

Tao Pan

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.

90 papers	9,698 citations	36 h-index	98 g-index
103 ext. papers	12,649 ext. citations	14.1 avg, IF	6.73 L-index

#	Paper	IF	Citations
90	tRNA modification dynamics from individual organisms to metaepitranscriptomics of microbiomes.. <i>Molecular Cell</i> , 2022 ,	17.6	2
89	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	5.7	0
88	A multiplex platform for small RNA sequencing elucidates multifaceted tRNA stress response and translational regulation.. <i>Nature Communications</i> , 2022 , 13, 2491	17.4	1
87	A high-throughput screening method for evolving a demethylase enzyme with improved and new functionalities. <i>Nucleic Acids Research</i> , 2021 , 49, e30	20.1	6
86	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,	11.5	2
85	Tissue-specific reprogramming of host tRNA transcriptome by the microbiome. <i>Genome Research</i> , 2021 , 31, 947-957	9.7	2
84	Pseudouridine RNA modification detection and quantification by RT-PCR. <i>Methods</i> , 2021 ,	4.6	2
83	ALKBH7-mediated demethylation regulates mitochondrial polycistronic RNA processing. <i>Nature Cell Biology</i> , 2021 , 23, 684-691	23.4	10
82	Quantitative probing of glycosylated queuosine modifications in tRNA. <i>Methods in Enzymology</i> , 2021 , 658, 73-82	1.7	2
81	Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. <i>Genome Biology</i> , 2021 , 22, 330	18.3	6
80	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	20.1	7
79	tRNA Queuosine Modification Enzyme Modulates the Growth and Microbiome Recruitment to Breast Tumors. <i>Cancers</i> , 2020 , 12,	6.6	10
78	HIV protease cleaves the antiviral m6A reader protein YTHDF3 in the viral particle. <i>PLoS Pathogens</i> , 2020 , 16, e1008305	7.6	25
77	A dual function PUS enzyme. <i>Nature Chemical Biology</i> , 2020 , 16, 107-108	11.7	1
76	5-Methylcytosine RNA Modifications Promote Retrovirus Replication in an ALYREF Reader Protein-Dependent Manner. <i>Journal of Virology</i> , 2020 , 94,	6.6	13
75	Detection and quantification of glycosylated queuosine modified tRNAs by acid denaturing and APB gels. <i>Rna</i> , 2020 , 26, 1291-1298	5.8	6
74	Regulation of Co-transcriptional Pre-mRNA Splicing by mA through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019 , 76, 70-81.e9	17.6	124

73	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	11.5	16
72	Sensitive and quantitative probing of pseudouridine modification in mRNA and long noncoding RNA. <i>Rna</i> , 2019 , 25, 1218-1225	5.8	21
71	Quantification of Queuosine Modification Levels in tRNA from Human Cells Using APB Gel and Northern Blot. <i>Bio-protocol</i> , 2019 , 9, e3191	0.9	1
70	Transcriptome-wide reprogramming of N-methyladenosine modification by the mouse microbiome. <i>Cell Research</i> , 2019 , 29, 167-170	24.7	19
69	NMethyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. <i>Nature Chemical Biology</i> , 2019 , 15, 88-94	11.7	149
68	Modifications and functional genomics of human transfer RNA. <i>Cell Research</i> , 2018 , 28, 395-404	24.7	155
67	An additional class of mA readers. <i>Nature Cell Biology</i> , 2018 , 20, 230-232	23.4	22
66	Pseudouridines have context-dependent mutation and stop rates in high-throughput sequencing. <i>RNA Biology</i> , 2018 , 15, 892-900	4.8	18
65	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018 , 9, 5353	17.4	31
64	RNA modification landscape of the human mitochondrial tRNA regulates protein synthesis. <i>Nature Communications</i> , 2018 , 9, 3966	17.4	36
63	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. <i>Rna</i> , 2018 , 24, 1305-1313	3.8	56
62	RNA modifications and structures cooperate to guide RNA-protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2017 , 18, 202-210	48.7	153
61	Function and origin of mistranslation in distinct cellular contexts. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017 , 52, 205-219	8.7	25
60	tRNA Misacylation with Methionine in the Mouse Gut Microbiome in Situ. <i>Microbial Ecology</i> , 2017 , 74, 10-14	4.4	4
59	N6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017 , 45, 6051-6063	20.1	339
58	Identification of N-methyladenosine reader proteins. <i>Methods</i> , 2017 , 126, 105-111	4.6	4
57	Dynamic RNA Modifications in Gene Expression Regulation. <i>Cell</i> , 2017 , 169, 1187-1200	56.2	1250
56	Determination of tRNA aminoacylation levels by high-throughput sequencing. <i>Nucleic Acids Research</i> , 2017 , 45, e133	20.1	33

