Hosein Mohimani

List of Publications by Citations

32 papers	**3,099** citations
20 h-index	**34** g-index
34 ext. papers	**4,429** ext. citations
11.8 avg, IF	**4.5** L-index

#	Paper	IF	Citations
32	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. *Nature Biotechnology*, **2016**, 34, 828-837	44.5	1566
31	American Gut: an Open Platform for Citizen Science Microbiome Research. *MSystems*, **2018**, 3,	7.6	336
30	Feature-based molecular networking in the GNPS analysis environment. *Nature Methods*, **2020**, 17, 905-908	28.6	207
29	Dereplication of peptidic natural products through database search of mass spectra. *Nature Chemical Biology*, **2017**, 13, 30-37	11.7	131
28	Automated genome mining of ribosomal peptide natural products. *ACS Chemical Biology*, **2014**, 9, 1545-51	4.9	114
27	Dereplication of microbial metabolites through database search of mass spectra. *Nature Communications*, **2018**, 9, 4035	17.4	109
26	Cytotoxic veraguamides, alkynyl bromide-containing cyclic depsipeptides from the marine cyanobacterium cf. Oscillatoria margaritifera. *Journal of Natural Products*, **2011**, 74, 928-36	4.9	84
25	NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery. *Journal of Natural Products*, **2014**, 77, 1902-9	4.9	64
24	Dereplication, sequencing and identification of peptidic natural products: from genome mining to peptidogenomics to spectral networks. *Natural Product Reports*, **2016**, 33, 73-86	15.1	54
23	Linking genomics and metabolomics to chart specialized metabolic diversity. *Chemical Society Reviews*, **2020**, 49, 3297-3314	58.5	52
22	Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. *Nature Microbiology*, **2018**, 3, 319-327	26.6	49
21	Multiplex de novo sequencing of peptide antibiotics. *Journal of Computational Biology*, **2011**, 18, 1371-81	1.7	36
20	Cycloquest: identification of cyclopeptides via database search of their mass spectra against genome databases. *Journal of Proteome Research*, **2011**, 10, 4505-12	5.6	33
19	Sequencing cyclic peptides by multistage mass spectrometry. *Proteomics*, **2011**, 11, 3642-50	4.8	32
18	A community resource for paired genomic and metabolomic data mining. *Nature Chemical Biology*, **2021**, 17, 363-368	11.7	32
17	Feature-based Molecular Networking in the GNPS Analysis Environment		29
16	BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. *Genome Research*, **2019**, 29, 1352-1362	9.7	26

List of Publications

15	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. *Cell Systems*, **2019**, 9, 600-608.e4	10.6	26
14	Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. *MSystems*, **2017**, 2,	7.6	23
13	Spatial Molecular Architecture of the Microbial Community of a Lichen. *MSystems*, **2016**, 1,	7.6	22
12	A new approach to evaluating statistical significance of spectral identifications. *Journal of Proteome Research*, **2013**, 12, 1560-8	5.6	16
11	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. *Cell Systems*, **2020**, 10, 99-108.e5	10.6	16
10	A Metabolome- and Metagenome-Wide Association Network Reveals Microbial Natural Products and Microbial Biotransformation Products from the Human Microbiota. *MSystems*, **2019**, 4,	7.6	15
9	Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. *Nature Communications*, **2021**, 12, 3225	17.4	8
8	MolDiscovery: learning mass spectrometry fragmentation of small molecules. *Nature Communications*, **2021**, 12, 3718	17.4	8
7	. *IEEE Transactions on Information Theory*, **2011**, 57, 7840-7855	2.8	5
6	Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. *Metabolites*, **2021**, 11,	5.6	2
5	Repository scale classification and decomposition of tandem mass spectral data. *Scientific Reports*, **2021**, 11, 8314	4.9	2
4	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides		1
3	MolDiscovery: Learning Mass Spectrometry Fragmentation of Small Molecules		1
2	MS2Planner: improved fragmentation spectra coverage in untargeted mass spectrometry by iterative optimized data acquisition. *Bioinformatics*, **2021**, 37, i231-i236	7.2	0
1	ForestDSH: a universal hash design for discrete probability distributions. *Data Mining and Knowledge Discovery*, **2021**, 35, 748-795	5.6	