

# Li Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

14,516  
citations

81743

39  
h-index

98622

67  
g-index

76  
all docs

76  
docs citations

76  
times ranked

13793  
citing authors

#	ARTICLE	IF	CITATIONS
1	Knockout of circRNAs by base editing back-splice sites of circularized exons. <i>Genome Biology</i> , 2022, 23, 16.	3.8	16
2	RNA circles with minimized immunogenicity as potent PKR inhibitors. <i>Molecular Cell</i> , 2022, 82, 420-434.e6.	4.5	52
3	Highly efficient prime editing by introducing same-sense mutations in pegRNA or stabilizing its structure. <i>Nature Communications</i> , 2022, 13, 1669.	5.8	52
4	Genomic and Transcriptomic Analyses of Prime Editing Guide RNA-Independent Off-Target Effects by Prime Editors. <i>CRISPR Journal</i> , 2022, 5, 276-293.	1.4	31
5	Multi-color RNA imaging with CRISPR-Cas13b systems in living cells. , 2022, 1, 100044.		13
6	Screening for functional circular RNAs using the CRISPR-Cas13 system. <i>Nature Methods</i> , 2021, 18, 51-59.	9.0	179
7	CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. <i>Methods</i> , 2021, 196, 3-10.	1.9	18
8	Mapping circular RNA structures in living cells by SHAPE-MaP. <i>Methods</i> , 2021, 196, 47-55.	1.9	8
9	Fast and furious: insights of back splicing regulation during nascent RNA synthesis. <i>Science China Life Sciences</i> , 2021, 64, 1050-1061.	2.3	1
10	Silencing of circular RNA_0000326 inhibits cervical cancer cell proliferation, migration and invasion by boosting microRNA-338-3p-dependent down-regulation of CDK4. <i>Aging</i> , 2021, 13, 9119-9134.	1.4	12
11	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. <i>Nature Cell Biology</i> , 2021, 23, 552-563.	4.6	50
12	Linking circular intronic RNA degradation and function in transcription by RNase H1. <i>Science China Life Sciences</i> , 2021, 64, 1795-1809.	2.3	43
13	SCAPTURE: a deep learning-embedded pipeline that captures polyadenylation information from 3' tag-based RNA-seq of single cells. <i>Genome Biology</i> , 2021, 22, 221.	3.8	15
14	Progression and application of CRISPR-Cas genomic editors. <i>Methods</i> , 2021, 194, 65-74.	1.9	9
15	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2021, 2372, 179-192.	0.4	8
16	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. <i>Nature Biotechnology</i> , 2020, 38, 856-860.	9.4	165
17	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723.	2.9	62
18	A Tale of Two Moieties: Rapidly Evolving CRISPR/Cas-Based Genome Editing. <i>Trends in Biochemical Sciences</i> , 2020, 45, 874-888.	3.7	23

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19	Silencing of circular RNA HIPK2 in neural stem cells enhances functional recovery following ischaemic stroke. <i>EBioMedicine</i> , 2020, 52, 102660.	2.7	37
20	Distinct Processing of lncRNAs Contributes to Non-conserved Functions in Stem Cells. <i>Cell</i> , 2020, 181, 621-636.e22.	13.5	192
21	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. <i>Genome Biology</i> , 2019, 20, 218.	3.8	23
22	Structure and Degradation of Circular RNAs Regulate PKR Activation in Innate Immunity. <i>Cell</i> , 2019, 177, 865-880.e21.	13.5	543
23	To BE or not to BE, that is the question. <i>Nature Biotechnology</i> , 2019, 37, 520-522.	9.4	11
24	Development and Application of Base Editors. <i>CRISPR Journal</i> , 2019, 2, 91-104.	1.4	46
25	CIRCexplorer3: A CLEAR Pipeline for Direct Comparison of Circular and Linear RNA Expression. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 511-521.	3.0	55
26	One Prime for All Editing. <i>Cell</i> , 2019, 179, 1448-1450.	13.5	23
27	Circular RNA profiling provides insights into their subcellular distribution and molecular characteristics in HepG2 cells. <i>RNA Biology</i> , 2019, 16, 220-232.	1.5	48
28	Genome-Wide Annotation of circRNAs and Their Alternative Back-Splicing/Splicing with CIRCexplorer Pipeline. <i>Methods in Molecular Biology</i> , 2019, 1870, 137-149.	0.4	41
29	N6-Methyladenosines Modulate A-to-I RNA Editing. <i>Molecular Cell</i> , 2018, 69, 126-135.e6.	4.5	108
30	Base editing with a Cpf1-cytidine deaminase fusion. <i>Nature Biotechnology</i> , 2018, 36, 324-327.	9.4	333
31	APOBEC3 induces mutations during repair of CRISPR-Cas9-generated DNA breaks. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 45-52.	3.6	42
32	Genome-wide screening of NEAT1 regulators reveals cross-regulation between paraspeckles and mitochondria. <i>Nature Cell Biology</i> , 2018, 20, 1145-1158.	4.6	124
33	CIRCpedia v2: An Updated Database for Comprehensive Circular RNA Annotation and Expression Comparison. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 226-233.	3.0	206
34	The Biogenesis, Functions, and Challenges of Circular RNAs. <i>Molecular Cell</i> , 2018, 71, 428-442.	4.5	1,511
35	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. <i>Nature Biotechnology</i> , 2018, 36, 946-949.	9.4	190
36	ALU ternative Regulation for Gene Expression. <i>Trends in Cell Biology</i> , 2017, 27, 480-490.	3.6	108