55	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	3.6	3
54	Hili Inhibits HIV Replication in Activated T Cells. <i>Journal of Virology</i> , 2017 , 91,	6.6	12
53	Selective Enzymatic Demethylation of N ² ,N ² -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 5017-5020	16.4	30
52	Determining the fidelity of tRNA aminoacylation via microarrays. <i>Methods</i> , 2017 , 113, 27-33	4.6	7
51	N(6)-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016 , 428, 822-833	6.5	122
50	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	16.4	27
49	Stress Response and Adaptation Mediated by Amino Acid Misincorporation during Protein Synthesis. <i>Advances in Nutrition</i> , 2016 , 7, 773S-9S	10	14
48	Structures of the m(6)A Methyltransferase Complex: Two Subunits with Distinct but Coordinated Roles. <i>Molecular Cell</i> , 2016 , 63, 183-185	17.6	22
47	ALKBH1-Mediated tRNA Demethylation Regulates Translation. <i>Cell</i> , 2016 , 167, 816-828.e16	56.2	197
46	Interaction of tRNA with MEK2 in pancreatic cancer cells. <i>Scientific Reports</i> , 2016 , 6, 28260	4.9	8
45	The dynamic N(1)-methyladenosine methylome in eukaryotic messenger RNA. <i>Nature</i> , 2016 , 530, 441-6	50.4	523
44	N6-methyladenosine-encoded epitranscriptomics. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 98-102	17.6	188
43	Temperature dependent mistranslation in a hyperthermophile adapts proteins to lower temperatures. <i>Nucleic Acids Research</i> , 2016 , 44, 294-303	20.1	31
42	A dual fluorescent reporter for the investigation of methionine mistranslation in live cells. <i>Rna</i> , 2016 , 22, 467-76	5.8	11
41	Probing N ⁶ -methyladenosine (m ⁶ A) RNA Modification in Total RNA with SCARLET. <i>Methods in Molecular Biology</i> , 2016 , 1358, 285-92	1.4	16
40	RNA modifications: what have we learned and where are we headed?. <i>Nature Reviews Genetics</i> , 2016 , 17, 365-72	30.1	144
39	tRNA base methylation identification and quantification via high-throughput sequencing. <i>Rna</i> , 2016 , 22, 1771-1784	5.8	100
38	Codon optimality controls differential mRNA translation during amino acid starvation. <i>Rna</i> , 2016 , 22, 1719-1727	5.8	29

37	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, 10292-10303	20.1	19
36	N(6)-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , 2015 , 518, 560-4	50.4	988
35	Efficient and quantitative high-throughput tRNA sequencing. <i>Nature Methods</i> , 2015 , 12, 835-837	21.6	291
34	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. <i>Cell</i> , 2015 , 162, 1286-98	56.2	264
33	RNA epigenetics. <i>Translational Research</i> , 2015 , 165, 28-35	11	86
32	High-Resolution N6-Methyladenosine (m6A) Map Using Photo-Crosslinking-Assisted m6A Sequencing. <i>Angewandte Chemie</i> , 2015 , 127, 1607-1610	3.6	26
31	Probing RNA Modification Status at Single-Nucleotide Resolution in Total RNA. <i>Methods in Enzymology</i> , 2015 , 560, 149-59	1.7	28
30	My adventure in tRNA biology, so far. <i>Rna</i> , 2015 , 21, 707-8	5.8	2
29	Methionine Mistranslation Bypasses the Restraint of the Genetic Code to Generate Mutant Proteins with Distinct Activities. <i>PLoS Genetics</i> , 2015 , 11, e1005745	6	18
28	Methionine Misacylation of tRNA on CaMKII in Response to ER Stress. <i>FASEB Journal</i> , 2015 , 29, 892.7	0.9	
27	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014 , 505, 117-20	50.4	1949
26	Angiogenin-cleaved tRNA halves interact with cytochrome c, protecting cells from apoptosis during osmotic stress. <i>Molecular and Cellular Biology</i> , 2014 , 34, 2450-63	4.8	172
25	A nutrient-driven tRNA modification alters translational fidelity and genome-wide protein coding across an animal genus. <i>PLoS Biology</i> , 2014 , 12, e1002015	9.7	70
24	Adaptive translation as a mechanism of stress response and adaptation. <i>Annual Review of Genetics</i> , 2013 , 47, 121-37	14.5	79
23	N6-methyl-adenosine modification in messenger and long non-coding RNA. <i>Trends in Biochemical Sciences</i> , 2013 , 38, 204-9	10.3	137
22	Diversity of human tRNA genes from the 1000-genomes project. <i>RNA Biology</i> , 2013 , 10, 1853-67	4.8	62
21	Mis-translation as a potential, new mechanism of adaption and stress response. <i>FASEB Journal</i> , 2013 , 27, 325.2	0.9	
20	A role for tRNA modifications in genome structure and codon usage. <i>Cell</i> , 2012 , 149, 202-13	56.2	176

