

# Hosein Mohimani

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9086686/publications.pdf>

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  | TransDiscovery: Discovering Biotransformation from Human Microbiota by Integrating Metagenomic and Metabolomic Data. <i>Metabolites</i> , 2022, 12, 119.   | 2.9  | 2         |
| 2  | A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.   | 8.0  | 81        |
| 3  | ForestDSH: a universal hash design for discrete probability distributions. <i>Data Mining and Knowledge Discovery</i> , 2021, 35, 748-795.   | 3.7  | 0         |
| 4  | Repository scale classification and decomposition of tandem mass spectral data. <i>Scientific Reports</i> , 2021, 11, 8314.  | 3.3  | 3         |
| 5  | Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. <i>Nature Communications</i> , 2021, 12, 3225.   | 12.8 | 31        |
| 6  | MolDiscovery: learning mass spectrometry fragmentation of small molecules. <i>Nature Communications</i> , 2021, 12, 3718.  | 12.8 | 44        |
| 7  | MS2Planner: improved fragmentation spectra coverage in untargeted mass spectrometry by iterative optimized data acquisition. <i>Bioinformatics</i> , 2021, 37, i231-i236.                          | 4.1  | 10        |
| 8  | Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. <i>Metabolites</i> , 2021, 11, 693.   | 2.9  | 11        |
| 9  | 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        |
| 10 | Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.  | 19.0 | 650       |
| 11 | Linking genomics and metabolomics to chart specialized metabolic diversity. <i>Chemical Society Reviews</i> , 2020, 49, 3297-3314.   | 38.1 | 114       |
| 12 | 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        |
| 13 | 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        |
| 14 | BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019, 29, 1352-1362.  | 5.5  | 55        |
| 15 | 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        |
| 16 | Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018, 9, 4035.  | 12.8 | 220       |
| 17 | American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .   | 3.8  | 604       |
| 18 | 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        |

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|----|--|------|-----------|
| 19 | Dereplication of peptidic natural products through database search of mass spectra. <i>Nature Chemical Biology</i> , 2017, 13, 30-37.  | 8.0  | 184       |
| 20 | Spatial Molecular Architecture of the Microbial Community of a <i>Peltigera</i> Lichen. <i>MSystems</i> , 2016, 1, .   | 3.8  | 36        |
| 21 | 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     |
| 22 | 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        |
| 23 | Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.   | 3.4  | 133       |
| 24 | NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery. <i>Journal of Natural Products</i> , 2014, 77, 1902-1909.   | 3.0  | 81        |
| 25 | A New Approach to Evaluating Statistical Significance of Spectral Identifications. <i>Journal of Proteome Research</i> , 2013, 12, 1560-1568.  | 3.7  | 20        |
| 26 | Multiplex De Novo Sequencing of Peptide Antibiotics. <i>Journal of Computational Biology</i> , 2011, 18, 1371-1381.  | 1.6  | 39        |
| 27 | 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        |
| 28 | 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        |
| 29 | 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         |
| 30 | Sequencing cyclic peptides by multistage mass spectrometry. <i>Proteomics</i> , 2011, 11, 3642-3650.   | 2.2  | 37        |