Maude Pupin

List of Publications by Year
in descending order

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	The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. Nature, 1997, 390, 249-256.	13.7	3,519
2	Comparing sequences without using alignments: application to HIV/SIV subtyping. BMC Bioinformatics, 2007, 8, 1.	1.2	520
3	NORINE: a database of nonribosomal peptides. Nucleic Acids Research, 2007, 36, D326-D331.	6.5	226
4	Diversity of Monomers in Nonribosomal Peptides: towards the Prediction of Origin and Biological Activity. Journal of Bacteriology, 2010, 192, 5143-5150.	1.0	102
5	Burkholderia genome mining for nonribosomal peptideÂsynthetases reveals a great potential for novelÂsiderophores and lipopeptides synthesis. MicrobiologyOpen, 2016, 5, 512-526.	1.2	86
6	A revised annotation and comparative analysis of Helicobacter pylori genomes. Nucleic Acids Research, 2003, 31, 1704-1714.	6.5	74
7	Structure, biosynthesis, and properties of kurstakins, nonribosomal lipopeptides from Bacillus spp.. Applied Microbiology and Biotechnology, 2012, 95, 593-600.	1.7	72
8	OUP accepted manuscript. Nucleic Acids Research, 2020, 48, D465-D469.	6.5	51
9	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
10	Norine, the knowledgebase dedicated to non-ribosomal peptides, is now open to crowdsourcing. Nucleic Acids Research, 2016, 44, D1113-D1118.	6.5	47
11	Norine: A powerful resource for novel nonribosomal peptide discovery. Synthetic and Systems Biotechnology, 2016, 1, 89-94.	1.8	28
12	Prediction of Monomer Isomery in Florine: A Workflow Dedicated to Nonribosomal Peptide Discovery. PLoS ONE, 2014, 9, e85667.	1.1	25
13	Prediction of New Bioactive Molecules using a Bayesian Belief Network. Journal of Chemical Information and Modeling, 2014, 54, 30-36.	2.5	24
14	Structural pattern matching of nonribosomal peptides. BMC Structural Biology, 2009, 9, 15.	2.3	18
15	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. Analytical Chemistry, 2020, 92, 15862-15871.	3.2	18
16	rBAN: retro-biosynthetic analysis of nonribosomal peptides. Journal of Cheminformatics, 2019, 11, 13.	2.8	16
17	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
18	Local Decoding of Sequences and Alignment-Free Comparison. Journal of Computational Biology, 2006, 13, 1465-1476.	0.8	13

#	Article	IF	Citations
19	A new fingerprint to predict nonribosomal peptides activity. Journal of Computer-Aided Molecular Design, 2012, 26, 1187-1194.	1.3	11
20	Smiles2Monomers: a link between chemical and biological structures for polymers. Journal of Cheminformatics, 2015, 7, 62.	2.8	10
21	Bioinformatics tools for the discovery of new lipopeptides with biocontrol applications. European Journal of Plant Pathology, 2018, 152, 993-1001.	0.8	9
22	HIV-1 and HIV-2 LTR Nucleotide Sequences: Assessment of the Alignment by N-block Presentation, â€œRetroviral Signaturesâ€•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
23	Bioinformatics Tools for the Discovery of New Nonribosomal Peptides. Methods in Molecular Biology, 2016, 1401, 209-232.	0.4	8
24	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
25	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
26	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