

Elena Rivas

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3393595/publications.pdf>

Version: 2024-02-01

24
papers

4,038
citations

430874

18
h-index

794594

19
g-index

30
all docs

30
docs citations

30
times ranked

5065
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	A dynamic programming algorithm for RNA structure prediction including pseudoknots 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 285, 2053-2068.	4.2	649
3	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	14.5	475
4	Noncoding RNA gene detection using comparative sequence analysis. <i>BMC Bioinformatics</i> , 2001, 2, 8.	2.6	402
5	Computational identification of noncoding RNAs in <i>E. coli</i> by comparative genomics. <i>Current Biology</i> , 2001, 11, 1369-1373.	3.9	363
6	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. <i>Nature Methods</i> , 2017, 14, 45-48.	19.0	300
7	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. <i>Bioinformatics</i> , 2000, 16, 583-605.	4.1	267
8	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
9	Identification of differentially expressed small non-coding RNAs in the legume endosymbiont <i>Sinorhizobium meliloti</i> by comparative genomics. <i>Molecular Microbiology</i> , 2007, 66, 1080-1091.	2.5	106
10	A range of complex probabilistic models for RNA secondary structure prediction that includes the nearest-neighbor model and more. <i>Rna</i> , 2012, 18, 193-212.	3.5	103
11	Estimating the power of sequence covariation for detecting conserved RNA structure. <i>Bioinformatics</i> , 2020, 36, 3072-3076.	4.1	69
12	Evolutionary models for insertions and deletions in a probabilistic modeling framework. <i>BMC Bioinformatics</i> , 2005, 6, 63.	2.6	57
13	Probabilistic Phylogenetic Inference with Insertions and Deletions. <i>PLoS Computational Biology</i> , 2008, 4, e1000172.	3.2	51
14	The four ingredients of single-sequence RNA secondary structure prediction. A unifying perspective. <i>RNA Biology</i> , 2013, 10, 1185-1196.	3.1	48
15	RNA structure prediction using positive and negative evolutionary information. <i>PLoS Computational Biology</i> , 2020, 16, e1008387.	3.2	46
16	Evolutionary conservation of <i>scp</i> RNA sequence and structure. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1649.	6.4	29
17	Parameterizing sequence alignment with an explicit evolutionary model. <i>BMC Bioinformatics</i> , 2015, 16, 406.	2.6	26
18	Discovery of 17 conserved structural RNAs in fungi. <i>Nucleic Acids Research</i> , 2021, 49, 6128-6143.	14.5	7

#	ARTICLE	IF	CITATIONS
19	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
20	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
21	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
22	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
23	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
24	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0