

Li Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1836971/publications.pdf>

Version: 2024-02-01

69

papers

14,516

citations

81900

39

h-index

98798

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.	8.8	16
2	RNA circles with minimized immunogenicity as potent PKR inhibitors. <i>Molecular Cell</i> , 2022, 82, 420-434.e6.	9.7	52
3	Highly efficient prime editing by introducing same-sense mutations in pegRNA or stabilizing its structure. <i>Nature Communications</i> , 2022, 13, 1669.	12.8	52
4	Genomic and Transcriptomic Analyses of Prime Editing Guide RNAâ€“Independent Off-Target Effects by Prime Editors. <i>CRISPR Journal</i> , 2022, 5, 276-293.	2.9	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 CRISPRâ€“Cas13 system. <i>Nature Methods</i> , 2021, 18, 51-59.	19.0	179
7	CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. <i>Methods</i> , 2021, 196, 3-10.	3.8	18
8	Mapping circular RNA structures in living cells by SHAPE-MaP. <i>Methods</i> , 2021, 196, 47-55.	3.8	8
9	Fast and furious: insights of back splicing regulation during nascent RNA synthesis. <i>Science China Life Sciences</i> , 2021, 64, 1050-1061.	4.9	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.	3.1	12
11	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. <i>Nature Cell Biology</i> , 2021, 23, 552-563.	10.3	50
12	Linking circular intronic RNA degradation and function in transcription by RNase H1. <i>Science China Life Sciences</i> , 2021, 64, 1795-1809.	4.9	43
13	SCAPTURE: a deep learning-embedded pipeline that captures polyadenylation information from 3â€² tag-based RNA-seq of single cells. <i>Genome Biology</i> , 2021, 22, 221.	8.8	15
14	Progression and application of CRISPR-Cas genomic editors. <i>Methods</i> , 2021, 194, 65-74.	3.8	9
15	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2021, 2372, 179-192.	0.9	8
16	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. <i>Nature Biotechnology</i> , 2020, 38, 856-860.	17.5	165
17	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723.	6.4	62
18	A Tale of Two Moieties: Rapidly Evolving CRISPR/Cas-Based Genome Editing. <i>Trends in Biochemical Sciences</i> , 2020, 45, 874-888.	7.5	23

#	ARTICLE	IF	CITATIONS
19	Silencing of circular RNA HIPK2 in neural stem cells enhances functional recovery following ischaemic stroke. EBioMedicine, 2020, 52, 102660.	6.1	37
20	Distinct Processing of lncRNAs Contributes to Non-conserved Functions in Stem Cells. Cell, 2020, 181, 621-636.e22.	28.9	192
21	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. Genome Biology, 2019, 20, 218.	8.8	23
22	Structure and Degradation of Circular RNAs Regulate PKR Activation in Innate Immunity. Cell, 2019, 177, 865-880.e21.	28.9	543
23	To BE or not to BE, that is the question. Nature Biotechnology, 2019, 37, 520-522.	17.5	11
24	Development and Application of Base Editors. CRISPR Journal, 2019, 2, 91-104.	2.9	46
25	CIRCexplorer3: A CLEAR Pipeline for Direct Comparison of Circular and Linear RNA Expression. Genomics, Proteomics and Bioinformatics, 2019, 17, 511-521.	6.9	55
26	One Prime for All Editing. Cell, 2019, 179, 1448-1450.	28.9	23
27	Circular RNA profiling provides insights into their subcellular distribution and molecular characteristics in HepG2 cells. RNA Biology, 2019, 16, 220-232.	3.1	48
28	Genome-Wide Annotation of circRNAs and Their Alternative Back-Splicing/Splicing with CIRCexplorer Pipeline. Methods in Molecular Biology, 2019, 1870, 137-149.	0.9	41
29	N6-Methyladenosines Modulate A-to-I RNA Editing. Molecular Cell, 2018, 69, 126-135.e6.	9.7	108
30	Base editing with a Cpf1-cytidine deaminase fusion. Nature Biotechnology, 2018, 36, 324-327.	17.5	333
31	APOBEC3 induces mutations during repair of CRISPR-Cas9-generated DNA breaks. Nature Structural and Molecular Biology, 2018, 25, 45-52.	8.2	42
32	Genome-wide screening of NEAT1 regulators reveals cross-regulation between paraspeckles and mitochondria. Nature Cell Biology, 2018, 20, 1145-1158.	10.3	124
33	CIRCpedia v2: An Updated Database for Comprehensive Circular RNA Annotation and Expression Comparison. Genomics, Proteomics and Bioinformatics, 2018, 16, 226-233.	6.9	206
34	The Biogenesis, Functions, and Challenges of Circular RNAs. Molecular Cell, 2018, 71, 428-442.	9.7	1,511
35	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. Nature Biotechnology, 2018, 36, 946-949.	17.5	190
36	ALU alternative Regulation for Gene Expression. Trends in Cell Biology, 2017, 27, 480-490.	7.9	108

