

# Tao Pan

## List of Publications by Year in descending order

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89  
papers

14,953  
citations

93792

39  
h-index

51423

90  
g-index

103  
all docs

103  
docs citations

103  
times ranked

14129  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pseudouridine RNA modification detection and quantification by RT-PCR. <i>Methods</i> , 2022, 203, 1-4.	1.9	6
2	tRNA modification dynamics from individual organisms to metaepitranscriptomics of microbiomes. <i>Molecular Cell</i> , 2022, 82, 891-906.	4.5	44
3	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.	1.8	2
4	A multiplex platform for small RNA sequencing elucidates multifaceted tRNA stress response and translational regulation. <i>Nature Communications</i> , 2022, 13, 2491.	5.8	21
5	Analysis of queuosine and 2-thio tRNA modifications by high throughput sequencing. <i>Nucleic Acids Research</i> , 2022, 50, e99-e99.	6.5	8
6	Quantitative probing of glycosylated queuosine modifications in tRNA. <i>Methods in Enzymology</i> , 2021, 658, 73-82.	0.4	4
7	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, .	3.3	16
8	Tissue-specific reprogramming of host tRNA transcriptome by the microbiome. <i>Genome Research</i> , 2021, 31, 947-957.	2.4	11
9	ALKBH7-mediated demethylation regulates mitochondrial polycistronic RNA processing. <i>Nature Cell Biology</i> , 2021, 23, 684-691.	4.6	41
10	A high-throughput screening method for evolving a demethylase enzyme with improved and new functionalities. <i>Nucleic Acids Research</i> , 2021, 49, e30-e30.	6.5	11
11	Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. <i>Genome Biology</i> , 2021, 22, 330.	3.8	44
12	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.	6.5	10
13	tRNA Queuosine Modification Enzyme Modulates the Growth and Microbiome Recruitment to Breast Tumors. <i>Cancers</i> , 2020, 12, 628.	1.7	38
14	HIV protease cleaves the antiviral m6A reader protein YTHDF3 in the viral particle. <i>PLoS Pathogens</i> , 2020, 16, e1008305.	2.1	40
15	A dual function PUS enzyme. <i>Nature Chemical Biology</i> , 2020, 16, 107-108.	3.9	1
16	5-Methylcytosine RNA Modifications Promote Retrovirus Replication in an ALYREF Reader Protein-Dependent Manner. <i>Journal of Virology</i> , 2020, 94, .	1.5	22
17	Detection and quantification of glycosylated queuosine modified tRNAs by acid denaturing and APB gels. <i>Rna</i> , 2020, 26, 1291-1298.	1.6	13
18	Regulation of Co-transcriptional Pre-mRNA Splicing by m6A through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019, 76, 70-81.e9.	4.5	248

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19	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.	3.3	28
20	Sensitive and quantitative probing of pseudouridine modification in mRNA and long noncoding RNA. <i>Rna</i> , 2019, 25, 1218-1225.	1.6	41
21	Transcriptome-wide reprogramming of N6-methyladenosine modification by the mouse microbiome. <i>Cell Research</i> , 2019, 29, 167-170.	5.7	38
22	N6-Methyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. <i>Nature Chemical Biology</i> , 2019, 15, 88-94.	3.9	258
23	Quantification of Queuosine Modification Levels in tRNA from Human Cells Using APB Gel and Northern Blot. <i>Bio-protocol</i> , 2019, 9, e3191.	0.2	4
24	Modifications and functional genomics of human transfer RNA. <i>Cell Research</i> , 2018, 28, 395-404.	5.7	260
25	An additional class of m6A readers. <i>Nature Cell Biology</i> , 2018, 20, 230-232.	4.6	37
26	Pseudouridines have context-dependent mutation and stop rates in high-throughput sequencing. <i>RNA Biology</i> , 2018, 15, 892-900.	1.5	25
27	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018, 9, 5353.	5.8	48
28	RNA modification landscape of the human mitochondrial tRNA <sup>Lys</sup> regulates protein synthesis. <i>Nature Communications</i> , 2018, 9, 3966.	5.8	61
29	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. <i>Rna</i> , 2018, 24, 1305-1313.	1.6	92
30	RNA modifications and structures cooperate to guide RNA-protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 202-210.	16.1	225
31	Function and origin of mistranslation in distinct cellular contexts. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 205-219.	2.3	38
32	tRNA Misacylation with Methionine in the Mouse Gut Microbiome in Situ. <i>Microbial Ecology</i> , 2017, 74, 10-14.	1.4	6
33	N 6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017, 45, 6051-6063.	6.5	586
34	Identification of N 6 -methyladenosine reader proteins. <i>Methods</i> , 2017, 126, 105-111.	1.9	5
35	Dynamic RNA Modifications in Gene Expression Regulation. <i>Cell</i> , 2017, 169, 1187-1200.	13.5	2,222
36	Determination of tRNA aminoacylation levels by high-throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, e133-e133.	6.5	72

