

Chengqi Yi

List of Publications by Year in Descending Order

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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.

83

papers

7,064

citations

33

h-index

84

g-index

99

ext. papers

8,927

ext. citations

13.3

avg, IF

6.02

L-index

#	Paper	IF	Citations
83	Metatranscriptomic analysis of host response and vaginal microbiome of patients with severe COVID-19.. <i>Science China Life Sciences</i> , 2022 , 1	8.5	0
82	N-methyladenosine methylation in tRNA drives liver tumorigenesis by regulating cholesterol metabolism. <i>Nature Communications</i> , 2021 , 12, 6314	17.4	6
81	The epitranscriptome of small non-coding RNAs. <i>Non-coding RNA Research</i> , 2021 , 6, 167-173	6	2
80	Increasing the efficiency and precision of prime editing with guide RNA pairs. <i>Nature Chemical Biology</i> , 2021 ,	11.7	7
79	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. <i>Cell Discovery</i> , 2021 , 7, 19	22.3	3
78	Transformation of 5-Carboxylcytosine to Cytosine Through C-C Bond Cleavage in Human Cells Constitutes a Novel Pathway for DNA Demethylation. <i>CCS Chemistry</i> , 2021 , 3, 994-1008	7.2	9
77	The mA Consensus Motif Provides a Paradigm of Epitranscriptomic Studies. <i>Biochemistry</i> , 2021 , 60, 3410-3412	32.12	4
76	Detect-seq reveals out-of-protospacer editing and target-strand editing by cytosine base editors. <i>Nature Methods</i> , 2021 , 18, 643-651	21.6	9
75	Tissue-specific 5-hydroxymethylcytosine landscape of the human genome. <i>Nature Communications</i> , 2021 , 12, 4249	17.4	5
74	Direct decarboxylation of ten-eleven translocation-produced 5-carboxylcytosine in mammalian genomes forms a new mechanism for active DNA demethylation. <i>Chemical Science</i> , 2021 , 12, 11322-11329	9.4	8
73	The mA methylome of SARS-CoV-2 in host cells. <i>Cell Research</i> , 2021 , 31, 404-414	24.7	28
72	DNA repair glycosylase hNEIL1 triages damaged bases via competing interaction modes. <i>Nature Communications</i> , 2021 , 12, 4108	17.4	1
71	Targeting PUS7 suppresses tRNA pseudouridylation and glioblastoma tumorigenesis.. <i>Nature Cancer</i> , 2021 , 2, 932-949	15.4	6
70	mAm-seq reveals the dynamic mAm methylation in the human transcriptome. <i>Nature Communications</i> , 2021 , 12, 4778	17.4	5
69	Advances in single-cell multi-omics profiling. <i>RSC Chemical Biology</i> , 2021 , 2, 441-449	3	5
68	Epitranscriptomic technologies and analyses. <i>Science China Life Sciences</i> , 2020 , 63, 501-515	8.5	4
67	Transposase-assisted tagmentation of RNA/DNA hybrid duplexes. <i>ELife</i> , 2020 , 9,	8.9	16

66	Mapping the epigenetic modifications of DNA and RNA. <i>Protein and Cell</i> , 2020 , 11, 792-808	7.2	55
65	Landscape and Regulation of mA and mAm Methylome across Human and Mouse Tissues. <i>Molecular Cell</i> , 2020 , 77, 426-440.e6	17.6	77
64	Structural Insights into the Specific Recognition of 5-methylcytosine and 5-hydroxymethylcytosine by TAL Effectors. <i>Journal of Molecular Biology</i> , 2020 , 432, 1035-1047	6.5	4
63	Differential roles of human PUS10 in miRNA processing and tRNA pseudouridylation. <i>Nature Chemical Biology</i> , 2020 , 16, 160-169	11.7	28
62	Advances in the Profiling of Single-Cell DNA Modifications. <i>Small Methods</i> , 2019 , 3, 1900137	12.8	3
61	Single-Cell 5fC Sequencing. <i>Methods in Molecular Biology</i> , 2019 , 1979, 251-267	1.4	0
60	Compilation of Modern Technologies To Map Genome-Wide Cytosine Modifications in DNA. <i>ChemBioChem</i> , 2019 , 20, 1898-1905	3.8	8
59	Acetylation Enhances mRNA Stability and Translation. <i>Biochemistry</i> , 2019 , 58, 1553-1554	3.2	1
58	Unnatural Cytosine Bases Recognized as Thymines by DNA Polymerases by the Formation of the Watson-Crick Geometry. <i>Angewandte Chemie</i> , 2019 , 131, 136-139	3.6	1
57	Unnatural Cytosine Bases Recognized as Thymines by DNA Polymerases by the Formation of the Watson-Crick Geometry. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 130-133	16.4	5
56	Cap-specific, terminal N-methylation by a mammalian mAm methyltransferase. <i>Cell Research</i> , 2019 , 29, 80-82	24.7	86
55	Coupling Transcription and Translation via the Epitranscriptomic mA Mark. <i>Biochemistry</i> , 2019 , 58, 297-298	2.8	2
54	Reading Chemical Modifications in the Transcriptome. <i>Journal of Molecular Biology</i> , 2019 , 432, 1824-1826	6.5	10
53	Liquid biopsies: DNA methylation analyses in circulating cell-free DNA. <i>Journal of Genetics and Genomics</i> , 2018 , 45, 185-192	4	24
52	N-methyladenosine methylome in messenger RNA and non-coding RNA. <i>Current Opinion in Chemical Biology</i> , 2018 , 45, 179-186	9.7	37
51	Perspectives on topology of the human mA methylome at single nucleotide resolution. <i>Rna</i> , 2018 , 24, 1437-1442	5.8	11
50	Bisulfite-Free, Nanoscale Analysis of 5-Hydroxymethylcytosine at Single Base Resolution. <i>Journal of the American Chemical Society</i> , 2018 , 140, 13190-13194	16.4	42
49	Genome-wide mapping reveals that deoxyuridine is enriched in the human centromeric DNA. <i>Nature Chemical Biology</i> , 2018 , 14, 680-687	11.7	28

