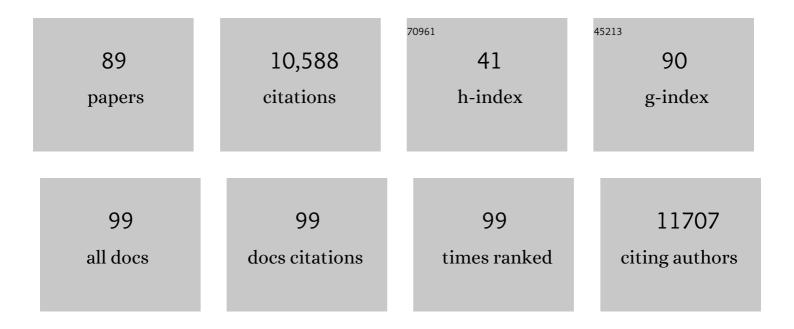
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	N6-Methyladenosine in nuclear RNA is a major substrate of the obesity-associated FTO. Nature Chemical Biology, 2011, 7, 885-887.	3.9	2,936
2	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. Nature Biotechnology, 2011, 29, 68-72.	9.4	955
3	Transcriptome-wide mapping reveals reversible and dynamic N1-methyladenosine methylome. Nature Chemical Biology, 2016, 12, 311-316.	3.9	502
4	Chemical pulldown reveals dynamic pseudouridylation of the mammalian transcriptome. Nature Chemical Biology, 2015, 11, 592-597.	3.9	428
5	Efficient and quantitative high-throughput tRNA sequencing. Nature Methods, 2015, 12, 835-837.	9.0	426
6	Epitranscriptome sequencing technologies: decoding RNA modifications. Nature Methods, 2017, 14, 23-31.	9.0	360
7	Oxidative demethylation of 3â€methylthymine and 3â€methyluracil in singleâ€stranded DNA and RNA by mouse and human FTO. FEBS Letters, 2008, 582, 3313-3319.	1.3	359
8	Base-Resolution Mapping Reveals Distinct m1A Methylome in Nuclear- and Mitochondrial-Encoded Transcripts. Molecular Cell, 2017, 68, 993-1005.e9.	4.5	344
9	Crystal structures of DNA/RNA repair enzymes AlkB and ABH2 bound to dsDNA. Nature, 2008, 452, 961-965.	13.7	230
10	Mapping recently identified nucleotide variants in the genome and transcriptome. Nature Biotechnology, 2012, 30, 1107-1116.	9.4	197
11	Landscape and Regulation of m6A and m6Am Methylome across Human and Mouse Tissues. Molecular Cell, 2020, 77, 426-440.e6.	4.5	179
12	Mapping the epigenetic modifications of DNA and RNA. Protein and Cell, 2020, 11, 792-808.	4.8	174
13	Jasmonate-Activated MYC2 Represses ETHYLENE INSENSITIVE3 Activity to Antagonize Ethylene-Promoted Apical Hook Formation in <i>Arabidopsis</i> ÂÂ. Plant Cell, 2014, 26, 1105-1117.	3.1	171
14	Protein cysteine phosphorylation of SarA/MgrA family transcriptional regulators mediates bacterial virulence and antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15461-15466.	3.3	151
15	Bisulfite-free, base-resolution analysis of 5-formylcytosine at the genome scale. Nature Methods, 2015, 12, 1047-1050.	9.0	141
16	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. Cell Stem Cell, 2017, 20, 720-731.e5.	5.2	135
17	Chemical Modifications to RNA: A New Layer of Gene Expression Regulation. ACS Chemical Biology, 2017, 12, 316-325.	1.6	134
18	Analysis of RNA base modification and structural rearrangement by single-molecule real-time detection of reverse transcription. Journal of Nanobiotechnology, 2013, 11, 8.	4.2	131

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19	Cap-specific, terminal N6-methylation by a mammalian m6Am methyltransferase. Cell Research, 2019, 29, 80-82.	5.7	131
20	DNA Repair by Reversal of DNA Damage. Cold Spring Harbor Perspectives in Biology, 2013, 5, a012575-a012575.	2.3	121
21	Iron-catalysed oxidation intermediates captured in a DNA repair dioxygenase. Nature, 2010, 468, 330-333.	13.7	120
22	Pseudouridine: the fifth RNA nucleotide with renewed interests. Current Opinion in Chemical Biology, 2016, 33, 108-116.	2.8	120
23	Transcriptome-wide dynamics of RNA pseudouridylation. Nature Reviews Molecular Cell Biology, 2015, 16, 581-585.	16.1	107
24	A Non-Heme Iron-Mediated Chemical Demethylation in DNA and RNA. Accounts of Chemical Research, 2009, 42, 519-529.	7.6	102
25	Cellular Dynamics of RNA Modification. Accounts of Chemical Research, 2011, 44, 1380-1388.	7.6	98
26	The m6A methylome of SARS-CoV-2 in host cells. Cell Research, 2021, 31, 404-414.	5.7	95
27	N1-methyladenosineÂmethylation in tRNA drives liver tumourigenesis by regulating cholesterol metabolism. Nature Communications, 2021, 12, 6314.	5.8	81
28	Dynamics of spontaneous flipping of a mismatched base in DNA duplex. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8043-8048.	3.3	79
29	N1-methyladenosine methylome in messenger RNA and non-coding RNA. Current Opinion in Chemical Biology, 2018, 45, 179-186.	2.8	72
30	Bisulfite-Free, Nanoscale Analysis of 5-Hydroxymethylcytosine at Single Base Resolution. Journal of the American Chemical Society, 2018, 140, 13190-13194.	6.6	71