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37	Selective Enzymatic Demethylation of <i>N<sup>2</sup>,N<sup>2</sup></i> -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie</i> , 2017, 129, 5099-5102.	1.6	3
38	Hili Inhibits HIV Replication in Activated T Cells. <i>Journal of Virology</i> , 2017, 91, .	1.5	15
39	Selective Enzymatic Demethylation of <i>N<sup>2</sup>,N<sup>2</sup></i> -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5017-5020.	7.2	44
40	Determining the fidelity of tRNA aminoacylation via microarrays. <i>Methods</i> , 2017, 113, 27-33.	1.9	11
41	RNA modifications: what have we learned and where are we headed?. <i>Nature Reviews Genetics</i> , 2016, 17, 365-372.	7.7	215
42	tRNA base methylation identification and quantification via high-throughput sequencing. <i>Rna</i> , 2016, 22, 1771-1784.	1.6	148
43	Codon optimality controls differential mRNA translation during amino acid starvation. <i>Rna</i> , 2016, 22, 1719-1727.	1.6	47
44	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.	6.5	31
45	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.	6.6	35
46	Stress Response and Adaptation Mediated by Amino Acid Misincorporation during Protein Synthesis. <i>Advances in Nutrition</i> , 2016, 7, 773S-779S.	2.9	24
47	Structures of the m <sup>6</sup> A Methyltransferase Complex: Two Subunits with Distinct but Coordinated Roles. <i>Molecular Cell</i> , 2016, 63, 183-185.	4.5	40
48	ALKBH1-Mediated tRNA Demethylation Regulates Translation. <i>Cell</i> , 2016, 167, 816-828.e16.	13.5	366
49	Interaction of tRNA with MEK2 in pancreatic cancer cells. <i>Scientific Reports</i> , 2016, 6, 28260.	1.6	8
50	The dynamic N1-methyladenosine methylome in eukaryotic messenger RNA. <i>Nature</i> , 2016, 530, 441-446.	13.7	765
51	N6-methyladenosine-encoded epitranscriptomics. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 98-102.	3.6	266
52	Temperature dependent mistranslation in a hyperthermophile adapts proteins to lower temperatures. <i>Nucleic Acids Research</i> , 2016, 44, 294-303.	6.5	67
53	A dual fluorescent reporter for the investigation of methionine mistranslation in live cells. <i>Rna</i> , 2016, 22, 467-476.	1.6	14
54	N6-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016, 428, 822-833.	2.0	164

