

Tao Pan

List of Publications by Year in descending order

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89
papers

14,953
citations

81900

39
h-index

45317

90
g-index

103
all docs

103
docs citations

103
times ranked

12867
citing authors

#	ARTICLE	IF	CITATIONS
1	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014, 505, 117-120.	27.8	3,138
2	Dynamic RNA Modifications in Gene Expression Regulation. <i>Cell</i> , 2017, 169, 1187-1200.	28.9	2,222
3	N6-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , 2015, 518, 560-564.	27.8	1,482
4	The dynamic N1-methyladenosine methylome in eukaryotic messenger RNA. <i>Nature</i> , 2016, 530, 441-446.	27.8	765
5	N 6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017, 45, 6051-6063.	14.5	586
6	Efficient and quantitative high-throughput tRNA sequencing. <i>Nature Methods</i> , 2015, 12, 835-837.	19.0	426
7	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. <i>Cell</i> , 2015, 162, 1286-1298.	28.9	395
8	ALKBH1-Mediated tRNA Demethylation Regulates Translation. <i>Cell</i> , 2016, 167, 816-828.e16.	28.9	366
9	N6-methyladenosine-encoded epitranscriptomics. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 98-102.	8.2	266
10	Modifications and functional genomics of human transfer RNA. <i>Cell Research</i> , 2018, 28, 395-404.	12.0	260
11	N6-Methyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. <i>Nature Chemical Biology</i> , 2019, 15, 88-94.	8.0	258
12	Regulation of Co-transcriptional Pre-mRNA Splicing by m6A through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019, 76, 70-81.e9.	9.7	248
13	A Role for tRNA Modifications in Genome Structure and Codon Usage. <i>Cell</i> , 2012, 149, 202-213.	28.9	239
14	Angiogenin-Cleaved tRNA Halves Interact with Cytochrome <i>c</i> , Protecting Cells from Apoptosis during Osmotic Stress. <i>Molecular and Cellular Biology</i> , 2014, 34, 2450-2463.	2.3	236
15	RNA FOLDING DURING TRANSCRIPTION. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 161-175.	18.3	227
16	RNA modifications and structures cooperate to guide RNA-protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 202-210.	37.0	225
17	RNA modifications: what have we learned and where are we headed?. <i>Nature Reviews Genetics</i> , 2016, 17, 365-372.	16.3	215
18	Intermediates and kinetic traps in the folding of a large ribozyme revealed by circular dichroism and UV absorbance spectroscopies and catalytic activity. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 931-938.	8.2	184

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19	N6-methyl-adenosine modification in messenger and long non-coding RNA. Trends in Biochemical Sciences, 2013, 38, 204-209.	7.5	181
20	Diversity of tRNA genes in eukaryotes. Nucleic Acids Research, 2006, 34, 6137-6146.	14.5	180
21	N6-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. Journal of Molecular Biology, 2016, 428, 822-833.	4.2	164
22	tRNA base methylation identification and quantification via high-throughput sequencing. Rna, 2016, 22, 1771-1784.	3.5	148
23	The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA. Angewandte Chemie - International Edition, 2010, 49, 8885-8888.	13.8	129
24	Mg ²⁺ -Dependent Compaction and Folding of Yeast tRNA ^{Phe} and the Catalytic Domain of the B. subtilis RNase P RNA Determined by Small-Angle X-ray Scattering. Biochemistry, 2000, 39, 11107-11113.	2.5	118
25	RNA epigenetics. Translational Research, 2015, 165, 28-35.	5.0	111
26	Recognition of the T Stem Loop of a Pre-tRNA Substrate by the Ribozyme from Bacillus subtilis Ribonuclease P. Biochemistry, 1997, 36, 6317-6325.	2.5	109
27	Mg ²⁺ -dependent folding of a large ribozyme without kinetic traps. Nature Structural Biology, 1999, 6, 1091-1095.	9.7	108
28	Adaptive Translation as a Mechanism of Stress Response and Adaptation. Annual Review of Genetics, 2013, 47, 121-137.	7.6	102
29	A Thermodynamic Framework and Cooperativity in the Tertiary Folding of a Mg ²⁺ -Dependent Ribozyme. Biochemistry, 1999, 38, 16840-16846.	2.5	99
30	A Nutrient-Driven tRNA Modification Alters Translational Fidelity and Genome-wide Protein Coding across an Animal Genus. PLoS Biology, 2014, 12, e1002015.	5.6	93
31	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. Rna, 2018, 24, 1305-1313.	3.5	92
32	Diversity of human tRNA genes from the 1000-genomes project. RNA Biology, 2013, 10, 1853-1867.	3.1	79
33	Determination of tRNA aminoacylation levels by high-throughput sequencing. Nucleic Acids Research, 2017, 45, e133-e133.	14.5	72
34	Temperature dependent mistranslation in a hyperthermophile adapts proteins to lower temperatures. Nucleic Acids Research, 2016, 44, 294-303.	14.5	67
35	RNA modification landscape of the human mitochondrial tRNA ^{Lys} regulates protein synthesis. Nature Communications, 2018, 9, 3966.	12.8	61
36	Recognition of the 5' Leader and the Acceptor Stem of a Pre-tRNA Substrate by the Ribozyme from Bacillus subtilis RNase P. Biochemistry, 1998, 37, 10126-10133.	2.5	57

