

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	Circular Intronic Long Noncoding RNAs. <i>Molecular Cell</i> , 2013, 51, 792-806.	9.7	1,858
2	Complementary Sequence-Mediated Exon Circularization. <i>Cell</i> , 2014, 159, 134-147.	28.9	1,638
3	Regulation of circRNA biogenesis. <i>RNA Biology</i> , 2015, 12, 381-388.	3.1	1,525
4	The Biogenesis, Functions, and Challenges of Circular RNAs. <i>Molecular Cell</i> , 2018, 71, 428-442.	9.7	1,511
5	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016, 26, 1277-1287.	5.5	799
6	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
7	Structure and Degradation of Circular RNAs Regulate PKR Activation in Innate Immunity. <i>Cell</i> , 2019, 177, 865-880.e21.	28.9	543
8	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. <i>Molecular Cell</i> , 2017, 67, 214-227.e7.	9.7	533
9	The Biogenesis of Nascent Circular RNAs. <i>Cell Reports</i> , 2016, 15, 611-624.	6.4	465
10	Long Noncoding RNAs with snoRNA Ends. <i>Molecular Cell</i> , 2012, 48, 219-230.	9.7	389
11	Genomewide characterization of non-polyadenylated RNAs. <i>Genome Biology</i> , 2011, 12, R16.	9.6	365
12	Base editing with a Cpf1-cytidine deaminase fusion. <i>Nature Biotechnology</i> , 2018, 36, 324-327.	17.5	333
13	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
14	The Diversity of Long Noncoding RNAs and Their Generation. <i>Trends in Genetics</i> , 2017, 33, 540-552.	6.7	265
15	CIRCpedia v2: An Updated Database for Comprehensive Circular RNA Annotation and Expression Comparison. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 226-233.	6.9	206
16	SLERT Regulates DDX21 Rings Associated with Pol I Transcription. <i>Cell</i> , 2017, 169, 664-678.e16.	28.9	205
17	Distinct Processing of lncRNAs Contributes to Non-conserved Functions in Stem Cells. <i>Cell</i> , 2020, 181, 621-636.e22.	28.9	192
18	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. <i>Nature Biotechnology</i> , 2018, 36, 946-949.	17.5	190

#	ARTICLE	IF	CITATIONS
19	Screening for functional circular RNAs using the CRISPR-Cas13 system. <i>Nature Methods</i> , 2021, 18, 51-59.	19.0	179
20	Increased complexity of circRNA expression during species evolution. <i>RNA Biology</i> , 2017, 14, 1064-1074.	3.1	166
21	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. <i>Nature Biotechnology</i> , 2020, 38, 856-860.	17.5	165
22	Genome-wide screening of NEAT1 regulators reveals cross-regulation between paraspeckles and mitochondria. <i>Nature Cell Biology</i> , 2018, 20, 1145-1158.	10.3	124
23	Unusual Processing Generates SPA LncRNAs that Sequester Multiple RNA Binding Proteins. <i>Molecular Cell</i> , 2016, 64, 534-548.	9.7	123
24	ALU alternative Regulation for Gene Expression. <i>Trends in Cell Biology</i> , 2017, 27, 480-490.	7.9	108
25	N6-Methyladenosines Modulate A-to-I RNA Editing. <i>Molecular Cell</i> , 2018, 69, 126-135.e6.	9.7	108
26	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
27	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. <i>Cell Research</i> , 2017, 27, 1289-1292.	12.0	99
28	CircRNA-derived pseudogenes. <i>Cell Research</i> , 2016, 26, 747-750.	12.0	96
29	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
30	Protein arginine methyltransferase CARM1 attenuates the paraspeckle-mediated nuclear retention of mRNAs containing IRAlus. <i>Genes and Development</i> , 2015, 29, 630-645.	5.9	80
31	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
32	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723.	6.4	62
33	CIRCexplorer3: A CLEAR Pipeline for Direct Comparison of Circular and Linear RNA Expression. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 511-521.	6.9	55
34	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2016, 1402, 215-227.	0.9	52
35	RNA circles with minimized immunogenicity as potent PKR inhibitors. <i>Molecular Cell</i> , 2022, 82, 420-434.e6.	9.7	52
36	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