48	Epitranscriptomics: Toward A Better Understanding of RNA Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2017 , 15, 147-153	6.5	18
47	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. <i>Cell Stem Cell</i> , 2017 , 20, 720-731.e5	18	93
46	Transcriptome-Wide Mapping of N ⁶ -Methyladenosine Methylome. <i>Methods in Molecular Biology</i> , 2017 , 1562, 245-255	1.4	8
45	Chemical Modifications to RNA: A New Layer of Gene Expression Regulation. <i>ACS Chemical Biology</i> , 2017 , 12, 316-325	4.9	95
44	A Radiolabeling-Free, qPCR-Based Method for Locus-Specific Pseudouridine Detection. <i>Angewandte Chemie</i> , 2017 , 129, 15074-15078	3.6	0
43	A Radiolabeling-Free, qPCR-Based Method for Locus-Specific Pseudouridine Detection. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 14878-14882	16.4	21
42	Deciphering TAL effectors for 5-methylcytosine and 5-hydroxymethylcytosine recognition. <i>Nature Communications</i> , 2017 , 8, 901	17.4	19
41	Allosteric histidine switch for regulation of intracellular zinc(II) fluctuation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 13661-13666	11.5	15
40	Base-Resolution Mapping Reveals Distinct mA Methylome in Nuclear- and Mitochondrial-Encoded Transcripts. <i>Molecular Cell</i> , 2017 , 68, 993-1005.e9	17.6	210
39	Epitranscriptome sequencing technologies: decoding RNA modifications. <i>Nature Methods</i> , 2016 , 14, 23-31	11.6	241
38	Base-Resolution Analysis of Cisplatin-DNA Adducts at the Genome Scale. <i>Angewandte Chemie</i> , 2016 , 128, 14458-14461	3.6	14
37	Pseudouridine: the fifth RNA nucleotide with renewed interests. <i>Current Opinion in Chemical Biology</i> , 2016 , 33, 108-16	9.7	76
36	Tautomerization-dependent recognition and excision of oxidation damage in base-excision DNA repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 7792-7	11.5	29
35	Transcriptome-wide mapping reveals reversible and dynamic N ¹ -methyladenosine methylome. <i>Nature Chemical Biology</i> , 2016 , 12, 311-6	11.7	337
34	Single-base resolution analysis of DNA epigenome via high-throughput sequencing. <i>Science China Life Sciences</i> , 2016 , 59, 219-26	8.5	5
33	Base-Resolution Analysis of Cisplatin-DNA Adducts at the Genome Scale. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 14246-14249	16.4	51
32	Chemical pulldown reveals dynamic pseudouridylation of the mammalian transcriptome. <i>Nature Chemical Biology</i> , 2015 , 11, 592-7	11.7	295
31	Pseudouridine Chemical Labeling and Profiling. <i>Methods in Enzymology</i> , 2015 , 560, 247-72	1.7	4