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37	SLERT Regulates DDX21 Rings Associated with Pol I Transcription. <i>Cell</i> , 2017, 169, 664-678.e16.	13.5	205
38	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. <i>Molecular Cell</i> , 2017, 67, 214-227.e7.	4.5	533
39	The Diversity of Long Noncoding RNAs and Their Generation. <i>Trends in Genetics</i> , 2017, 33, 540-552.	2.9	265
40	Increased complexity of circRNA expression during species evolution. <i>RNA Biology</i> , 2017, 14, 1064-1074.	1.5	166
41	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. <i>Cell Research</i> , 2017, 27, 1289-1292.	5.7	99
42	Multifaceted roles of complementary sequences on circRNA formation. <i>Quantitative Biology</i> , 2017, 5, 205-209.	0.3	0
43	The Output of Protein-Coding Genes Shifts to Circular RNAs When the Pre-mRNA Processing Machinery Is Limiting. <i>Molecular Cell</i> , 2017, 68, 940-954.e3.	4.5	319
44	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016, 26, 1277-1287.	2.4	799
45	CircRNA-derived pseudogenes. <i>Cell Research</i> , 2016, 26, 747-750.	5.7	96
46	The Biogenesis of Nascent Circular RNAs. <i>Cell Reports</i> , 2016, 15, 611-624.	2.9	465
47	Unusual Processing Generates SPA LncRNAs that Sequester Multiple RNA Binding Proteins. <i>Molecular Cell</i> , 2016, 64, 534-548.	4.5	123
48	RNA Structure Switches RBP Binding. <i>Molecular Cell</i> , 2016, 64, 219-220.	4.5	11
49	Parthenogenetic haploid embryonic stem cells efficiently support mouse generation by oocyte injection. <i>Cell Research</i> , 2016, 26, 131-134.	5.7	38
50	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2016, 1402, 215-227.	0.4	52
51	Splicing noncoding <sc>RNAs</sc> from the inside out. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 651-660.	3.2	45
52	Protein arginine methyltransferase CARM1 attenuates the paraspeckle-mediated nuclear retention of mRNAs containing IR<i>Alu</i>s. <i>Genes and Development</i> , 2015, 29, 630-645.	2.7	80
53	SnoVectors for nuclear expression of RNA. <i>Nucleic Acids Research</i> , 2015, 43, e5-e5.	6.5	43
54	Gear Up in Circles. <i>Molecular Cell</i> , 2015, 58, 715-717.	4.5	4

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55	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. <i>Cell Research</i> , 2015, 25, 459-476.	5.7	73
56	The long noncoding RNA regulation at the MYC locus. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 41-48.	1.5	26
57	CRISPR-Cas9-Mediated Genetic Screening in Mice with Haploid Embryonic Stem Cells Carrying a Guide RNA Library. <i>Cell Stem Cell</i> , 2015, 17, 221-232.	5.2	91
58	Regulation of circRNA biogenesis. <i>RNA Biology</i> , 2015, 12, 381-388.	1.5	1,525
59	Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. <i>Cell Research</i> , 2014, 24, 513-531.	5.7	588
60	Microexons Go Big. <i>Cell</i> , 2014, 159, 1488-1489.	13.5	14
61	Life without A tail: New formats of long noncoding RNAs. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 54, 338-349.	1.2	104
62	Competition of RNA splicing: line in or circle up. <i>Science China Life Sciences</i> , 2014, 57, 1232-1233.	2.3	2
63	Complementary Sequence-Mediated Exon Circularization. <i>Cell</i> , 2014, 159, 134-147.	13.5	1,638
64	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. <i>BMC Genomics</i> , 2014, 15, 287.	1.2	42
65	Prediction of constitutive A-to-I editing sites from human transcriptomes in the absence of genomic sequences. <i>BMC Genomics</i> , 2013, 14, 206.	1.2	32
66	Circular Intronic Long Noncoding RNAs. <i>Molecular Cell</i> , 2013, 51, 792-806.	4.5	1,858
67	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013, 3, 226-241.	1.8	13
68	Long Noncoding RNAs with snoRNA Ends. <i>Molecular Cell</i> , 2012, 48, 219-230.	4.5	389
69	Genomewide characterization of non-polyadenylated RNAs. <i>Genome Biology</i> , 2011, 12, R16.	13.9	365