

Schraga Schwartz

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

9,359
citations

279798

23
h-index

345221

36
g-index

46
all docs

46
docs citations

46
times ranked

8170
citing authors

#	ARTICLE	IF	CITATIONS
1	Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq. <i>Nature</i> , 2012, 485, 201-206.	27.8	3,661
2	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5' Sites. <i>Cell Reports</i> , 2014, 8, 284-296.	6.4	972
3	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	28.9	770
4	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. <i>Cell</i> , 2013, 155, 1409-1421.	28.9	554
5	The m1A landscape on cytosolic and mitochondrial mRNA at single-base resolution. <i>Nature</i> , 2017, 551, 251-255.	27.8	440
6	The epitranscriptome beyond m6A. <i>Nature Reviews Genetics</i> , 2021, 22, 119-131.	16.3	353
7	Deciphering the "m6A Code" via Antibody-Independent Quantitative Profiling. <i>Cell</i> , 2019, 178, 731-747.e16.	28.9	341
8	Accurate detection of m6A RNA modifications in native RNA sequences. <i>Nature Communications</i> , 2019, 10, 4079.	12.8	322
9	m6A modification controls the innate immune response to infection by targeting type I interferons. <i>Nature Immunology</i> , 2019, 20, 173-182.	14.5	317
10	Transcriptome-Wide Mapping of 5-methylcytidine RNA Modifications in Bacteria, Archaea, and Yeast Reveals m5C within Archaeal mRNAs. <i>PLoS Genetics</i> , 2013, 9, e1003602.	3.5	274
11	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	27.8	175
12	Context-dependent functional compensation between Ythdf m ⁶ A reader proteins. <i>Genes and Development</i> , 2020, 34, 1373-1391.	5.9	158
13	Quantitative profiling of pseudouridylation dynamics in native RNAs with nanopore sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1278-1291.	17.5	144
14	TRUB1 is the predominant pseudouridine synthase acting on mammalian mRNA via a predictable and conserved code. <i>Genome Research</i> , 2017, 27, 393-406.	5.5	106
15	Next-generation sequencing technologies for detection of modified nucleotides in RNAs. <i>RNA Biology</i> , 2017, 14, 1124-1137.	3.1	91
16	Variants in PUS7 Cause Intellectual Disability with Speech Delay, Microcephaly, Short Stature, and Aggressive Behavior. <i>American Journal of Human Genetics</i> , 2018, 103, 1045-1052.	6.2	89
17	Germline NPM1 mutations lead to altered rRNA 2'-O-methylation and cause dyskeratosis congenita. <i>Nature Genetics</i> , 2019, 51, 1518-1529.	21.4	84
18	Cracking the epitranscriptome. <i>Rna</i> , 2016, 22, 169-174.	3.5	73

#	ARTICLE	IF	CITATIONS
19	Multiplexed profiling facilitates robust m6A quantification at site, gene and sample resolution. <i>Nature Methods</i> , 2021, 18, 1060-1067.	19.0	57
20	RNA editing in bacteria recodes multiple proteins and regulates an evolutionarily conserved toxin-antitoxin system. <i>Genome Research</i> , 2017, 27, 1696-1703.	5.5	51
21	m ¹ A within cytoplasmic mRNAs at single nucleotide resolution: a reconciled transcriptome-wide map. <i>Rna</i> , 2018, 24, 1427-1436.	3.5	49
22	A network-based analysis of colon cancer splicing changes reveals a tumorigenesis-favoring regulatory pathway emanating from ELK1. <i>Genome Research</i> , 2016, 26, 541-553.	5.5	45
23	Quantitative nucleotide resolution profiling of RNA cytidine acetylation by ac4C-seq. <i>Nature Protocols</i> , 2021, 16, 2286-2307.	12.0	40
24	The germinal center reaction depends on RNA methylation and divergent functions of specific methyl readers. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	25
25	Probing small ribosomal subunit RNA helix 45 acetylation across eukaryotic evolution. <i>Nucleic Acids Research</i> , 2022, 50, 6284-6299.	14.5	21
26	Deciphering the principles of the RNA editing code via large-scale systematic probing. <i>Molecular Cell</i> , 2021, 81, 2374-2387.e3.	9.7	20
27	Misincorporation signatures for detecting modifications in mRNA: Not as simple as it sounds. <i>Methods</i> , 2019, 156, 53-59.	3.8	19
28	A late-stage assembly checkpoint of the human mitochondrial ribosome large subunit. <i>Nature Communications</i> , 2022, 13, 929.	12.8	13
29	A systematic dissection of determinants and consequences of snoRNA-guided pseudouridylation of human mRNA. <i>Nucleic Acids Research</i> , 2022, 50, 4900-4916.	14.5	11
30	The ribosome epitranscriptome: inert or a platform for functional plasticity?. <i>Rna</i> , 2021, 27, 1293-1301.	3.5	9
31	Decoupling of degradation from deadenylation reshapes poly(A) tail length in yeast meiosis. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 1038-1049.	8.2	8
32	Cloning of DNA oligo pools for in vitro expression. <i>STAR Protocols</i> , 2022, 3, 101103.	1.2	4
33	How many tRNAs are out there?. <i>Molecular Cell</i> , 2021, 81, 1595-1597.	9.7	3
34	mito-Seq: A High-Throughput Method for Systematic Mapping of Pseudouridine Within Mitochondrial RNA. <i>Methods in Molecular Biology</i> , 2021, 2192, 103-115.	0.9	3