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55	Probing N 6-methyladenosine (m6A) RNA Modification in Total RNA with SCARLET. <i>Methods in Molecular Biology</i> , 2016, 1358, 285-292.	0.4	21
56	Probing RNA Modification Status at Single-Nucleotide Resolution in Total RNA. <i>Methods in Enzymology</i> , 2015, 560, 149-159.	0.4	37
57	My adventure in tRNA biology, so far. <i>Rna</i> , 2015, 21, 707-708.	1.6	3
58	N6-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. <i>Nature</i> , 2015, 518, 560-564.	13.7	1,482
59	Efficient and quantitative high-throughput tRNA sequencing. <i>Nature Methods</i> , 2015, 12, 835-837.	9.0	426
60	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. <i>Cell</i> , 2015, 162, 1286-1298.	13.5	395
61	RNA epigenetics. <i>Translational Research</i> , 2015, 165, 28-35.	2.2	111
62	Methionine mistranslation bypasses the restraint of the genetic code to generate mutant proteins with distinct activities. <i>PLoS Genetics</i> , 2015, 11, e1005745.	1.5	21
63	Methionine misacylation of tRNA on CaMKII in response to ER stress. <i>FASEB Journal</i> , 2015, 29, 892.7.	0.2	0
64	A nutrient-driven tRNA modification alters translational fidelity and genome-wide protein coding across an animal genus. <i>PLoS Biology</i> , 2014, 12, e1002015.	2.6	93
65	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014, 505, 117-120.	13.7	3,138
66	Angiogenin-cleaved tRNA halves interact with cytochrome c, protecting cells from apoptosis during osmotic stress. <i>Molecular and Cellular Biology</i> , 2014, 34, 2450-2463.	1.1	236
67	Adaptive translation as a mechanism of stress response and adaptation. <i>Annual Review of Genetics</i> , 2013, 47, 121-137.	3.2	102
68	N6-methyl-adenosine modification in messenger and long non-coding RNA. <i>Trends in Biochemical Sciences</i> , 2013, 38, 204-209.	3.7	181
69	Diversity of human tRNA genes from the 1000-genomes project. <i>RNA Biology</i> , 2013, 10, 1853-1867.	1.5	79
70	Mistranslation as a potential, new mechanism of adaptation and stress response. <i>FASEB Journal</i> , 2013, 27, 325.2.	0.2	0
71	A role for tRNA modifications in genome structure and codon usage. <i>Cell</i> , 2012, 149, 202-213.	13.5	239
72	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.	1.6	0

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73	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, 8885-8888.	7.2	129
74	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.	7.2	2
75	RNA FOLDING DURING TRANSCRIPTION. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 161-175.	18.3	227
76	Diversity of tRNA genes in eukaryotes. <i>Nucleic Acids Research</i> , 2006, 34, 6137-6146.	6.5	180
77	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.	1.2	32
78	Altering the Intermediate in the Equilibrium Folding of Unmodified Yeast tRNA <sup>Phe</sup> with Monovalent and Divalent Cations. <i>Biochemistry</i> , 2001, 40, 3629-3638.	1.2	34
79	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.	6.5	34
80	The <i>Bacillus subtilis</i> RNase P holoenzyme contains two RNase P RNA and two RNase P protein subunits. <i>Rna</i> , 2001, 7, 233-241.	1.6	54
81	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.	1.6	20
82	Mg <sup>2+</sup> -Dependent Compaction and Folding of Yeast tRNA <sup>Phe</sup> and the Catalytic Domain of the <i>B. subtilis</i> RNase P RNA Determined by Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2000, 39, 11107-11113.	1.2	118
83	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.	6.5	18
84	Mg <sup>2+</sup> -dependent folding of a large ribozyme without kinetic traps. <i>Nature Structural Biology</i> , 1999, 6, 1091-1095.	9.7	108
85	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.	1.2	46
86	A Thermodynamic Framework and Cooperativity in the Tertiary Folding of a Mg <sup>2+</sup> -Dependent Ribozyme. <i>Biochemistry</i> , 1999, 38, 16840-16846.	1.2	99
87	Recognition of the 5' Leader and the Acceptor Stem of a Pre-tRNA Substrate by the Ribozyme from <i>Bacillus subtilis</i> RNase P. <i>Biochemistry</i> , 1998, 37, 10126-10133.	1.2	57
88	Recognition of the T Stem-Loop of a Pre-tRNA Substrate by the Ribozyme from <i>Bacillus subtilis</i> RNase P. <i>Biochemistry</i> , 1997, 36, 6317-6325.	1.2	109
89	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.	3.6	184