19	The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA. <i>Angewandte Chemie</i> , 2010 , 122, 9069-9072	3.6	6
18	Titelbild: The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA (Angew. Chem. 47/2010). <i>Angewandte Chemie</i> , 2010 , 122, 8947-8947	3.6	
17	The AlkB domain of mammalian ABH8 catalyzes hydroxylation of 5-methoxycarbonylmethyluridine at the wobble position of tRNA. <i>Angewandte Chemie - International Edition</i> , 2010 , 49, 8885-8	16.4	113
16	Cover Picture: The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA (Angew. Chem. Int. Ed. 47/2010). <i>Angewandte Chemie - International Edition</i> , 2010 , 49, 8765-8765	16.4	2
15	Diversity of tRNA genes in eukaryotes. <i>Nucleic Acids Research</i> , 2006 , 34, 6137-46	20.1	145
14	RNA folding during transcription. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006 , 35, 161-75		177
13	Modular construction of a tertiary RNA structure: the specificity domain of the Bacillus subtilis RNase P RNA. <i>Biochemistry</i> , 2001 , 40, 11202-10	3.2	31
12	Altering the intermediate in the equilibrium folding of unmodified yeast tRNAPhe with monovalent and divalent cations. <i>Biochemistry</i> , 2001 , 40, 3629-38	3.2	25
11	Modular construction for function of a ribonucleoprotein enzyme: the catalytic domain of Bacillus subtilis RNase P complexed with B. subtilis RNase P protein. <i>Nucleic Acids Research</i> , 2001 , 29, 1892-7	20.1	29
10	The Bacillus subtilis RNase P holoenzyme contains two RNase P RNA and two RNase P protein subunits. <i>Rna</i> , 2001 , 7, 233-41	5.8	50
9	The 3Tsubstrate determinants for the catalytic efficiency of the Bacillus subtilis RNase P holoenzyme suggest autolytic processing of the RNase P RNA in vivo. <i>Rna</i> , 2000 , 6, 1413-22	5.8	18
8	Mg2+-dependent compaction and folding of yeast tRNAPhe and the catalytic domain of the B. subtilis RNase P RNA determined by small-angle X-ray scattering. <i>Biochemistry</i> , 2000 , 39, 11107-13	3.2	109
7	Design and isolation of ribozyme-substrate pairs using RNase P-based ribozymes containing altered substrate binding sites. <i>Nucleic Acids Research</i> , 1999 , 27, 4298-304	20.1	17
6	Mg2+-dependent folding of a large ribozyme without kinetic traps. <i>Nature Structural Biology</i> , 1999 , 6, 1091-5		99
5	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, 8612-20	3.2	46
4	A thermodynamic framework and cooperativity in the tertiary folding of a Mg2+-dependent ribozyme. <i>Biochemistry</i> , 1999 , 38, 16840-6	3.2	92
3	Recognition of the 5Tleader and the acceptor stem of a pre-tRNA substrate by the ribozyme from Bacillus subtilis RNase P. <i>Biochemistry</i> , 1998 , 37, 10126-33	3.2	55
2	Recognition of the T stem-loop of a pre-tRNA substrate by the ribozyme from Bacillus subtilis ribonuclease P. <i>Biochemistry</i> , 1997 , 36, 6317-25	3.2	108

- 1 Intermediates and kinetic traps in the folding of a large ribozyme revealed by circular dichroism and UV absorbance spectroscopies and catalytic activity. *Nature Structural and Molecular Biology*, **1997**, 4, 931-8 17.6 170