

# Ting Ni

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

2,597  
citations

279798  
23  
h-index

206112  
48  
g-index

62  
all docs

62  
docs citations

62  
times ranked

5164  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lung cancer cells expressing a shortened <i>CDK16</i> 3'UTR escape senescence through impaired miR-485-5p targeting. <i>Molecular Oncology</i> , 2022, 16, 1347-1364.	4.6	8
2	An enhancer variant at 16q22.1 predisposes to hepatocellular carcinoma via regulating PRMT7 expression. <i>Nature Communications</i> , 2022, 13, 1232.	12.8	6
3	Transcription factor ASCL1 acts as a novel potential therapeutic target for the treatment of the Cushing's disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, , .	3.6	2
4	Comprehensive analysis reveals distinct mutational signature and its mechanistic insights of alcohol consumption in human cancers. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	14
5	opvCRISPR: One-pot visual RT-LAMP-CRISPR platform for SARS-cov-2 detection. <i>Biosensors and Bioelectronics</i> , 2021, 172, 112766.	10.1	207
6	Independent component analysis based gene co-expression network inference (ICAnet) to decipher functional modules for better single-cell clustering and batch integration. <i>Nucleic Acids Research</i> , 2021, 49, e54-e54.	14.5	20
7	Systematic evaluation of the effect of polyadenylation signal variants on the expression of disease-associated genes. <i>Genome Research</i> , 2021, 31, 890-899.	5.5	8
8	SMYD3-PARP16 axis accelerates unfolded protein response and mediates neointima formation. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1261-1273.	12.0	11
9	H3K4 Methyltransferase Smyd3 Mediates Vascular Smooth Muscle Cell Proliferation, Migration, and Neointima Formation. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 1901-1914.	2.4	7
10	HCV poly U/UC sequence-induced inflammation leads to metabolic disorders in vulvar lichen sclerosis. <i>Life Science Alliance</i> , 2021, 4, e202000906.	2.8	4
11	Comprehensive characterization of somatic variants associated with intronic polyadenylation in human cancers. <i>Nucleic Acids Research</i> , 2021, 49, 10369-10381.	14.5	14
12	Cancer-associated dynamics and potential regulators of intronic polyadenylation revealed by IPAFinder using standard RNA-seq data. <i>Genome Research</i> , 2021, 31, 2095-2106.	5.5	20
13	Prevalent intron retention fine-tunes gene expression and contributes to cellular senescence. <i>Aging Cell</i> , 2020, 19, e13276.	6.7	25
14	Histone methyltransferase Smyd3 is a new regulator for vascular senescence. <i>Aging Cell</i> , 2020, 19, e13212.	6.7	24
15	Single-Cell Transcriptome Analysis Reveals Six Subpopulations Reflecting Distinct Cellular Fates in Senescent Mouse Embryonic Fibroblasts. <i>Frontiers in Genetics</i> , 2020, 11, 867.	2.3	16
16	A bioenergetic shift is required for spermatogonial differentiation. <i>Cell Discovery</i> , 2020, 6, 56.	6.7	21
17	Tempo-spatial alternative polyadenylation analysis reveals that 3' UTR lengthening of Mdm2 regulates p53 expression and cellular senescence in aged rat testis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 1046-1052.	2.1	6
18	Smyd3-PARP16 axis accelerates unfolded protein response and vascular aging. <i>Aging</i> , 2020, 12, 21423-21445.	3.1	12

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19	Metastasis-related methyltransferase 1 (Merm1) represses the methyltransferase activity of Dnmt3a and facilitates RNA polymerase I transcriptional elongation. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 78-90.	3.3	1
20	Endogenous Retrovirus-Derived Long Noncoding RNA Enhances Innate Immune Responses via Derepressing RELA Expression. <i>MBio</i> , 2019, 10, .	4.1	39
21	Global downregulation of pigmentation-associated genes in human premature hair graying. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 1155-1163.	1.8	5
22	Exploitation of nuclear protein SFPQ by the encephalomyocarditis virus to facilitate its replication. <i>Biochemical and Biophysical Research Communications</i> , 2019, 510, 65-71.	2.1	13
23	Spliceosome disassembly factors ILP1 and NTR1 promote miRNA biogenesis in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2019, 47, 7886-7900.	14.5	31
24	Chromatin remodeling factor BAZ1A regulates cellular senescence in both cancer and normal cells. <i>Life Sciences</i> , 2019, 229, 225-232.	4.3	12
25	Alternative polyadenylation dependent function of splicing factor SRSF3 contributes to cellular senescence. <i>Aging</i> , 2019, 11, 1356-1388.	3.1	33
26	HNRNPA1-mediated 3' UTR length changes of <i>HN1</i> contributes to cancer- and senescence-associated phenotypes. <i>Aging</i> , 2019, 11, 4407-4437.	3.1	19
27	Down-regulation of cancer-associated gene CDC73 contributes to cellular senescence. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 809-814.	2.1	2
28	3' UTR lengthening as a novel mechanism in regulating cellular senescence. <i>Genome Research</i> , 2018, 28, 285-294.	5.5	90
29	Antisense transcription regulates the expression of sense gene via alternative polyadenylation. <i>Protein and Cell</i> , 2018, 9, 540-552.	11.0	3
30	Position-specific intron retention is mediated by the histone methyltransferase SDG725. <i>BMC Biology</i> , 2018, 16, 44.	3.8	41
31	Disruption of <i>Gen1</i> Causes Congenital Anomalies of the Kidney and Urinary Tract in Mice. <i>International Journal of Biological Sciences</i> , 2018, 14, 10-20.	6.4	11
32	The correlation of copy number variations with longevity in a genome-wide association study of Han Chinese. <i>Aging</i> , 2018, 10, 1206-1222.	3.1	25
33	An episomal vector-based CRISPR/Cas9 system for highly efficient gene knockout in human pluripotent stem cells. <i>Scientific Reports</i> , 2017, 7, 2320.	3.3	91
34	Dynamic landscape of alternative polyadenylation during retinal development. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 1721-1739.	5.4	20
35	Alternative splicing in aging and age-related diseases. <i>Translational Medicine of Aging</i> , 2017, 1, 32-40.	1.3	28
36	Alternative Polyadenylation: Methods, Findings, and Impacts. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 287-300.	6.9	100

