

Eric P Nawrocki

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3591347/publications.pdf>

Version: 2024-02-01

17
papers

10,776
citations

623734

14
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

15552
citing authors

#	ARTICLE	IF	CITATIONS
1	NCBI prokaryotic genome annotation pipeline. <i>Nucleic Acids Research</i> , 2016, 44, 6614-6624.	14.5	4,711
2	Infernal 1.1: 100-fold faster RNA homology searches. <i>Bioinformatics</i> , 2013, 29, 2933-2935.	4.1	2,281
3	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	14.5	1,000
4	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , 2018, 46, D335-D342.	14.5	819
5	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	14.5	475
6	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	14.5	355
7	Virus Variation Resource "improved response to emergent viral outbreaks. <i>Nucleic Acids Research</i> , 2017, 45, D482-D490.	14.5	342
8	Non-coding RNA Analysis Using the Rfam Database. <i>Current Protocols in Bioinformatics</i> , 2018, 62, e51.	25.8	309
9	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
10	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	6.5	110
11	R2DT is a framework for predicting and visualising RNA secondary structure using templates. <i>Nature Communications</i> , 2021, 12, 3494.	12.8	58
12	Identification and Characterization of a Class of MALAT1-like Genomic Loci. <i>Cell Reports</i> , 2017, 19, 1723-1738.	6.4	55
13	VADR: validation and annotation of virus sequence submissions to GenBank. <i>BMC Bioinformatics</i> , 2020, 21, 211.	2.6	46
14	VecScreen_plus_taxonomy: imposing a tax(onomy) increase on vector contamination screening. <i>Bioinformatics</i> , 2018, 34, 755-759.	4.1	23
15	Group I introns are widespread in archaea. <i>Nucleic Acids Research</i> , 2018, 46, 7970-7976.	14.5	20
16	Rapid automated validation, annotation and publication of SARS-CoV-2 sequences to GenBank. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	4
17	Ribovore: ribosomal RNA sequence analysis for GenBank submissions and database curation. <i>BMC Bioinformatics</i> , 2021, 22, 400.	2.6	3