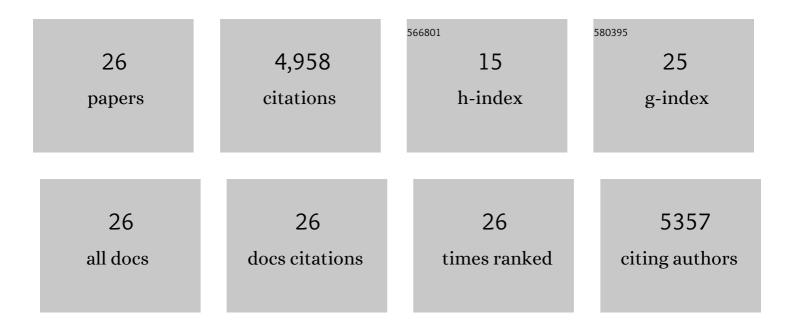
Maude Pupin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. Analytical Chemistry, 2020, 92, 15862-15871.	3.2	18
2	Monomer structure fingerprints: an extension of the monomer composition version for peptide databases. Journal of Computer-Aided Molecular Design, 2020, 34, 1147-1156.	1.3	0
3	Palantir: a springboard for the analysis of secondary metabolite gene clusters in large-scale genome mining projects. Bioinformatics, 2020, 36, 4345-4347.	1.8	16
4	OUP accepted manuscript. Nucleic Acids Research, 2020, 48, D465-D469.	6.5	51
5	Kendrick Mass Defect Approach Combined to NORINE Database for Molecular Formula Assignment of Nonribosomal Peptides. Journal of the American Society for Mass Spectrometry, 2019, 30, 2608-2616.	1.2	3
6	rBAN: retro-biosynthetic analysis of nonribosomal peptides. Journal of Cheminformatics, 2019, 11, 13.	2.8	16
7	Bioinformatics tools for the discovery of new lipopeptides with biocontrol applications. European Journal of Plant Pathology, 2018, 152, 993-1001.	0.8	9
8	Nonribosomal peptides and polyketides of Burkholderia: new compounds potentially implicated in biocontrol and pharmaceuticals. Environmental Science and Pollution Research, 2018, 25, 29794-29807.	2.7	48
9	<i>Burkholderia</i> genome mining for nonribosomal peptideÂsynthetases reveals a great potential for novelÂsiderophores and lipopeptides synthesis. MicrobiologyOpen, 2016, 5, 512-526.	1.2	86
10	Norine: A powerful resource for novel nonribosomal peptide discovery. Synthetic and Systems Biotechnology, 2016, 1, 89-94.	1.8	28
11	Norine, the knowledgebase dedicated to non-ribosomal peptides, is now open to crowdsourcing. Nucleic Acids Research, 2016, 44, D1113-D1118.	6.5	47
12	Bioinformatics Tools for the Discovery of New Nonribosomal Peptides. Methods in Molecular Biology, 2016, 1401, 209-232.	0.4	8
13	Smiles2Monomers: a link between chemical and biological structures for polymers. Journal of Cheminformatics, 2015, 7, 62.	2.8	10
14	Prediction of Monomer Isomery in Florine: A Workflow Dedicated to Nonribosomal Peptide Discovery. PLoS ONE, 2014, 9, e85667.	1.1	25
15	Prediction of New Bioactive Molecules using a Bayesian Belief Network. Journal of Chemical Information and Modeling, 2014, 54, 30-36.	2.5	24
16	A new fingerprint to predict nonribosomal peptides activity. Journal of Computer-Aided Molecular Design, 2012, 26, 1187-1194.	1.3	11
17	Structure, biosynthesis, and properties of kurstakins, nonribosomal lipopeptides from Bacillus spp Applied Microbiology and Biotechnology, 2012, 95, 593-600.	1.7	72
18	Diversity of Monomers in Nonribosomal Peptides: towards the Prediction of Origin and Biological Activity. Journal of Bacteriology, 2010, 192, 5143-5150.	1.0	102

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#	Article	IF	CITATIONS
19	Structural pattern matching of nonribosomal peptides. BMC Structural Biology, 2009, 9, 15.	2.3	18
20	NORINE: a database of nonribosomal peptides. Nucleic Acids Research, 2007, 36, D326-D331.	6.5	226
21	Comparing sequences without using alignments: application to HIV/SIV subtyping. BMC Bioinformatics, 2007, 8, 1.	1.2	520
22	Local Decoding of Sequences and Alignment-Free Comparison. Journal of Computational Biology, 2006, 13, 1465-1476.	0.8	13
23	A revised annotation and comparative analysis of Helicobacter pylori genomes. Nucleic Acids Research, 2003, 31, 1704-1714.	6.5	74
24	HIV-1 and HIV-2 LTR Nucleotide Sequences: Assessment of the Alignment by N-block Presentation, "Retroviral Signatures―of Overrepeated Oligonucleotides, and a Probable Important Role of Scrambled Stepwise Duplications/Deletions in Molecular Evolution. Molecular Biology and Evolution, 2001, 18, 1231-1245.	3.5	8
25	Detecting localized repeats in genomic sequences: a new strategy and its application to Bacillus subtilis and Arabidopsis thaliana sequences. Computers & Chemistry, 2000, 24, 57-70.	1.2	6
26	The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. Nature, 1997, 390, 249-256.	13.7	3,519