

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.

73 papers	9,506 citations	34 h-index	76 g-index
76 ext. papers	12,586 ext. citations	17.7 avg, IF	6.79 L-index

#	Paper	IF	Citations
73	Circular intronic long noncoding RNAs. <i>Molecular Cell</i> , 2013 , 51, 792-806	17.6	1352
72	Complementary sequence-mediated exon circularization. <i>Cell</i> , 2014 , 159, 134-147	56.2	1144
71	Regulation of circRNA biogenesis. <i>RNA Biology</i> , 2015 , 12, 381-8	4.8	1049
70	The Biogenesis, Functions, and Challenges of Circular RNAs. <i>Molecular Cell</i> , 2018 , 71, 428-442	17.6	902
69	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016 , 26, 1277-87	9.7	482
68	Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. <i>Cell Research</i> , 2014 , 24, 513-31	24.7	471
67	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. <i>Molecular Cell</i> , 2017 , 67, 214-227.e7	17.6	334
66	The Biogenesis of Nascent Circular RNAs. <i>Cell Reports</i> , 2016 , 15, 611-624	10.6	324
65	Structure and Degradation of Circular RNAs Regulate PKR Activation in Innate Immunity. <i>Cell</i> , 2019 , 177, 865-880.e21	56.2	312
64	Long noncoding RNAs with snoRNA ends. <i>Molecular Cell</i> , 2012 , 48, 219-30	17.6	304
63	Genomewide characterization of non-polyadenylated RNAs. <i>Genome Biology</i> , 2011 , 12, R16	18.3	286
62	Base editing with a Cpf1-cytidine deaminase fusion. <i>Nature Biotechnology</i> , 2018 , 36, 324-327	44.5	232
61	The Output of Protein-Coding Genes Shifts to Circular RNAs When the Pre-mRNA Processing Machinery Is Limiting. <i>Molecular Cell</i> , 2017 , 68, 940-954.e3	17.6	213
60	The Diversity of Long Noncoding RNAs and Their Generation. <i>Trends in Genetics</i> , 2017 , 33, 540-552	8.5	167
59	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. <i>Nature Biotechnology</i> , 2018 , 36, 946-949	44.5	137
58	SLERT Regulates DDX21 Rings Associated with Pol I Transcription. <i>Cell</i> , 2017 , 169, 664-678.e16	56.2	125
57	Increased complexity of circRNA expression during species evolution. <i>RNA Biology</i> , 2017 , 14, 1064-1074	4.8	117

56	CIRCpedia v2: An Updated Database for Comprehensive Circular RNA Annotation and Expression Comparison. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 226-233	6.5	117
55	Genome-wide screening of NEAT1 regulators reveals cross-regulation between paraspeckles and mitochondria. <i>Nature Cell Biology</i> , 2018 , 20, 1145-1158	23.4	85
54	Unusual Processing Generates SPA lncRNAs that Sequester Multiple RNA Binding Proteins. <i>Molecular Cell</i> , 2016 , 64, 534-548	17.6	79
53	Life without A tail: new formats of long noncoding RNAs. <i>International Journal of Biochemistry and Cell Biology</i> , 2014 , 54, 338-49	5.6	78
52	Distinct Processing of lncRNAs Contributes to Non-conserved Functions in Stem Cells. <i>Cell</i> , 2020 , 181, 621-636.e22	56.2	75
51	CircRNA-derived pseudogenes. <i>Cell Research</i> , 2016 , 26, 747-50	24.7	72
50	ALU alternative Regulation for Gene Expression. <i>Trends in Cell Biology</i> , 2017 , 27, 480-490	18.3	71
49	CRISPR-Cas9-Mediated Genetic Screening in Mice with Haploid Embryonic Stem Cells Carrying a Guide RNA Library. <i>Cell Stem Cell</i> , 2015 , 17, 221-32	18	70
48	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. <i>Nature Biotechnology</i> , 2020 , 38, 856-860	44.5	69
47	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. <i>Cell Research</i> , 2017 , 27, 1289-1292	24.7	63
46	Protein arginine methyltransferase CARM1 attenuates the paraspeckle-mediated nuclear retention of mRNAs containing IRAlus. <i>Genes and Development</i> , 2015 , 29, 630-45	12.6	61
45	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. <i>Cell Research</i> , 2015 , 25, 459-76	24.7	60
44	N-Methyladenosines Modulate A-to-I RNA Editing. <i>Molecular Cell</i> , 2018 , 69, 126-135.e6	17.6	58
43	Screening for functional circular RNAs using the CRISPR-Cas13 system. <i>Nature Methods</i> , 2021 , 18, 51-59	21.6	57
42	Splicing noncoding RNAs from the inside out. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015 , 6, 651-60	9.3	37
41	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. <i>BMC Genomics</i> , 2014 , 15, 287	4.5	35
40	APOBEC3 induces mutations during repair of CRISPR-Cas9-generated DNA breaks. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 45-52	17.6	35
39	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2016 , 1402, 215-227	1.4	30

