-Based Genome Mining Improves Discovery of Biosynthetic Gene Clusters and their Products from Salinispora Species. Chemistry and Biology, 2015, 22, 460-471.	6.2	150
16	Assembling the Community-Scale Discoverable Human Proteome. Cell Systems, 2018, 7, 412-421.e5.	2.9	136
17	Automated Genome Mining of Ribosomal Peptide Natural Products. ACS Chemical Biology, 2014, 9, 1545-1551.	1.6	133
18	NPClassifier: A Deep Neural Network-Based Structural Classification Tool for Natural Products. Journal of Natural Products, 2021, 84, 2795-2807.	1.5	131

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19	Significance estimation for large scale metabolomics annotations by spectral matching. Nature Communications, 2017, 8, 1494.	5.8	128
20	Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. Nature Communications, 2021, 12, 3832.	5.8	119
21	A Convolutional Neural Network-Based Approach for the Rapid Annotation of Molecularly Diverse Natural Products. Journal of the American Chemical Society, 2020, 142, 4114-4120.	6.6	114
22	Three-Dimensional Microbiome and Metabolome Cartography of a Diseased Human Lung. Cell Host and Microbe, 2017, 22, 705-716.e4.	5.1	111
23	A community resource for paired genomic and metabolomic data mining. Nature Chemical Biology, 2021, 17, 363-368.	3.9	81
24	ReDU: a framework to find and reanalyze public mass spectrometry data. Nature Methods, 2020, 17, 901-904.	9.0	79
25	Auto-deconvolution and molecular networking of gas chromatographyâ€“mass spectrometry data. Nature Biotechnology, 2021, 39, 169-173.	9.4	78
26	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. Nature Chemical Biology, 2021, 17, 146-151.	3.9	73
27	SPLASH, a hashed identifier for mass spectra. Nature Biotechnology, 2016, 34, 1099-1101.	9.4	61
28	Lifestyle chemistries from phones for individual profiling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7645-E7654.	3.3	55
29	SweetNET: A Bioinformatics Workflow for Glycopeptide MS/MS Spectral Analysis. Journal of Proteome Research, 2016, 15, 2826-2840.	1.8	49
30	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	5.8	45
31	GNPS Dashboard: collaborative exploration of mass spectrometry data in the web browser. Nature Methods, 2022, 19, 134-136.	9.0	35
32	Non-targeted tandem mass spectrometry enables the visualization of organic matter chemotype shifts in coastal seawater. Chemosphere, 2021, 271, 129450.	4.2	33
33	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. ELife, 2017, 6, .	2.8	33
34	Enhancing untargeted metabolomics using metadata-based source annotation. Nature Biotechnology, 2022, 40, 1774-1779.	9.4	25
35	Spectral Library Generating Function for Assessing Spectrum-Spectrum Match Significance. Journal of Proteome Research, 2013, 12, 3944-3951.	1.8	23
36	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. MSystems, 2019, 4, .	1.7	23

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37	Chemical Proportionality within Molecular Networks. Analytical Chemistry, 2021, 93, 12833-12839.	3.2	22
38	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. Marine Drugs, 2021, 19, 20.	2.2	19
39	Initial Development toward Non-Invasive Drug Monitoring via Untargeted Mass Spectrometric Analysis of Human Skin. Analytical Chemistry, 2019, 91, 8062-8069.	3.2	17
40	Tandem Mass Spectrometry Molecular Networking as a Powerful and Efficient Tool for Drug Metabolism Studies. Analytical Chemistry, 2022, 94, 1456-1464.	3.2	17
41	SIMILE enables alignment of tandem mass spectra with statistical significance. Nature Communications, 2022, 13, 2510.	5.8	16
42	Protocol for communityâ€created public MS/MS reference spectra within the Global Natural Products Social Molecular Networking infrastructure. Rapid Communications in Mass Spectrometry, 2020, 34, e8725.	0.7	14
43	Fungalâ€“bacterial interaction selects for quorum sensing mutants with increased production of natural antifungal compounds. Communications Biology, 2020, 3, 670.	2.0	12
44	Whole Cell MALDI Fingerprinting Is a Robust Tool for Differential Profiling of Two-Component Mammalian Cell Mixtures. Journal of the American Society for Mass Spectrometry, 2019, 30, 344-354.	1.2	11
45	Quick-start infrastructure for untargeted metabolomics analysis in GNPS. Nature Metabolism, 2021, 3, 880-882.	5.1	11
46	foodMASST a mass spectrometry search tool for foods and beverages. Npj Science of Food, 2022, 6, 22.	2.5	9
47	Chemical Gradients of Plant Substrates in an Atta texana Fungus Garden. MSystems, 2021, 6, e0060121.	1.7	2
48	TIMSCONVERT: a workflow to convert trapped ion mobility data to open data formats. Bioinformatics, 2022, 38, 4046-4047.	1.8	1
49	Three Dimensional Cartography of Microbiome and Metabolome Data onto Radiological Images of the Human Lung. SSRN Electronic Journal, 0, , .	0.4	0