#	ARTICLE	IF	CITATIONS
37	SLERT Regulates DDX21 Rings Associated with Pol I Transcription. <i>Cell</i> , 2017, 169, 664-678.e16.	28.9	205
38	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. <i>Molecular Cell</i> , 2017, 67, 214-227.e7.	9.7	533
39	The Diversity of Long Noncoding RNAs and Their Generation. <i>Trends in Genetics</i> , 2017, 33, 540-552.	6.7	265
40	Increased complexity of circRNA expression during species evolution. <i>RNA Biology</i> , 2017, 14, 1064-1074.	3.1	166
41	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. <i>Cell Research</i> , 2017, 27, 1289-1292.	12.0	99
42	Multifaceted roles of complementary sequences on circRNA formation. <i>Quantitative Biology</i> , 2017, 5, 205-209.	0.5	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.	9.7	319
44	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016, 26, 1277-1287.	5.5	799
45	CircRNA-derived pseudogenes. <i>Cell Research</i> , 2016, 26, 747-750.	12.0	96
46	The Biogenesis of Nascent Circular RNAs. <i>Cell Reports</i> , 2016, 15, 611-624.	6.4	465
47	Unusual Processing Generates SPA LncRNAs that Sequester Multiple RNA Binding Proteins. <i>Molecular Cell</i> , 2016, 64, 534-548.	9.7	123
48	RNA Structure Switches RBP Binding. <i>Molecular Cell</i> , 2016, 64, 219-220.	9.7	11
49	Parthenogenetic haploid embryonic stem cells efficiently support mouse generation by oocyte injection. <i>Cell Research</i> , 2016, 26, 131-134.	12.0	38
50	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2016, 1402, 215-227.	0.9	52
51	Splicing noncoding <scp>RNAs</scp> from the inside out. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 651-660.	6.4	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.	5.9	80
53	SnoVectors for nuclear expression of RNA. <i>Nucleic Acids Research</i> , 2015, 43, e5-e5.	14.5	43
54	Gear Up in Circles. <i>Molecular Cell</i> , 2015, 58, 715-717.	9.7	4

#	ARTICLE	IF	CITATIONS
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.	12.0	73
56	The long noncoding RNA regulation at the MYC locus. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 41-48.	3.3	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.	11.1	91
58	Regulation of circRNA biogenesis. <i>RNA Biology</i> , 2015, 12, 381-388.	3.1	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.	12.0	588
60	Microexons Go Big. <i>Cell</i> , 2014, 159, 1488-1489.	28.9	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.	2.8	104
62	Competition of RNA splicing: line in or circle up. <i>Science China Life Sciences</i> , 2014, 57, 1232-1233.	4.9	2
63	Complementary Sequence-Mediated Exon Circularization. <i>Cell</i> , 2014, 159, 134-147.	28.9	1,638
64	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. <i>BMC Genomics</i> , 2014, 15, 287.	2.8	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.	2.8	32
66	Circular Intronic Long Noncoding RNAs. <i>Molecular Cell</i> , 2013, 51, 792-806.	9.7	1,858
67	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013, 3, 226-241.	4.0	13
68	Long Noncoding RNAs with snoRNA Ends. <i>Molecular Cell</i> , 2012, 48, 219-230.	9.7	389
69	Genomewide characterization of non-polyadenylated RNAs. <i>Genome Biology</i> , 2011, 12, R16.	9.6	365