38	Development and Application of Base Editors. <i>CRISPR Journal</i> , 2019 , 2, 91-104	2.5	29
37	Circular RNA profiling provides insights into their subcellular distribution and molecular characteristics in HepG2 cells. <i>RNA Biology</i> , 2019 , 16, 220-232	4.8	29
36	Parthenogenetic haploid embryonic stem cells efficiently support mouse generation by oocyte injection. <i>Cell Research</i> , 2016 , 26, 131-4	24.7	28
35	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020 , 31, 107723	10.6	27
34	Prediction of constitutive A-to-I editing sites from human transcriptomes in the absence of genomic sequences. <i>BMC Genomics</i> , 2013 , 14, 206	4.5	27
33	SnoVectors for nuclear expression of RNA. <i>Nucleic Acids Research</i> , 2015 , 43, e5	20.1	25
32	Silencing of circular RNA HIPK2 in neural stem cells enhances functional recovery following ischaemic stroke. <i>EBioMedicine</i> , 2020 , 52, 102660	8.8	23
31	The long noncoding RNA regulation at the MYC locus. <i>Current Opinion in Genetics and Development</i> , 2015 , 33, 41-8	4.9	22
30	CIRCexplorer3: A CLEAR Pipeline for Direct Comparison of Circular and Linear RNA Expression. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 511-521	6.5	21
29	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. <i>Genome Biology</i> , 2019 , 20, 218	18.3	16
28	One Prime for All Editing. <i>Cell</i> , 2019 , 179, 1448-1450	56.2	15
27	Genome-Wide Annotation of circRNAs and Their Alternative Back-Splicing/Splicing with CIRCexplorer Pipeline. <i>Methods in Molecular Biology</i> , 2019 , 1870, 137-149	1.4	15
26	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. <i>Nature Cell Biology</i> , 2021 , 23, 552-563	23.4	14
25	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013 , 3, 226-41	5.9	12
24	A Tale of Two Moieties: Rapidly Evolving CRISPR/Cas-Based Genome Editing. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 874-888	10.3	11
23	Microexons go big. <i>Cell</i> , 2014 , 159, 1488-9	56.2	10
22	RNA Structure Switches RBP Binding. <i>Molecular Cell</i> , 2016 , 64, 219-220	17.6	8
21	Linking circular intronic RNA degradation and function in transcription by RNase H1. <i>Science China Life Sciences</i> , 2021 , 64, 1795-1809	8.5	8

20	To BE or not to BE, that is the question. <i>Nature Biotechnology</i> , 2019 , 37, 520-522	44.5	7
19	RNA circles with minimized immunogenicity as potent PKR inhibitors.. <i>Molecular Cell</i> , 2021 ,	17.6	7
18	Silencing of circular RNA_0000326 inhibits cervical cancer cell proliferation, migration and invasion by boosting microRNA-338-3p-dependent down-regulation of CDK4. <i>Aging</i> , 2021 , 13, 9119-9134	5.6	6
17	Screening for functional circular RNAs using the CRISPR-Cas13 system		5
16	CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. <i>Methods</i> , 2021 , 196, 3-10	4.6	5
15	Genomic and Transcriptomic Analyses of Prime Editing Guide RNA-Independent Off-Target Effects by Prime Editors.. <i>CRISPR Journal</i> , 2022 ,	2.5	5
14	Gear Up in Circles. <i>Molecular Cell</i> , 2015 , 58, 715-7	17.6	4
13	Highly efficient prime editing by introducing same-sense mutations in pegRNA or stabilizing its structure.. <i>Nature Communications</i> , 2022 , 13, 1669	17.4	4
12	SCAPTURE: a deep learning-embedded pipeline that captures polyadenylation information from 3' tag-based RNA-seq of single cells. <i>Genome Biology</i> , 2021 , 22, 221	18.3	3
11	Progression and application of CRISPR-Cas genomic editors. <i>Methods</i> , 2021 , 194, 65-74	4.6	3
10	Competition of RNA splicing: line in or circle up. <i>Science China Life Sciences</i> , 2014 , 57, 1232-3	8.5	2
9	Knockout of circRNAs by base editing back-splice sites of circularized exons.. <i>Genome Biology</i> , 2022 , 23, 16	18.3	2
8	No observable guide-RNA-independent off-target mutation induced by prime editor		2
7	Mapping circular RNA structures in living cells by SHAPE-MaP. <i>Methods</i> , 2021 , 196, 47-55	4.6	2
6	A CLEAR pipeline for direct comparison of circular and linear RNA expression		1
5	SCAPTURE: a deep learning-embedded pipeline that captures polyadenylation information from 3' tag-based RNA-seq of single cells		1
4	Fast and furious: insights of back splicing regulation during nascent RNA synthesis. <i>Science China Life Sciences</i> , 2021 , 64, 1050-1061	8.5	1
3	Knockout of circRNAs by base editing back-splice sites of circularized exons		1

- 2 Characterization of Circular RNAs. *Methods in Molecular Biology*, **2021**, 2372, 179-192 1.4 O
- 1 Multifaceted roles of complementary sequences on circRNA formation. *Quantitative Biology*, **2017**, 5, 205-209 3.9