

# Maude Pupin

## List of Publications by Year in descending order

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26  
papers

4,958  
citations

566801

15  
h-index

580395

25  
g-index

26  
all docs

26  
docs citations

26  
times ranked

5357  
citing authors

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

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19	Structural pattern matching of nonribosomal peptides. <i>BMC Structural Biology</i> , 2009, 9, 15.	2.3	18
20	NORINE: a database of nonribosomal peptides. <i>Nucleic Acids Research</i> , 2007, 36, D326-D331.	6.5	226
21	Comparing sequences without using alignments: application to HIV/SIV subtyping. <i>BMC Bioinformatics</i> , 2007, 8, 1.	1.2	520
22	Local Decoding of Sequences and Alignment-Free Comparison. <i>Journal of Computational Biology</i> , 2006, 13, 1465-1476.	0.8	13
23	A revised annotation and comparative analysis of <i>Helicobacter pylori</i> genomes. <i>Nucleic Acids Research</i> , 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. <i>Molecular Biology and Evolution</i> , 2001, 18, 1231-1245.	3.5	8
25	Detecting localized repeats in genomic sequences: a new strategy and its application to <i>Bacillus subtilis</i> and <i>Arabidopsis thaliana</i> sequences. <i>Computers &amp; Chemistry</i> , 2000, 24, 57-70.	1.2	6
26	The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . <i>Nature</i> , 1997, 390, 249-256.	13.7	3,519