

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	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , 2022, 40, 74-85.	17.5	152
2	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	27.8	228
3	Giotto: a toolbox for integrative analysis and visualization of spatial expression data. <i>Genome Biology</i> , 2021, 22, 78.	8.8	367
4	Imaging cell lineage with a synthetic digital recording system. <i>Science</i> , 2021, 372, .	12.6	78
5	Spatial transcriptomics of planktonic and sessile bacterial populations at single-cell resolution. <i>Science</i> , 2021, 373, .	12.6	140
6	Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594.	12.6	74
7	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	3.8	3
8	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
9	Detecting protein and post-translational modifications in single cells with iDentification and qUantification sEparaTion (DUET). <i>Communications Biology</i> , 2020, 3, 420.	4.4	3
10	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. <i>Cell</i> , 2019, 179, 713-728.e17.	28.9	186
11	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
12	Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+. <i>Nature</i> , 2019, 568, 235-239.	27.8	1,088
13	The adult human testis transcriptional cell atlas. <i>Cell Research</i> , 2018, 28, 1141-1157.	12.0	426
14	Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data. <i>Nature Biotechnology</i> , 2018, 36, 1183-1190.	17.5	179
15	Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. <i>Cell</i> , 2018, 174, 744-757.e24.	28.9	649
16	Dynamics and Spatial Genomics of the Nascent Transcriptome by Intron seqFISH. <i>Cell</i> , 2018, 174, 363-376.e16.	28.9	242
17	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
18	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

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19	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
20	Profiling the transcriptome with RNA SPOTs. <i>Nature Methods</i> , 2017, 14, 1153-1155.	19.0	93
21	Identification of a neural crest stem cell niche by Spatial Genomic Analysis. <i>Nature Communications</i> , 2017, 8, 1830.	12.8	82
22	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	8.8	258
23	Synthetic recording and in situ readout of lineage information in single cells. <i>Nature</i> , 2017, 541, 107-111.	27.8	348
24	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
25	In Situ Transcription Profiling of Single Cells Reveals Spatial Organization of Cells in the Mouse Hippocampus. <i>Neuron</i> , 2016, 92, 342-357.	8.1	540
26	Dense transcript profiling in single cells by image correlation decoding. <i>Nature Methods</i> , 2016, 13, 657-660.	19.0	66
27	Noncommutative Biology: Sequential Regulation of Complex Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005089.	3.2	16
28	Whole-body tissue stabilization and selective extractions via tissue-hydrogel hybrids for high-resolution intact circuit mapping and phenotyping. <i>Nature Protocols</i> , 2015, 10, 1860-1896.	12.0	234
29	Combinatorial gene regulation by modulation of relative pulse timing. <i>Nature</i> , 2015, 527, 54-58.	27.8	117
30	Single-cell in situ RNA profiling by sequential hybridization. <i>Nature Methods</i> , 2014, 11, 360-361.	19.0	724
31	Pulsatile Dynamics in the Yeast Proteome. <i>Current Biology</i> , 2014, 24, 2189-2194.	3.9	73
32	Single-Cell Phenotyping within Transparent Intact Tissue through Whole-Body Clearing. <i>Cell</i> , 2014, 158, 945-958.	28.9	833
33	Dynamic Heterogeneity and DNA Methylation in Embryonic Stem Cells. <i>Molecular Cell</i> , 2014, 55, 319-331.	9.7	271
34	Turning single cells into microarrays by super-resolution barcoding. <i>Briefings in Functional Genomics</i> , 2013, 12, 75-80.	2.7	10
35	Single-cell systems biology by super-resolution imaging and combinatorial labeling. <i>Nature Methods</i> , 2012, 9, 743-748.	19.0	394
36	Frequency-modulated nuclear localization bursts coordinate gene regulation. <i>Nature</i> , 2008, 455, 485-490.	27.8	445

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37	Stochastic protein expression in individual cells at the single molecule level. <i>Nature</i> , 2006, 440, 358-362.	27.8	1,081
38	Manipulating Molecules via Combined Electrostatic and Pulsed Nonresonant Laser Fields. <i>ACS Symposium Series</i> , 2002, , 286-303.	0.5	3
39	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
40	Supplementary Protocol for RNA SPOTs. <i>Protocol Exchange</i> , 0, , .	0.3	1
41	RNA seqFISH+ Supplementary Protocol. <i>Protocol Exchange</i> , 0, , .	0.3	1