Elena Rivas

List of Publications by Year
in descending order

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 14: expanded coverage of metagenomic, viral and microRNA families. Nucleic Acids Research, 2021, 49, D192-D200.	14.5	475
2	Evolutionary conservation of <scp>RNA</scp> sequence and structure. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1649.	6.4	29
3	Discovery of 17 conserved structural RNAs in fungi. Nucleic Acids Research, 2021, 49, 6128-6143.	14.5	7
4	Estimating the power of sequence covariation for detecting conserved RNA structure. Bioinformatics, 2020, 36, 3072-3076.	4.1	69
5	RNA structure prediction using positive and negative evolutionary information. PLoS Computational Biology, 2020, 16, e1008387.	3.2	46
6	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
7	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
8	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
9	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
10	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
11	RNA structure prediction using positive and negative evolutionary information. , 2020, 16, e1008387.		0
12	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
13	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. Nucleic Acids Research, 2018, 46, D335-D342.	14.5	819
14	A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs. Nature Methods, 2017, 14, 45-48.	19.0	300
15	Parameterizing sequence alignment with an explicit evolutionary model. BMC Bioinformatics, 2015, 16, 406.	2.6	26
16	The four ingredients of single-sequence RNA secondary structure prediction. A unifying perspective. RNA Biology, 2013, 10, 1185-1196.	3.1	48
17	A range of complex probabilistic models for RNA secondary structure prediction that includes the nearest-neighbor model and more. Rna, 2012, 18, 193-212.	3.5	103
18	Probabilistic Phylogenetic Inference with Insertions and Deletions. PLoS Computational Biology, 2008, 4, e1000172.	3.2	51

#	Article	IF	Citations
19	Identification of differentially expressed small non‐coding RNAs in the legume endosymbiont <i>Sinorhizobium meliloti</i> by comparative genomics. Molecular Microbiology, 2007, 66, 1080-1091.	2.5	106
20	Evolutionary models for insertions and deletions in a probabilistic modeling framework. BMC Bioinformatics, 2005, 6, 63.	2.6	57
21	Computational identification of noncoding RNAs in E. coli by comparative genomics. Current Biology, 2001, 11, 1369-1373.	3.9	363
22	Noncoding RNA gene detection using comparative sequence analysis. BMC Bioinformatics, 2001, 2, 8.	2.6	402
23	Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs. Bioinformatics, 2000, 16, 583-605.	4.1	267
24	A dynamic programming algorithm for RNA structure prediction including pseudoknots 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1999, 285, 2053-2068.	4.2	649