

# 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	Pseudouridine RNA modification detection and quantification by RT-PCR. <i>Methods</i> , 2022, 203, 1-4.	3.8	6
2	tRNA modification dynamics from individual organisms to metaepitranscriptomics of microbiomes. <i>Molecular Cell</i> , 2022, 82, 891-906.	9.7	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.	3.7	2
4	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
5	Analysis of queuosine and 2-thio tRNA modifications by high throughput sequencing. <i>Nucleic Acids Research</i> , 2022, 50, e99-e99.	14.5	8
6	Quantitative probing of glycosylated queuosine modifications in tRNA. <i>Methods in Enzymology</i> , 2021, 658, 73-82.	1.0	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, .	7.1	16
8	Tissue-specific reprogramming of host tRNA transcriptome by the microbiome. <i>Genome Research</i> , 2021, 31, 947-957.	5.5	11
9	ALKBH7-mediated demethylation regulates mitochondrial polycistronic RNA processing. <i>Nature Cell Biology</i> , 2021, 23, 684-691.	10.3	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.	14.5	11
11	Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. <i>Genome Biology</i> , 2021, 22, 330.	8.8	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.	14.5	10
13	tRNA Queuosine Modification Enzyme Modulates the Growth and Microbiome Recruitment to Breast Tumors. <i>Cancers</i> , 2020, 12, 628.	3.7	38
14	HIV protease cleaves the antiviral m6A reader protein YTHDF3 in the viral particle. <i>PLoS Pathogens</i> , 2020, 16, e1008305.	4.7	40
15	A dual function PUS enzyme. <i>Nature Chemical Biology</i> , 2020, 16, 107-108.	8.0	1
16	5-Methylcytosine RNA Modifications Promote Retrovirus Replication in an ALYREF Reader Protein-Dependent Manner. <i>Journal of Virology</i> , 2020, 94, .	3.4	22
17	Detection and quantification of glycosylated queuosine modified tRNAs by acid denaturing and APB gels. <i>Rna</i> , 2020, 26, 1291-1298.	3.5	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.	9.7	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. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19440-19448.	7.1	28
20	Sensitive and quantitative probing of pseudouridine modification in mRNA and long noncoding RNA. Rna, 2019, 25, 1218-1225.	3.5	41
21	Transcriptome-wide reprogramming of N6-methyladenosine modification by the mouse microbiome. Cell Research, 2019, 29, 167-170.	12.0	38
22	N6-Methyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. Nature Chemical Biology, 2019, 15, 88-94.	8.0	258
23	Quantification of Queuosine Modification Levels in tRNA from Human Cells Using APB Gel and Northern Blot. Bio-protocol, 2019, 9, e3191.	0.4	4
24	Modifications and functional genomics of human transfer RNA. Cell Research, 2018, 28, 395-404.	12.0	260
25	An additional class of m6A readers. Nature Cell Biology, 2018, 20, 230-232.	10.3	37
26	Pseudouridines have context-dependent mutation and stop rates in high-throughput sequencing. RNA Biology, 2018, 15, 892-900.	3.1	25
27	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. Nature Communications, 2018, 9, 5353.	12.8	48
28	RNA modification landscape of the human mitochondrial tRNA <sup>Lys</sup> regulates protein synthesis. Nature Communications, 2018, 9, 3966.	12.8	61
29	Queuosine modification protects cognate tRNAs against ribonuclease cleavage. Rna, 2018, 24, 1305-1313.	3.5	92
30	RNA modifications and structures cooperate to guide RNA-protein interactions. Nature Reviews Molecular Cell Biology, 2017, 18, 202-210.	37.0	225
31	Function and origin of mistranslation in distinct cellular contexts. Critical Reviews in Biochemistry and Molecular Biology, 2017, 52, 205-219.	5.2	38
32	tRNA Misacylation with Methionine in the Mouse Gut Microbiome in Situ. Microbial Ecology, 2017, 74, 10-14.	2.8	6
33	N 6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. Nucleic Acids Research, 2017, 45, 6051-6063.	14.5	586
34	Identification of N 6 -methyladenosine reader proteins. Methods, 2017, 126, 105-111.	3.8	5
35	Dynamic RNA Modifications in Gene Expression Regulation. Cell, 2017, 169, 1187-1200.	28.9	2,222
36	Determination of tRNA aminoacylation levels by high-throughput sequencing. Nucleic Acids Research, 2017, 45, e133-e133.	14.5	72