#	ARTICLE	IF	CITATIONS
37	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. <i>Nature Cell Biology</i> , 2021, 23, 552-563.	10.3	50
38	Circular RNA profiling provides insights into their subcellular distribution and molecular characteristics in HepG2 cells. <i>RNA Biology</i> , 2019, 16, 220-232.	3.1	48
39	Development and Application of Base Editors. <i>CRISPR Journal</i> , 2019, 2, 91-104.	2.9	46
40	Splicing noncoding <sc>RNAs</sc> from the inside out. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 651-660.	6.4	45
41	SnoVectors for nuclear expression of RNA. <i>Nucleic Acids Research</i> , 2015, 43, e5-e5.	14.5	43
42	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
43	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. <i>BMC Genomics</i> , 2014, 15, 287.	2.8	42
44	APOBEC3 induces mutations during repair of CRISPR-Cas9-generated DNA breaks. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 45-52.	8.2	42
45	Genome-Wide Annotation of circRNAs and Their Alternative Back-Splicing/Splicing with CIRCexplorer Pipeline. <i>Methods in Molecular Biology</i> , 2019, 1870, 137-149.	0.9	41
46	Parthenogenetic haploid embryonic stem cells efficiently support mouse generation by oocyte injection. <i>Cell Research</i> , 2016, 26, 131-134.	12.0	38
47	Silencing of circular RNA HIPK2 in neural stem cells enhances functional recovery following ischaemic stroke. <i>EBioMedicine</i> , 2020, 52, 102660.	6.1	37
48	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
49	Genomic and Transcriptomic Analyses of Prime Editing Guide RNA-Independent Off-Target Effects by Prime Editors. <i>CRISPR Journal</i> , 2022, 5, 276-293.	2.9	31
50	The long noncoding RNA regulation at the MYC locus. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 41-48.	3.3	26
51	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. <i>Genome Biology</i> , 2019, 20, 218.	8.8	23
52	One Prime for All Editing. <i>Cell</i> , 2019, 179, 1448-1450.	28.9	23
53	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
54	CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. <i>Methods</i> , 2021, 196, 3-10.	3.8	18

#	ARTICLE	IF	CITATIONS
55	Knockout of circRNAs by base editing back-splice sites of circularized exons. <i>Genome Biology</i> , 2022, 23, 16.	8.8	16
56	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.	8.8	15
57	Microexons Go Big. <i>Cell</i> , 2014, 159, 1488-1489.	28.9	14
58	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013, 3, 226-241.	4.0	13
59	Multi-color RNA imaging with CRISPR-Cas13b systems in living cells. , 2022, 1, 100044.		13
60	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
61	RNA Structure Switches RBP Binding. <i>Molecular Cell</i> , 2016, 64, 219-220.	9.7	11
62	To BE or not to BE, that is the question. <i>Nature Biotechnology</i> , 2019, 37, 520-522.	17.5	11
63	Progression and application of CRISPR-Cas genomic editors. <i>Methods</i> , 2021, 194, 65-74.	3.8	9
64	Mapping circular RNA structures in living cells by SHAPE-MaP. <i>Methods</i> , 2021, 196, 47-55.	3.8	8
65	Characterization of Circular RNAs. <i>Methods in Molecular Biology</i> , 2021, 2372, 179-192.	0.9	8
66	Gear Up in Circles. <i>Molecular Cell</i> , 2015, 58, 715-717.	9.7	4
67	Competition of RNA splicing: line in or circle up. <i>Science China Life Sciences</i> , 2014, 57, 1232-1233.	4.9	2
68	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
69	Multifaceted roles of complementary sequences on circRNA formation. <i>Quantitative Biology</i> , 2017, 5, 205-209.	0.5	0