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37	The Bacillus subtilis RNase P holoenzyme contains two RNase P RNA and two RNase P protein subunits. <i>Rna</i> , 2001, 7, 233-241.	3.5	54
38	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018, 9, 5353.	12.8	48
39	Codon optimality controls differential mRNA translation during amino acid starvation. <i>Rna</i> , 2016, 22, 1719-1727.	3.5	47
40	The Cleavage Step of Ribonuclease P Catalysis Is Determined by Ribozyme-Substrate Interactions both Distal and Proximal to the Cleavage Site. <i>Biochemistry</i> , 1999, 38, 8612-8620.	2.5	46
41	Selective Enzymatic Demethylation of <i>N²,N²</i> -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5017-5020.	13.8	44
42	tRNA modification dynamics from individual organisms to metaepitranscriptomics of microbiomes. <i>Molecular Cell</i> , 2022, 82, 891-906.	9.7	44
43	Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. <i>Genome Biology</i> , 2021, 22, 330.	8.8	44
44	Sensitive and quantitative probing of pseudouridine modification in mRNA and long noncoding RNA. <i>Rna</i> , 2019, 25, 1218-1225.	3.5	41
45	ALKBH7-mediated demethylation regulates mitochondrial polycistronic RNA processing. <i>Nature Cell Biology</i> , 2021, 23, 684-691.	10.3	41
46	Structures of the m ⁶ A Methyltransferase Complex: Two Subunits with Distinct but Coordinated Roles. <i>Molecular Cell</i> , 2016, 63, 183-185.	9.7	40
47	HIV protease cleaves the antiviral m ⁶ A reader protein YTHDF3 in the viral particle. <i>PLoS Pathogens</i> , 2020, 16, e1008305.	4.7	40
48	Function and origin of mistranslation in distinct cellular contexts. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 205-219.	5.2	38
49	Transcriptome-wide reprogramming of N ⁶ -methyladenosine modification by the mouse microbiome. <i>Cell Research</i> , 2019, 29, 167-170.	12.0	38
50	tRNA Queuosine Modification Enzyme Modulates the Growth and Microbiome Recruitment to Breast Tumors. <i>Cancers</i> , 2020, 12, 628.	3.7	38
51	Probing RNA Modification Status at Single-Nucleotide Resolution in Total RNA. <i>Methods in Enzymology</i> , 2015, 560, 149-159.	1.0	37
52	An additional class of m ⁶ A readers. <i>Nature Cell Biology</i> , 2018, 20, 230-232.	10.3	37
53	Evolutionary Gain of Alanine Mischarging to Noncognate tRNAs with a G4:U69 Base Pair. <i>Journal of the American Chemical Society</i> , 2016, 138, 12948-12955.	13.7	35
54	Altering the Intermediate in the Equilibrium Folding of Unmodified Yeast tRNA ^{Phe} with Monovalent and Divalent Cations. <i>Biochemistry</i> , 2001, 40, 3629-3638.	2.5	34