31	Differential roles of human PUS10 in miRNA processing and tRNA pseudouridylation. Nature Chemical Biology, 2020, 16, 160-169.	3.9	68
32	Baseâ€Resolution Analysis of Cisplatin–DNA Adducts at the Genome Scale. Angewandte Chemie - International Edition, 2016, 55, 14246-14249.	7.2	64
33	Targeting PUS7 suppresses tRNA pseudouridylation and glioblastoma tumorigenesis. Nature Cancer, 2021, 2, 932-949.	5.7	64
34	Duplex interrogation by a direct DNA repair protein in search of base damage. Nature Structural and Molecular Biology, 2012, 19, 671-676.	3.6	62
35	Mitochondrial base editor induces substantial nuclear off-target mutations. Nature, 2022, 606, 804-811.	13.7	62
36	Increasing the efficiency and precision of prime editing with guide RNA pairs. Nature Chemical Biology, 2022, 18, 29-37.	3.9	60

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37	Targeting MgrA-Mediated Virulence Regulation in Staphylococcus aureus. Chemistry and Biology, 2011, 18, 1032-1041.	6.2	55
38	Switching Demethylation Activities between AlkB Family RNA/DNA Demethylases through Exchange of Activeâ€6ite Residues. Angewandte Chemie - International Edition, 2014, 53, 3659-3662.	7.2	53
39	Tautomerization-dependent recognition and excision of oxidation damage in base-excision DNA repair. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7792-7797.	3.3	50
40	Tissue-specific 5-hydroxymethylcytosine landscape of the human genome. Nature Communications, 2021, 12, 4249.	5.8	50
41	Genome-wide mapping reveals that deoxyuridine is enriched in the human centromeric DNA. Nature Chemical Biology, 2018, 14, 680-687.	3.9	45
42	Structure determination of DNA methylation lesions N 1 -meA and N 3 -meC in duplex DNA using a cross-linked protein–DNA system. Nucleic Acids Research, 2010, 38, 4415-4425.	6.5	43
43	Transposase-assisted tagmentation of RNA/DNA hybrid duplexes. ELife, 2020, 9, .	2.8	40
44	Structural insight into the oxidationâ€sensing mechanism of the antibiotic resistance of regulator MexR. EMBO Reports, 2010, 11, 685-690.	2.0	38
45	m6Am-seq reveals the dynamic m6Am methylation in the human transcriptome. Nature Communications, 2021, 12, 4778.	5.8	38
46	A Radiolabelingâ€Free, qPCRâ€Based Method for Locusâ€5pecific Pseudouridine Detection. Angewandte Chemie - International Edition, 2017, 56, 14878-14882.	7.2	36
47	Liquid biopsies: DNA methylation analyses in circulating cell-free DNA. Journal of Genetics and Genomics, 2018, 45, 185-192.	1.7	36
48	Detect-seq reveals out-of-protospacer editing and target-strand editing by cytosine base editors. Nature Methods, 2021, 18, 643-651.	9.0	36
49	Decoding pseudouridine: an emerging target for therapeutic development. Trends in Pharmacological Sciences, 2022, 43, 522-535.	4.0	32
50	Epitranscriptomics: Toward A Better Understanding of RNA Modifications. Genomics, Proteomics and Bioinformatics, 2017, 15, 147-153.	3.0	31
51	Direct decarboxylation of ten-eleven translocation-produced 5-carboxylcytosine in mammalian genomes forms a new mechanism for active DNA demethylation. Chemical Science, 2021, 12, 11322-11329.	3.7	29
52	Genome-wide Mapping of Cellular Protein–RNA Interactions Enabled by Chemical Crosslinking. Genomics, Proteomics and Bioinformatics, 2014, 12, 72-78.	3.0	28
53	N6-methyladenosine regulates maternal RNA maintenance in oocytes and timely RNA decay during mouse maternal-to-zygotic transition. Nature Cell Biology, 2022, 24, 917-927.	4.6	28
54	Deciphering TAL effectors for 5-methylcytosine and 5-hydroxymethylcytosine recognition. Nature Communications, 2017, 8, 901.	5.8	26

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55	Biochemical and Structural Insights into the Mechanism of DNA Recognition by Arabidopsis ETHYLENE INSENSITIVE3. PLoS ONE, 2015, 10, e0137439.	1.1	24
56	Rationalization and prediction of selective decoding of pseudouridine-modified nonsense and sense codons. Rna, 2012, 18, 355-367.	1.6	23
57	Allosteric histidine switch for regulation of intracellular zinc(II) fluctuation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13661-13666.	3.3	22