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37	Selective Enzymatic Demethylation of <i>N</i> <sup>2</sup> , <i>N</i> <sup>2</sup> -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie</i> , 2017, 129, 5099-5102.	2.0	3
38	Hili Inhibits HIV Replication in Activated T Cells. <i>Journal of Virology</i> , 2017, 91, .	3.4	15
39	Selective Enzymatic Demethylation of <i>N</i> <sup>2</sup> , <i>N</i> <sup>2</sup> -Dimethylguanosine in RNA and Its Application in High-Throughput tRNA Sequencing. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5017-5020.	13.8	44
40	Determining the fidelity of tRNA aminoacylation via microarrays. <i>Methods</i> , 2017, 113, 27-33.	3.8	11
41	RNA modifications: what have we learned and where are we headed?. <i>Nature Reviews Genetics</i> , 2016, 17, 365-372.	16.3	215
42	tRNA base methylation identification and quantification via high-throughput sequencing. <i>Rna</i> , 2016, 22, 1771-1784.	3.5	148
43	Codon optimality controls differential mRNA translation during amino acid starvation. <i>Rna</i> , 2016, 22, 1719-1727.	3.5	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.	14.5	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.	13.7	35
46	Stress Response and Adaptation Mediated by Amino Acid Misincorporation during Protein Synthesis. <i>Advances in Nutrition</i> , 2016, 7, 773S-779S.	6.4	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.	9.7	40
48	ALKBH1-Mediated tRNA Demethylation Regulates Translation. <i>Cell</i> , 2016, 167, 816-828.e16.	28.9	366
49	Interaction of tRNA with MEK2 in pancreatic cancer cells. <i>Scientific Reports</i> , 2016, 6, 28260.	3.3	8
50	The dynamic N1-methyladenosine methylome in eukaryotic messenger RNA. <i>Nature</i> , 2016, 530, 441-446.	27.8	765
51	N6-methyladenosine-encoded epitranscriptomics. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 98-102.	8.2	266
52	Temperature dependent mistranslation in a hyperthermophile adapts proteins to lower temperatures. <i>Nucleic Acids Research</i> , 2016, 44, 294-303.	14.5	67
53	A dual fluorescent reporter for the investigation of methionine mistranslation in live cells. <i>Rna</i> , 2016, 22, 467-476.	3.5	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.	4.2	164

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55	Probing N 6-methyladenosine (m6A) RNA Modification in Total RNA with SCARLET. Methods in Molecular Biology, 2016, 1358, 285-292.	0.9	21
56	Probing RNA Modification Status at Single-Nucleotide Resolution in Total RNA. Methods in Enzymology, 2015, 560, 149-159.	1.0	37
57	My adventure in tRNA biology, so far. Rna, 2015, 21, 707-708.	3.5	3
58	N6-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions. Nature, 2015, 518, 560-564.	27.8	1,482
59	Efficient and quantitative high-throughput tRNA sequencing. Nature Methods, 2015, 12, 835-837.	19.0	426
60	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. Cell, 2015, 162, 1286-1298.	28.9	395
61	RNA epigenetics. Translational Research, 2015, 165, 28-35.	5.0	111
62	Methionine Mistranslation Bypasses the Restraint of the Genetic Code to Generate Mutant Proteins with Distinct Activities. PLoS Genetics, 2015, 11, e1005745.	3.5	21
63	Methionine Misacylation of tRNA on CaMKII in Response to ER Stress. FASEB Journal, 2015, 29, 892.7.	0.5	0
64	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
65	N6-methyladenosine-dependent regulation of messenger RNA stability. Nature, 2014, 505, 117-120.	27.8	3,138
66	Angiogenin-Cleaved tRNA Halves Interact with Cytochrome c, Protecting Cells from Apoptosis during Osmotic Stress. Molecular and Cellular Biology, 2014, 34, 2450-2463.	2.3	236
67	Adaptive Translation as a Mechanism of Stress Response and Adaptation. Annual Review of Genetics, 2013, 47, 121-137.	7.6	102
68	N6-methyl-adenosine modification in messenger and long non-coding RNA. Trends in Biochemical Sciences, 2013, 38, 204-209.	7.5	181
69	Diversity of human tRNA genes from the 1000-genomes project. RNA Biology, 2013, 10, 1853-1867.	3.1	79
70	Mis-translation as a potential, new mechanism of adaption and stress response. FASEB Journal, 2013, 27, 325.2.	0.5	0
71	A Role for tRNA Modifications in Genome Structure and Codon Usage. Cell, 2012, 149, 202-213.	28.9	239
72	Titelbild: The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA (Angew. Chem. 47/2010). Angewandte Chemie, 2010, 122, 8947-8947.	2.0	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.	13.8	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.	13.8	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.	14.5	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.	2.5	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.	2.5	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.	14.5	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.	3.5	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.	3.5	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.	2.5	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.	14.5	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.	2.5	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.	2.5	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.	2.5	57
88	Recognition of the T Stem-Loop of a Pre-tRNA Substrate by the Ribozyme from <i>Bacillus subtilis</i> Ribonuclease P. <i>Biochemistry</i> , 1997, 36, 6317-6325.	2.5	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.	8.2	184