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List of Publications by Year
in descending order

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Version: 2024-02-01

35 papers	5,000 citations	331259 21 h-index	395343 33 g-index
42 all docs	42 docs citations	42 times ranked	7308 citing authors

#	Article	IF	Citations
1	Transcriptome-Wide Profiling of RNA Stability. Methods in Molecular Biology, 2022, 2404, 311-330.	0.4	0
2	NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation. Genes and Development, 2022, 36, 348-367.	2.7	17
3	Systematic refinement of gene annotations by parsing mRNA 3â€² end sequencing datasets. Methods in Enzymology, 2021, 655, 205-223.	0.4	2
4	Structure-function analysis of microRNA 3â€²-end trimming by Nibbler. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30370-30379.	3.3	9
5	Conformation of sister chromatids in the replicated human genome. Nature, 2020, 586, 139-144.	13.7	68
6	Determining mRNA Stability by Metabolic RNA Labeling and Chemical Nucleoside Conversion. Methods in Molecular Biology, 2020, 2062, 169-189.	0.4	7
7	Time-Resolved Small RNA Sequencing Unravels the Molecular Principles of MicroRNA Homeostasis. Molecular Cell, 2019, 75, 756-768.e7.	4.5	116
8	Structural basis for acceptor RNA substrate selectivity of the 3â€² terminal uridylyl transferase Tailor. Nucleic Acids Research, 2019, 47, 1030-1042.	6.5	13
9	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. BMC Bioinformatics, 2019, 20, 258.	1.2	86
10	Sequencing cell-type-specific transcriptomes with SLAM-ITseq. Nature Protocols, 2019, 14, 2261-2278.	5.5	13
11	Cell-type specific sequencing of microRNAs from complex animal tissues. Nature Methods, 2018, 15, 283-289.	9.0	68
12	Positioning Europe for the EPITRANSCRIPTOMICS challenge. RNA Biology, 2018, 15, 1-3.	1.5	18
13	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. Science, 2018, 360, 800-805.	6.0	284
14	SLAM-ITseq: Sequencing cell type-specific transcriptomes without cell sorting. Development (Cambridge), 2018, 145, .	1.2	29
15	Analysis of 3â€² End Modifications in microRNAs by High-Throughput Sequencing. Methods in Molecular Biology, 2018, 1823, 115-139.	0.4	3
16	Small RNAs Are Trafficked from the Epididymis to Developing Mammalian Sperm. Developmental Cell, 2018, 46, 481-494.e6.	3.1	287
17	Thiol-linked alkylation of RNA to assess expression dynamics. Nature Methods, 2017, 14, 1198-1204.	9.0	411
18	Genetic and mechanistic diversity of piRNA 3â€²-end formation. Nature, 2016, 539, 588-592.	13.7	115

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19	Molecular basis for cytoplasmic <scp>RNA</scp> surveillance by uridylationâ€triggered decay in Drosophila. EMBO Journal, 2016, 35, 2417-2434.	3.5	50
20	Approaching the Golden Fleece a Molecule at a Time: Biophysical Insights into Argonaute-Instructed Nucleic Acid Interactions. Molecular Cell, 2015, 59, 4-7.	4.5	13
21	Selective Suppression of the Splicing-Mediated MicroRNA Pathway by the Terminal Uridyltransferase Tailor. Molecular Cell, 2015, 59, 217-228.	4.5	58
22	Uridylation of RNA Hairpins by Tailor Confines the Emergence of MicroRNAs in Drosophila. Molecular Cell, 2015, 59, 203-216.	4.5	62
23	Diversifying microRNA sequence and function. Nature Reviews Molecular Cell Biology, 2013, 14, 475-488.	16.1	1,066
24	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. Nature Methods, 2012, 9, 403-409.	9.0	188
25	The 3â€²-to-5â€² Exoribonuclease Nibbler Shapes the 3â€² Ends of MicroRNAs Bound to Drosophila Argonaute1. Current Biology, 2011, 21, 1878-1887.	1.8	143
26	MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression. Molecular Therapy, 2011, 19, 526-535.	3.7	143
27	Target RNA-directed tailing and trimming purifies the sorting of endo-siRNAs between the two Drosophila Argonaute proteins. Rna, 2011, 17, 54-63.	1.6	51
28	Riding in silence: a little snowboarding, a lot of small RNAs. Silence: A Journal of RNA Regulation, 2010, 1, 8.	8.0	4
29	Target RNAâ€“Directed Trimming and Tailing of Small Silencing RNAs. Science, 2010, 328, 1534-1539.	6.0	514
30	The impact of target site accessibility on the design of effective siRNAs. Nature Biotechnology, 2008, 26, 578-583.	9.4	262
31	RNA chaperone activity of L1 ribosomal proteins: phylogenetic conservation and splicing inhibition. Nucleic Acids Research, 2007, 35, 3752-3763.	6.5	14
32	Molecular Basis for Target RNA Recognition and Cleavage by Human RISC. Cell, 2007, 130, 101-112.	13.5	491
33	Cleavage of the siRNA passenger strand during RISC assembly in human cells. EMBO Reports, 2006, 7, 314-320.	2.0	340
34	Inducible DNA-loop formation blocks transcriptional activation by an SV40 enhancer. EMBO Journal, 2005, 24, 358-367.	3.5	44
35	MicroRNome by methylation-dependent sequencing (mime-seq). Protocol Exchange, 0, , .	0.3	1