30	Efficient and quantitative high-throughput tRNA sequencing. <i>Nature Methods</i> , 2015 , 12, 835-837	21.6	291
29	Transcriptome-wide dynamics of RNA pseudouridylation. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 581-5	48.7	75
28	Bisulfite-free, base-resolution analysis of 5-formylcytosine at the genome scale. <i>Nature Methods</i> , 2015 , 12, 1047-50	21.6	106
27	Biochemical and Structural Insights into the Mechanism of DNA Recognition by Arabidopsis ETHYLENE INSENSITIVE3. <i>PLoS ONE</i> , 2015 , 10, e0137439	3.7	12
26	Switching demethylation activities between AlkB family RNA/DNA demethylases through exchange of active-site residues. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 3659-62	16.4	43
25	Oxidative demethylation of DNA and RNA mediated by non-heme iron-dependent dioxygenases. <i>Chemistry - an Asian Journal</i> , 2014 , 9, 2018-29	4.5	6
24	Dynamics of spontaneous flipping of a mismatched base in DNA duplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8043-8	11.5	64
23	Jasmonate-activated MYC2 represses ETHYLENE INSENSITIVE3 activity to antagonize ethylene-promoted apical hook formation in Arabidopsis. <i>Plant Cell</i> , 2014 , 26, 1105-17	11.6	122
22	Genome-wide mapping of cellular protein-RNA interactions enabled by chemical crosslinking. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 72-8	6.5	21
21	Switching Demethylation Activities between AlkB Family RNA/DNA Demethylases through Exchange of Active-Site Residues. <i>Angewandte Chemie</i> , 2014 , 126, 3733-3736	3.6	5
20	Analysis of RNA base modification and structural rearrangement by single-molecule real-time detection of reverse transcription. <i>Journal of Nanobiotechnology</i> , 2013 , 11, 8	9.4	97
19	DNA repair by reversal of DNA damage. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5, a012575	10.2	91
18	Mapping recently identified nucleotide variants in the genome and transcriptome. <i>Nature Biotechnology</i> , 2012 , 30, 1107-16	44.5	179
17	Duplex interrogation by a direct DNA repair protein in search of base damage. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 671-6	17.6	49
16	Rationalization and prediction of selective decoding of pseudouridine-modified nonsense and sense codons. <i>Rna</i> , 2012 , 18, 355-67	5.8	20
15	Protein cysteine phosphorylation of SarA/MgrA family transcriptional regulators mediates bacterial virulence and antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15461-6	11.5	124
14	N6-methyladenosine in nuclear RNA is a major substrate of the obesity-associated FTO. <i>Nature Chemical Biology</i> , 2011 , 7, 885-7	11.7	1937
13	Cellular dynamics of RNA modification. <i>Accounts of Chemical Research</i> , 2011 , 44, 1380-8	24.3	83

12	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. <i>Nature Biotechnology</i> , 2011 , 29, 68-72	44.5	816
11	Targeting MgrA-mediated virulence regulation in <i>Staphylococcus aureus</i> . <i>Chemistry and Biology</i> , 2011 , 18, 1032-41		44
10	Probing enzyme-mediated oxidation reactions in crystallo. <i>Pure and Applied Chemistry</i> , 2011 , 83, 2199-2212		1
9	Structural insight into the oxidation-sensing mechanism of the antibiotic resistance of regulator MexR. <i>EMBO Reports</i> , 2010 , 11, 717-717	6.5	0
8	Structural insight into the oxidation-sensing mechanism of the antibiotic resistance of regulator MexR. <i>EMBO Reports</i> , 2010 , 11, 685-90	6.5	33
7	Iron-catalysed oxidation intermediates captured in a DNA repair dioxygenase. <i>Nature</i> , 2010 , 468, 330-3	50.4	109
6	Structure determination of DNA methylation lesions N1-meA and N3-meC in duplex DNA using a cross-linked protein-DNA system. <i>Nucleic Acids Research</i> , 2010 , 38, 4415-25	20.1	36
5	AlkB recognition of a bulky DNA base adduct stabilized by chemical cross-linking. <i>Science China Chemistry</i> , 2010 , 53, 86-90	7.9	2
4	A non-heme iron-mediated chemical demethylation in DNA and RNA. <i>Accounts of Chemical Research</i> , 2009 , 42, 519-29	24.3	90
3	Crystal structures of DNA/RNA repair enzymes AlkB and ABH2 bound to dsDNA. <i>Nature</i> , 2008 , 452, 961-5	50.4	203
2	Oxidative demethylation of 3-methylthymine and 3-methyluracil in single-stranded DNA and RNA by mouse and human FTO. <i>FEBS Letters</i> , 2008 , 582, 3313-9	3.8	302
1	Transposase assisted tagmentation of RNA/DNA hybrid duplexes		1