

Schraga Schwartz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4154033/publications.pdf>

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	Cloning of DNA oligo pools for inÂvitro expression. STAR Protocols, 2022, 3, 101103.	1.2	4
2	A late-stage assembly checkpoint of the human mitochondrial ribosome large subunit. Nature Communications, 2022, 13, 929.	12.8	13
3	A systematic dissection of determinants and consequences of snoRNA-guided pseudouridylation of human mRNA. Nucleic Acids Research, 2022, 50, 4900-4916.	14.5	11
4	Probing small ribosomal subunit RNA helix 45 acetylation across eukaryotic evolution. Nucleic Acids Research, 2022, 50, 6284-6299.	14.5	21
5	The epitranscriptome beyond m6A. Nature Reviews Genetics, 2021, 22, 119-131.	16.3	353
6	Quantitative nucleotide resolution profiling of RNA cytidine acetylation by ac4C-seq. Nature Protocols, 2021, 16, 2286-2307.	12.0	40
7	How many tRNAs are out there?. Molecular Cell, 2021, 81, 1595-1597.	9.7	3
8	Quantitative profiling of pseudouridylation dynamics in native RNAs with nanopore sequencing. Nature Biotechnology, 2021, 39, 1278-1291.	17.5	144
9	Deciphering the principles of the RNA editing code via large-scale systematic probing. Molecular Cell, 2021, 81, 2374-2387.e3.	9.7	20
10	The ribosome epitranscriptome: inertâ€”or a platform for functional plasticity?. Rna, 2021, 27, 1293-1301.	3.5	9
11	The germinal center reaction depends on RNA methylation and divergent functions of specific methyl readers. Journal of Experimental Medicine, 2021, 218, .	8.5	25
12	Multiplexed profiling facilitates robust m6A quantification at site, gene and sample resolution. Nature Methods, 2021, 18, 1060-1067.	19.0	57
13	mito-Î´-Seq: A High-Throughput Method for Systematic Mapping of Pseudouridine Within Mitochondrial RNA. Methods in Molecular Biology, 2021, 2192, 103-115.	0.9	3
14	Decoupling of degradation from deadenylation reshapes poly(A) tail length in yeast meiosis. Nature Structural and Molecular Biology, 2021, 28, 1038-1049.	8.2	8
15	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. Nature, 2020, 583, 638-643.	27.8	175
16	Context-dependent functional compensation between Ythdf m⁶A reader proteins. Genes and Development, 2020, 34, 1373-1391.	5.9	158
17	Accurate detection of m6A RNA modifications in native RNA sequences. Nature Communications, 2019, 10, 4079.	12.8	322
18	Deciphering the â€œm6A Codeâ€”via Antibody-Independent Quantitative Profiling. Cell, 2019, 178, 731-747.e16.	28.9	341

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19	Germline NPM1 mutations lead to altered rRNA 2â€²-O-methylation and cause dyskeratosis congenita. <i>Nature Genetics</i> , 2019, 51, 1518-1529.	21.4	84
20	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
21	Misincorporation signatures for detecting modifications in mRNA: Not as simple as it sounds. <i>Methods</i> , 2019, 156, 53-59.	3.8	19
22	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
23	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
24	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
25	The m1A landscape on cytosolic and mitochondrial mRNA at single-base resolution. <i>Nature</i> , 2017, 551, 251-255.	27.8	440
26	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
27	Next-generation sequencing technologies for detection of modified nucleotides in RNAs. <i>RNA Biology</i> , 2017, 14, 1124-1137.	3.1	91
28	Cracking the epitranscriptome. <i>Rna</i> , 2016, 22, 169-174.	3.5	73
29	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
30	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5â€² Sites. <i>Cell Reports</i> , 2014, 8, 284-296.	6.4	972
31	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	28.9	770
32	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. <i>Cell</i> , 2013, 155, 1409-1421.	28.9	554
33	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
34	Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq. <i>Nature</i> , 2012, 485, 201-206.	27.8	3,661