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37	NRF1 coordinates with DNA methylation to regulate spermatogenesis. <i>FASEB Journal</i> , 2017, 31, 4959-4970.	0.5	41
38	PA-seq for Global Identification of RNA Polyadenylation Sites of Kaposi's Sarcoma-Associated Herpesvirus Transcripts. <i>Current Protocols in Microbiology</i> , 2016, 41, 14E.7.1-14E.7.18.	6.5	2
39	Global intron retention mediated gene regulation during CD4 <sup>+</sup> T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	14.5	96
40	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016, 6, 21243.	3.3	145
41	Follicular CXCR5-expressing CD8 <sup>+</sup> T cells curtail chronic viral infection. <i>Nature</i> , 2016, 537, 412-416.	27.8	514
42	Expression dynamics, relationships, and transcriptional regulations of diverse transcripts in mouse spermatogenic cells. <i>RNA Biology</i> , 2016, 13, 1011-1024.	3.1	72
43	SET DOMAIN GROUP 708, a histone H3 lysine 36-specific methyltransferase, controls flowering time in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2016, 210, 577-588.	7.3	49
44	Interaction Between the <i>FOXO1A-209</i> Genotype and Tea Drinking Is Significantly Associated with Reduced Mortality at Advanced Ages. <i>Rejuvenation Research</i> , 2016, 19, 195-203.	1.8	14
45	RNA polymerase II-associated factor 1 regulates the release and phosphorylation of paused RNA polymerase II. <i>Science</i> , 2015, 350, 1383-1386.	12.6	189
46	MitoRCA-seq reveals unbalanced cytokine to thymine transition in Polg mutant mice. <i>Scientific Reports</i> , 2015, 5, 12049.	3.3	19
47	An intriguing RNA species—perspectives of circularized RNA. <i>Protein and Cell</i> , 2015, 6, 871-880.	11.0	88
48	GxE Interactions between FOXO Genotypes and Tea Drinking Are Significantly Associated with Cognitive Disability at Advanced Ages in China. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 426-433.	3.6	34
49	Certain Adenylated Non-Coding RNAs, Including 5' Leader Sequences of Primary MicroRNA Transcripts, Accumulate in Mouse Cells following Depletion of the RNA Helicase MTR4. <i>PLoS ONE</i> , 2014, 9, e99430.	2.5	5
50	A Novel Role of CDX1 in Embryonic Epicardial Development. <i>PLoS ONE</i> , 2014, 9, e103271.	2.5	8
51	Distinct polyadenylation landscapes of diverse human tissues revealed by a modified PA-seq strategy. <i>BMC Genomics</i> , 2013, 14, 615.	2.8	43
52	Genome-wide identification and predictive modeling of tissue-specific alternative polyadenylation. <i>Bioinformatics</i> , 2013, 29, i108-i116.	4.1	27
53	A Viral Genome Landscape of RNA Polyadenylation from KSHV Latent to Lytic Infection. <i>PLoS Pathogens</i> , 2013, 9, e1003749.	4.7	49
54	A paired-end sequencing strategy to map the complex landscape of transcription initiation. <i>Nature Methods</i> , 2010, 7, 521-527.	19.0	153

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55	The Prevalence and Regulation of Antisense Transcripts in <i>Schizosaccharomyces pombe</i> . PLoS ONE, 2010, 5, e15271.	2.5	50
56	Selective Gene Amplification for High-Throughput Sequencing. Recent Patents on DNA & Gene Sequences, 2009, 3, 29-38.	0.7	4