

Hosein Mohimani

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. <i>Metabolites</i> , 2021 , 11, | 5.6 | 2 |
| 31 | Repository scale classification and decomposition of tandem mass spectral data. <i>Scientific Reports</i> , 2021 , 11, 8314 | 4.9 | 2 |
| 30 | Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. <i>Nature Communications</i> , 2021 , 12, 3225 | 17.4 | 8 |
| 29 | MolDiscovery: learning mass spectrometry fragmentation of small molecules. <i>Nature Communications</i> , 2021 , 12, 3718 | 17.4 | 8 |
| 28 | A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021 , 17, 363-368 | 11.7 | 32 |
| 27 | ForestDSH: a universal hash design for discrete probability distributions. <i>Data Mining and Knowledge Discovery</i> , 2021 , 35, 748-795 | 5.6 | |
| 26 | MS2Planner: improved fragmentation spectra coverage in untargeted mass spectrometry by iterative optimized data acquisition. <i>Bioinformatics</i> , 2021 , 37, i231-i236 | 7.2 | 0 |
| 25 | Linking genomics and metabolomics to chart specialized metabolic diversity. <i>Chemical Society Reviews</i> , 2020 , 49, 3297-3314 | 58.5 | 52 |
| 24 | De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. <i>Cell Systems</i> , 2020 , 10, 99-108.e5 | 10.6 | 16 |
| 23 | Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020 , 17, 905-908 | 20.6 | 207 |
| 22 | A Metabolome- and Metagenome-Wide Association Network Reveals Microbial Natural Products and Microbial Biotransformation Products from the Human Microbiota. <i>MSystems</i> , 2019 , 4, | 7.6 | 15 |
| 21 | BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019 , 29, 1352-1362 | 9.7 | 26 |
| 20 | 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 | 10.6 | 26 |
| 19 | Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. <i>Nature Microbiology</i> , 2018 , 3, 319-327 | 26.6 | 49 |
| 18 | Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018 , 9, 4035 | 17.4 | 109 |
| 17 | American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3, | 7.6 | 336 |
| 16 | Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. <i>MSystems</i> , 2017 , 2, | 7.6 | 23 |

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| 15 | Dereplication of peptidic natural products through database search of mass spectra. <i>Nature Chemical Biology</i> , 2017 , 13, 30-37 | 11.7 | 131 |
| 14 | 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 | 15.1 | 54 |
| 13 | Spatial Molecular Architecture of the Microbial Community of a Lichen. <i>MSystems</i> , 2016 , 1, | 7.6 | 22 |
| 12 | Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016 , 34, 828-837 | 44.5 | 1566 |
| 11 | Automated genome mining of ribosomal peptide natural products. <i>ACS Chemical Biology</i> , 2014 , 9, 1545-519 | 11.9 | 114 |
| 10 | NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery. <i>Journal of Natural Products</i> , 2014 , 77, 1902-9 | 4.9 | 64 |
| 9 | A new approach to evaluating statistical significance of spectral identifications. <i>Journal of Proteome Research</i> , 2013 , 12, 1560-8 | 5.6 | 16 |
| 8 | Multiplex de novo sequencing of peptide antibiotics. <i>Journal of Computational Biology</i> , 2011 , 18, 1371-81.7 | 11.7 | 36 |
| 7 | Cycloquest: identification of cyclopeptides via database search of their mass spectra against genome databases. <i>Journal of Proteome Research</i> , 2011 , 10, 4505-12 | 5.6 | 33 |
| 6 | Cytotoxic veraguamides, alkynyl bromide-containing cyclic depsipeptides from the marine cyanobacterium cf. <i>Oscillatoria margaritifera</i> . <i>Journal of Natural Products</i> , 2011 , 74, 928-36 | 4.9 | 84 |
| 5 | . <i>IEEE Transactions on Information Theory</i> , 2011 , 57, 7840-7855 | 2.8 | 5 |
| 4 | Sequencing cyclic peptides by multistage mass spectrometry. <i>Proteomics</i> , 2011 , 11, 3642-50 | 4.8 | 32 |
| 3 | MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides | | 1 |
| 2 | MolDiscovery: Learning Mass Spectrometry Fragmentation of Small Molecules | | 1 |
| 1 | Feature-based Molecular Networking in the GNPS Analysis Environment | | 29 |