

# Long Cai

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

10,080  
citations

117625

34  
h-index

302126

39  
g-index

53  
all docs

53  
docs citations

53  
times ranked

12194  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+. Nature, 2019, 568, 235-239.	27.8	1,088
2	Stochastic protein expression in individual cells at the single molecule level. Nature, 2006, 440, 358-362.	27.8	1,081
3	Single-Cell Phenotyping within Transparent Intact Tissue through Whole-Body Clearing. Cell, 2014, 158, 945-958.	28.9	833
4	Single-cell in situ RNA profiling by sequential hybridization. Nature Methods, 2014, 11, 360-361.	19.0	724
5	Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. Cell, 2018, 174, 744-757.e24.	28.9	649
6	In Situ Transcription Profiling of Single Cells Reveals Spatial Organization of Cells in the Mouse Hippocampus. Neuron, 2016, 92, 342-357.	8.1	540
7	Frequency-modulated nuclear localization bursts coordinate gene regulation. Nature, 2008, 455, 485-490.	27.8	445
8	The adult human testis transcriptional cell atlas. Cell Research, 2018, 28, 1141-1157.	12.0	426
9	Single-cell systems biology by super-resolution imaging and combinatorial labeling. Nature Methods, 2012, 9, 743-748.	19.0	394
10	Giotto: a toolbox for integrative analysis and visualization of spatial expression data. Genome Biology, 2021, 22, 78.	8.8	367
11	Synthetic recording and in situ readout of lineage information in single cells. Nature, 2017, 541, 107-111.	27.8	348
12	Dynamic Heterogeneity and DNA Methylation in Embryonic Stem Cells. Molecular Cell, 2014, 55, 319-331.	9.7	271
13	Challenges and emerging directions in single-cell analysis. Genome Biology, 2017, 18, 84.	8.8	258
14	Dynamics and Spatial Genomics of the Nascent Transcriptome by Intron seqFISH. Cell, 2018, 174, 363-376.e16.	28.9	242
15	Whole-body tissue stabilization and selective extractions via tissue-hydrogel hybrids for high-resolution intact circuit mapping and phenotyping. Nature Protocols, 2015, 10, 1860-1896.	12.0	234
16	Integrated spatial genomics reveals global architecture of single nuclei. Nature, 2021, 590, 344-350.	27.8	228
17	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. Cell, 2019, 179, 713-728.e17.	28.9	186
18	Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data. Nature Biotechnology, 2018, 36, 1183-1190.	17.5	179

#	ARTICLE	IF	CITATIONS
19	Single-molecule RNA detection at depth via hybridization chain reaction and tissue hydrogel embedding and clearing. <i>Development (Cambridge)</i> , 2016, 143, 2862-7.	2.5	174
20	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , 2022, 40, 74-85.	17.5	152
21	Spatial transcriptomics of planktonic and sessile bacterial populations at single-cell resolution. <i>Science</i> , 2021, 373, .	12.6	140
22	Combinatorial gene regulation by modulation of relative pulse timing. <i>Nature</i> , 2015, 527, 54-58.	27.8	117
23	seqFISH Accurately Detects Transcripts in Single Cells and Reveals Robust Spatial Organization in the Hippocampus. <i>Neuron</i> , 2017, 94, 752-758.e1.	8.1	100
24	Profiling the transcriptome with RNA SPOTs. <i>Nature Methods</i> , 2017, 14, 1153-1155.	19.0	93
25	Identification of a neural crest stem cell niche by Spatial Genomic Analysis. <i>Nature Communications</i> , 2017, 8, 1830.	12.8	82
26	Single-Cell Analysis Reveals Regulatory Gene Expression Dynamics Leading to Lineage Commitment in Early T Cell Development. <i>Cell Systems</i> , 2019, 9, 321-337.e9.	6.2	80
27	Imaging cell lineage with a synthetic digital recording system. <i>Science</i> , 2021, 372, .	12.6	78
28	Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594.	12.6	74
29	Pulsatile Dynamics in the Yeast Proteome. <i>Current Biology</i> , 2014, 24, 2189-2194.	3.9	73
30	Multiplexed Dynamic Imaging of Genomic Loci by Combined CRISPR Imaging and DNA Sequential FISH. <i>Biophysical Journal</i> , 2017, 112, 1773-1776.	0.5	70
31	Dense transcript profiling in single cells by image correlation decoding. <i>Nature Methods</i> , 2016, 13, 657-660.	19.0	66
32	Directed Evolution of a Bright Near-Infrared Fluorescent Rhodopsin Using a Synthetic Chromophore. <i>Cell Chemical Biology</i> , 2017, 24, 415-425.	5.2	55
33	In situ readout of DNA barcodes and single base edits facilitated by in vitro transcription. <i>Nature Biotechnology</i> , 2020, 38, 66-75.	17.5	52
34	Misexpression of basic helix-loop-helix genes in the murine cerebral cortex affects cell fate choices and neuronal survival. <i>Development (Cambridge)</i> , 2000, 127, 3021-30.	2.5	51
35	Noncommutative Biology: Sequential Regulation of Complex Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005089.	3.2	16
36	Turning single cells into microarrays by super-resolution barcoding. <i>Briefings in Functional Genomics</i> , 2013, 12, 75-80.	2.7	10

#	ARTICLE	IF	CITATIONS
37	Manipulating Molecules via Combined Electrostatic and Pulsed Nonresonant Laser Fields. ACS Symposium Series, 2002, , 286-303.	0.5	3
38	Detecting protein and post-translational modifications in single cells with iDentification and qUantification sEparaTion (DUET). Communications Biology, 2020, 3, 420.	4.4	3
39	Single cell biologyâ€™a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
40	Supplementary Protocol for RNA SPOTs. Protocol Exchange, 0, , .	0.3	1
41	RNA seqFISH+ Supplementary Protocol. Protocol Exchange, 0, , .	0.3	1