58	Transformation of 5-Carboxylcytosine to Cytosine Through C–C Bond Cleavage in Human Cells Constitutes a Novel Pathway for DNA Demethylation. CCS Chemistry, 2021, 3, 994-1008.	4.6	21
59	Advances in single-cell multi-omics profiling. RSC Chemical Biology, 2021, 2, 441-449.	2.0	20
60	Perspectives on topology of the human m ¹ A methylome at single nucleotide resolution. Rna, 2018, 24, 1437-1442.	1.6	19
61	Reading Chemical Modifications in the Transcriptome. Journal of Molecular Biology, 2020, 432, 1824-1839.	2.0	18
62	The m ⁶ A Consensus Motif Provides a Paradigm of Epitranscriptomic Studies. Biochemistry, 2021, 60, 3410-3412.	1.2	16
63	m6Am methyltransferase PCIF1 is essential for aggressiveness of gastric cancer cells by inhibiting TM9SF1 mRNA translation. Cell Discovery, 2022, 8, .	3.1	16
64	Baseâ€Resolution Analysis of Cisplatin–DNA Adducts at the Genome Scale. Angewandte Chemie, 2016, 128, 14458-14461.	1.6	14
65	The epitranscriptome of small non-coding RNAs. Non-coding RNA Research, 2021, 6, 167-173.	2.4	13
66	Epitranscriptomic technologies and analyses. Science China Life Sciences, 2020, 63, 501-515.	2.3	12
67	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. Cell Discovery, 2021, 7, 19.	3.1	11
68	Transcriptome-Wide Mapping of N 1-Methyladenosine Methylome. Methods in Molecular Biology, 2017, 1562, 245-255.	0.4	10
69	Single-base resolution analysis of DNA epigenome via high-throughput sequencing. Science China Life Sciences, 2016, 59, 219-226.	2.3	9
70	Compilation of Modern Technologies To Map Genomeâ€Wide Cytosine Modifications in DNA. ChemBioChem, 2019, 20, 1898-1905.	1.3	9
71	Oxidative Demethylation of DNA and RNA Mediated by Nonâ€Heme Ironâ€Dependent Dioxygenases. Chemistry - an Asian Journal, 2014, 9, 2018-2029.	1.7	8
72	Unnatural Cytosine Bases Recognized as Thymines by DNA Polymerases by the Formation of the Watson–Crick Geometry. Angewandte Chemie - International Edition, 2019, 58, 130-133.	7.2	8

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73	DNA repair glycosylase hNEIL1 triages damaged bases via competing interaction modes. Nature Communications, 2021, 12, 4108.	5.8	8
74	Structural Insights into the Specific Recognition of 5-methylcytosine and 5-hydroxymethylcytosine by TAL Effectors. Journal of Molecular Biology, 2020, 432, 1035-1047.	2.0	6
75	m6Am RNA modification detection by m6Am-seq. Methods, 2022, 203, 242-248.	1.9	6
76	Pseudouridine Chemical Labeling and Profiling. Methods in Enzymology, 2015, 560, 247-272.	0.4	5
77	AlkB recognition of a bulky DNA base adduct stabilized by chemical cross-linking. Science China Chemistry, 2010, 53, 86-90.	4.2	4
78	Advances in the Profiling of Single ell DNA Modifications. Small Methods, 2019, 3, 1900137.	4.6	4
79	Metatranscriptomic analysis of host response and vaginal microbiome of patients with severe COVID-19. Science China Life Sciences, 2022, , 1.	2.3	4
80	Coupling Transcription and Translation via the Epitranscriptomic m6A Mark. Biochemistry, 2019, 58, 297-298.	1.2	3
81	Single-Cell 5fC Sequencing. Methods in Molecular Biology, 2019, 1979, 251-267.	0.4	2
82	Acetylation Enhances mRNA Stability and Translation. Biochemistry, 2019, 58, 1553-1554.	1.2	2
83	Structural insight into the oxidationâ€sensing mechanism of the antibiotic resistance of regulator MexR. EMBO Reports, 2010, 11, 717-717.	2.0	1
84	Probing enzyme-mediated oxidation reactions in crystallo. Pure and Applied Chemistry, 2011, 83, 2199-2212.	0.9	1
85	A Radiolabelingâ€Free, qPCRâ€Based Method for Locusâ€Specific Pseudouridine Detection. Angewandte Chemie, 2017, 129, 15074-15078.	1.6	1
86	Unnatural Cytosine Bases Recognized as Thymines by DNA Polymerases by the Formation of the Watson–Crick Geometry. Angewandte Chemie, 2019, 131, 136-139.	1.6	1
87	A Novel Epigenetic Mark Derived from Vitamin C. Biochemistry, 2020, 59, 8-9.	1.2	1
88	Characterization of m ⁶ A modifications in the contemporary Zika virus genome and host cellular transcripts. Journal of Medical Virology, 2022, 94, 4309-4318.	2.5	1
89	Mixed methods. PLoS Genetics, 2020, 16, e1008950.	1.5	0