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55	Modular construction for function of a ribonucleoprotein enzyme: the catalytic domain of <i>Bacillus subtilis</i> RNase P complexed with <i>B. subtilis</i> RNase P protein. <i>Nucleic Acids Research</i> , 2001, 29, 1892-1897.	14.5	34
56	Modular Construction of a Tertiary RNA Structure: The Specificity Domain of the <i>Bacillus subtilis</i> RNase P RNA. <i>Biochemistry</i> , 2001, 40, 11202-11210.	2.5	32
57	Global tRNA misacylation induced by anaerobiosis and antibiotic exposure broadly increases stress resistance in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, gkw856.	14.5	31
58	CMT disease severity correlates with mutation-induced open conformation of histidyl-tRNA synthetase, not aminoacylation loss, in patient cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19440-19448.	7.1	28
59	Pseudouridines have context-dependent mutation and stop rates in high-throughput sequencing. <i>RNA Biology</i> , 2018, 15, 892-900.	3.1	25
60	Stress Response and Adaptation Mediated by Amino Acid Misincorporation during Protein Synthesis. <i>Advances in Nutrition</i> , 2016, 7, 773S-779S.	6.4	24
61	5-Methylcytosine RNA Modifications Promote Retrovirus Replication in an ALYREF Reader Protein-Dependent Manner. <i>Journal of Virology</i> , 2020, 94, .	3.4	22
62	Probing N 6-methyladenosine (m6A) RNA Modification in Total RNA with SCARLET. <i>Methods in Molecular Biology</i> , 2016, 1358, 285-292.	0.9	21
63	Methionine Mistranslation Bypasses the Restraint of the Genetic Code to Generate Mutant Proteins with Distinct Activities. <i>PLoS Genetics</i> , 2015, 11, e1005745.	3.5	21
64	A multiplex platform for small RNA sequencing elucidates multifaceted tRNA stress response and translational regulation. <i>Nature Communications</i> , 2022, 13, 2491.	12.8	21
65	The 3' substrate determinants for the catalytic efficiency of the <i>Bacillus subtilis</i> RNase P holoenzyme suggest autolytic processing of the RNase P RNA in vivo. <i>Rna</i> , 2000, 6, 1413-1422.	3.5	20
66	Design and isolation of ribozyme-substrate pairs using RNase P-based ribozymes containing altered substrate binding sites. <i>Nucleic Acids Research</i> , 1999, 27, 4298-4304.	14.5	18
67	CMT2N-causing aminoacylation domain mutants enable Nrp1 interaction with AlaRS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	16
68	Hili Inhibits HIV Replication in Activated T Cells. <i>Journal of Virology</i> , 2017, 91, .	3.4	15
69	A dual fluorescent reporter for the investigation of methionine mistranslation in live cells. <i>Rna</i> , 2016, 22, 467-476.	3.5	14
70	Detection and quantification of glycosylated queuosine modified tRNAs by acid denaturing and APB gels. <i>Rna</i> , 2020, 26, 1291-1298.	3.5	13
71	Determining the fidelity of tRNA aminoacylation via microarrays. <i>Methods</i> , 2017, 113, 27-33.	3.8	11
72	Tissue-specific reprogramming of host tRNA transcriptome by the microbiome. <i>Genome Research</i> , 2021, 31, 947-957.	5.5	11

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73	A high-throughput screening method for evolving a demethylase enzyme with improved and new functionalities. <i>Nucleic Acids Research</i> , 2021, 49, e30-e30.	14.5	11
74	Cross-editing by a tRNA synthetase allows vertebrates to abundantly express mischargeable tRNA without causing mistranslation. <i>Nucleic Acids Research</i> , 2020, 48, 6445-6457.	14.5	10
75	Interaction of tRNA with MEK2 in pancreatic cancer cells. <i>Scientific Reports</i> , 2016, 6, 28260.	3.3	8
76	Analysis of queuosine and 2-thio tRNA modifications by high throughput sequencing. <i>Nucleic Acids Research</i> , 2022, 50, e99-e99.	14.5	8
77	tRNA Misacylation with Methionine in the Mouse Gut Microbiome in Situ. <i>Microbial Ecology</i> , 2017, 74, 10-14.	2.8	6
78	Pseudouridine RNA modification detection and quantification by RT-PCR. <i>Methods</i> , 2022, 203, 1-4.	3.8	6
79	Identification of N ⁶ -methyladenosine reader proteins. <i>Methods</i> , 2017, 126, 105-111.	3.8	5
80	Quantitative probing of glycosylated queuosine modifications in tRNA. <i>Methods in Enzymology</i> , 2021, 658, 73-82.	1.0	4
81	Quantification of Queuosine Modification Levels in tRNA from Human Cells Using APB Gel and Northern Blot. <i>Bio-protocol</i> , 2019, 9, e3191.	0.4	4
82	My adventure in tRNA biology, so far. <i>Rna</i> , 2015, 21, 707-708.	3.5	3
83	Selective Enzymatic Demethylation of N ² ,N ² -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie</i> , 2017, 129, 5099-5102.	2.0	3
84	Cover Picture: The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA (<i>Angew. Chem. Int. Ed.</i> 47/2010). <i>Angewandte Chemie - International Edition</i> , 2010, 49, 8765-8765.	13.8	2
85	Profiling Selective Packaging of Host RNA and Viral RNA Modification in SARS-CoV-2 Viral Preparations. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 768356.	3.7	2
86	A dual function PUS enzyme. <i>Nature Chemical Biology</i> , 2020, 16, 107-108.	8.0	1
87	Titelbild: The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA (<i>Angew. Chem.</i> 47/2010). <i>Angewandte Chemie</i> , 2010, 122, 8947-8947.	2.0	0
88	Mistranslation as a potential, new mechanism of adaption and stress response. <i>FASEB Journal</i> , 2013, 27, 325.2.	0.5	0
89	Methionine Misacylation of tRNA on CaMKII in Response to ER Stress. <i>FASEB Journal</i> , 2015, 29, 892.7.	0.5	0