

Stephan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54
papers

6,355
citations

27
h-index

58
g-index

58
ext. papers

8,346
ext. citations

9.1
avg, IF

5.48
L-index

#	Paper	IF	Citations
54	ViennaRNA Package 2.0. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 26	1.8	2351
53	The Vienna RNA websuite. <i>Nucleic Acids Research</i> , 2008 , 36, W70-4	20.1	1339
52	RNAalifold: improved consensus structure prediction for RNA alignments. <i>BMC Bioinformatics</i> , 2008 , 9, 474	3.6	390
51	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012 , 44, 1316-20	36.3	317
50	Thermodynamics of RNA-RNA binding. <i>Bioinformatics</i> , 2006 , 22, 1177-82	7.2	272
49	Partition function and base pairing probabilities of RNA heterodimers. <i>Algorithms for Molecular Biology</i> , 2006 , 1, 3	1.8	183
48	Local RNA base pairing probabilities in large sequences. <i>Bioinformatics</i> , 2006 , 22, 614-5	7.2	164
47	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. <i>Genome Research</i> , 2016 , 26, 256-62	9.7	159
46	Recurrent mTORC1-activating RRAGC mutations in follicular lymphoma. <i>Nature Genetics</i> , 2016 , 48, 183-836.3	36.3	116
45	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015 , 47, 1316-1325	36.3	101
44	The ViennaRNA web services. <i>Methods in Molecular Biology</i> , 2015 , 1269, 307-26	1.4	80
43	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5261-70	11.5	75
42	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2019 , 47, 10543-10552	20.1	70
41	Changes of bivalent chromatin coincide with increased expression of developmental genes in cancer. <i>Scientific Reports</i> , 2016 , 6, 37393	4.9	64
40	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , 2008 , 56, 129-44	2	57
39	Temperature-responsive in vitro RNA structurome of <i>Yersinia pseudotuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 7237-42	11.5	55
38	Strategies for measuring evolutionary conservation of RNA secondary structures. <i>BMC Bioinformatics</i> , 2008 , 9, 122	3.6	50

37	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019 , 10, 1459	17.4	49
36	A folding algorithm for extended RNA secondary structures. <i>Bioinformatics</i> , 2011 , 27, i129-36	7.2	46
35	RNAs everywhere: genome-wide annotation of structured RNAs. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007 , 308, 1-25	1.8	38
34	RNPomics: defining the ncRNA transcriptome by cDNA library generation from ribonucleo-protein particles. <i>Nucleic Acids Research</i> , 2010 , 38, e113	20.1	36
33	DREAM and RB cooperate to induce gene repression and cell-cycle arrest in response to p53 activation. <i>Nucleic Acids Research</i> , 2019 , 47, 9087-9103	20.1	32
32	2D meets 4G: G-quadruplexes in RNA secondary structure prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 832-44	3	31
31	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , 2016 , 101, 1380-1389	6.6	31
30	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016 , 6, 34589	4.9	30
29	Animal snoRNAs and scaRNAs with exceptional structures. <i>RNA Biology</i> , 2011 , 8, 938-46	4.8	27
28	Nematode sbRNAs: homologs of vertebrate Y RNAs. <i>Journal of Molecular Evolution</i> , 2010 , 70, 346-58	3.1	27
27	From consensus structure prediction to RNA gene finding. <i>Briefings in Functional Genomics & Proteomics</i> , 2009 , 8, 461-71		26
26	The DREAM complex through its subunit Lin37 cooperates with Rb to initiate quiescence. <i>ELife</i> , 2017 , 6,	8.9	24
25	The PCBP1 gene encoding poly(rC) binding protein I is recurrently mutated in Burkitt lymphoma. <i>Genes Chromosomes and Cancer</i> , 2015 , 54, 555-64	5	21
24	Folding RNA/DNA hybrid duplexes. <i>Bioinformatics</i> , 2012 , 28, 2530-1	7.2	14
23	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. <i>Genome Medicine</i> , 2020 , 12, 97	14.4	9
22	Identification of RNA 3' ends and termination sites in. <i>RNA Biology</i> , 2020 , 17, 663-676	4.8	8
21	Beyond the 3'UTR binding-microRNA-induced protein truncation via DNA binding. <i>Oncotarget</i> , 2018 , 9, 32855-32867	3.3	8
20	Reconstruction of rearranged T-cell receptor loci by whole genome and transcriptome sequencing gives insights into the initial steps of T-cell prolymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2020 , 59, 261-267	5	7

19	The Evolving Faces of the SARS-CoV-2 Genome. <i>Viruses</i> , 2021 , 13,	6.2	5
18	DIEGO: detection of differential alternative splicing using Aitchison's geometry. <i>Bioinformatics</i> , 2018 , 34, 1066-1068	7.2	4
17	MCPIP1 ribonuclease can bind and cleave mRNA in -amplified neuroblastoma cells. <i>RNA Biology</i> , 2021 , 18, 144-156	4.8	4
16	Transcription factor RFX7 governs a tumor suppressor network in response to p53 and stress. <i>Nucleic Acids Research</i> , 2021 , 49, 7437-7456	20.1	4
15	RBFOX2 and alternative splicing in B-cell lymphoma. <i>Blood Cancer Journal</i> , 2018 , 8, 77	7	3
14	RNA structure prediction. <i>Methods in Molecular Biology</i> , 2011 , 760, 307-23	1.4	3
13	Splicing Endonuclease Is an Important Player in rRNA and tRNA Maturation in Archaea. <i>Frontiers in Microbiology</i> , 2020 , 11, 594838	5.7	3
12	Effects of lifestyle interventions on epigenetic signatures of liver fat: Central randomized controlled trial. <i>Liver International</i> , 2021 , 41, 2101-2111	7.9	3
11	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021 , 35, 2002-2016	10.7	3
10	Noncoding RNA Transcripts during Differentiation of Induced Pluripotent Stem Cells into Hepatocytes. <i>Stem Cells International</i> , 2018 , 2018, 5692840	5	3
9	Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing. <i>Genome Biology</i> , 2020 , 21, 299	18.3	2
8	Energy-based RNA consensus secondary structure prediction in multiple sequence alignments. <i>Methods in Molecular Biology</i> , 2014 , 1097, 125-41	1.4	2
7	Lifestyle weight-loss intervention may attenuate methylation aging: the CENTRAL MRI randomized controlled trial. <i>Clinical Epigenetics</i> , 2021 , 13, 48	7.7	2
6	Absence of Non-Canonical, Inhibitory Splice Variants in B Cell Lymphomas Correlates With Sustained NF- κ B Signaling. <i>Frontiers in Immunology</i> , 2021 , 12, 616451	8.4	2
5	A probabilistic version of Sankoff's maximum parsimony algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2020 , 18, 2050004	1	1
4	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. <i>Blood Advances</i> , 2021 , 5, 5239-5257	7.8	1
3	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i>		1
2	The failure of B cells to induce non-canonical MYD88 splice variants correlates with lymphomagenesis via sustained NF- κ B signaling		1

- 1 Legal Action for Climate Protection – Impulses on the international level from the German Federal Constitutional Court: the Court Order from March 2021 on the Unconstitutionality of the Federal German Climate Protection Act. *Brazilian Journal of Environmental Sciences (Online)*, **2022**, 57, 158-165 1