

Hosein Mohimani

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

5,599
citations

304743

22
h-index

477307

29
g-index

34
all docs

34
docs citations

34
times ranked

7409
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.	17.5	2,802
2	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	19.0	650
3	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
4	Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018, 9, 4035.	12.8	220
5	Dereplication of peptidic natural products through database search of mass spectra. <i>Nature Chemical Biology</i> , 2017, 13, 30-37.	8.0	184
6	Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.	3.4	133
7	Linking genomics and metabolomics to chart specialized metabolic diversity. <i>Chemical Society Reviews</i> , 2020, 49, 3297-3314.	38.1	114
8	Cytotoxic Veraguamides, Alkynyl Bromide-Containing Cyclic Depsipeptides from the Marine Cyanobacterium cf. <i>Oscillatoria margaritifera</i> . <i>Journal of Natural Products</i> , 2011, 74, 928-936.	3.0	95
9	NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery. <i>Journal of Natural Products</i> , 2014, 77, 1902-1909.	3.0	81
10	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	8.0	81
11	Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. <i>Nature Microbiology</i> , 2018, 3, 319-327.	13.3	71
12	Dereplication, sequencing and identification of peptidic natural products: from genome mining to peptidogenomics to spectral networks. <i>Natural Product Reports</i> , 2016, 33, 73-86.	10.3	59
13	BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019, 29, 1352-1362.	5.5	55
14	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	6.2	46
15	MolDiscovery: learning mass spectrometry fragmentation of small molecules. <i>Nature Communications</i> , 2021, 12, 3718.	12.8	44
16	Multiplex De Novo Sequencing of Peptide Antibiotics. <i>Journal of Computational Biology</i> , 2011, 18, 1371-1381.	1.6	39
17	Cycloquest: Identification of Cyclopeptides via Database Search of Their Mass Spectra against Genome Databases. <i>Journal of Proteome Research</i> , 2011, 10, 4505-4512.	3.7	38
18	Sequencing cyclic peptides by multistage mass spectrometry. <i>Proteomics</i> , 2011, 11, 3642-3650.	2.2	37

#	ARTICLE	IF	CITATIONS
19	Spatial Molecular Architecture of the Microbial Community of a <i>Peltigera</i> Lichen. <i>MSystems</i> , 2016, 1, .	3.8	36
20	Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. <i>Nature Communications</i> , 2021, 12, 3225.	12.8	31
21	Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. <i>MSystems</i> , 2017, 2, .	3.8	30
22	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. <i>Cell Systems</i> , 2020, 10, 99-108.e5.	6.2	28
23	A Metabolome- and Metagenome-Wide Association Network Reveals Microbial Natural Products and Microbial Biotransformation Products from the Human Microbiota. <i>MSystems</i> , 2019, 4, .	3.8	23
24	A New Approach to Evaluating Statistical Significance of Spectral Identifications. <i>Journal of Proteome Research</i> , 2013, 12, 1560-1568.	3.7	20
25	Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. <i>Metabolites</i> , 2021, 11, 693.	2.9	11
26	MS2Planner: improved fragmentation spectra coverage in untargeted mass spectrometry by iterative optimized data acquisition. <i>Bioinformatics</i> , 2021, 37, i231-i236.	4.1	10
27	On the Error of Estimating the Sparsest Solution of Underdetermined Linear Systems. <i>IEEE Transactions on Information Theory</i> , 2011, 57, 7840-7855.	2.4	6
28	Repository scale classification and decomposition of tandem mass spectral data. <i>Scientific Reports</i> , 2021, 11, 8314.	3.3	3
29	TransDiscovery: Discovering Biotransformation from Human Microbiota by Integrating Metagenomic and Metabolomic Data. <i>Metabolites</i> , 2022, 12, 119.	2.9	2
30	ForestDSH: a universal hash design for discrete probability distributions. <i>Data Mining and Knowledge Discovery</i> , 2021, 35, 748-795.	3.7	0