

Long Cai

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5819608/publications.pdf>

Version: 2024-02-01

41
papers

10,080
citations

117453

34
h-index

301761

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. | 13.7 | 1,088 |
| 2 | Stochastic protein expression in individual cells at the single molecule level. Nature, 2006, 440, 358-362. | 13.7 | 1,081 |
| 3 | Single-Cell Phenotyping within Transparent Intact Tissue through Whole-Body Clearing. Cell, 2014, 158, 945-958. | 13.5 | 833 |
| 4 | Single-cell in situ RNA profiling by sequential hybridization. Nature Methods, 2014, 11, 360-361. | 9.0 | 724 |
| 5 | Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. Cell, 2018, 174, 744-757.e24. | 13.5 | 649 |
| 6 | In Situ Transcription Profiling of Single Cells Reveals Spatial Organization of Cells in the Mouse Hippocampus. Neuron, 2016, 92, 342-357. | 3.8 | 540 |
| 7 | Frequency-modulated nuclear localization bursts coordinate gene regulation. Nature, 2008, 455, 485-490. | 13.7 | 445 |
| 8 | The adult human testis transcriptional cell atlas. Cell Research, 2018, 28, 1141-1157. | 5.7 | 426 |
| 9 | Single-cell systems biology by super-resolution imaging and combinatorial labeling. Nature Methods, 2012, 9, 743-748. | 9.0 | 394 |
| 10 | Giotto: a toolbox for integrative analysis and visualization of spatial expression data. Genome Biology, 2021, 22, 78. | 3.8 | 367 |
| 11 | Synthetic recording and in situ readout of lineage information in single cells. Nature, 2017, 541, 107-111. | 13.7 | 348 |
| 12 | Dynamic Heterogeneity and DNA Methylation in Embryonic Stem Cells. Molecular Cell, 2014, 55, 319-331. | 4.5 | 271 |
| 13 | Challenges and emerging directions in single-cell analysis. Genome Biology, 2017, 18, 84. | 3.8 | 258 |
| 14 | Dynamics and Spatial Genomics of the Nascent Transcriptome by Intron seqFISH. Cell, 2018, 174, 363-376.e16. | 13.5 | 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. | 5.5 | 234 |
| 16 | Integrated spatial genomics reveals global architecture of single nuclei. Nature, 2021, 590, 344-350. | 13.7 | 228 |
| 17 | Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. Cell, 2019, 179, 713-728.e17. | 13.5 | 186 |
| 18 | Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data. Nature Biotechnology, 2018, 36, 1183-1190. | 9.4 | 179 |

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|----|---|------|-----------|
| 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. | 1.2 | 174 |
| 20 | Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , 2022, 40, 74-85. | 9.4 | 152 |
| 21 | Spatial transcriptomics of planktonic and sessile bacterial populations at single-cell resolution. <i>Science</i> , 2021, 373, . | 6.0 | 140 |
| 22 | Combinatorial gene regulation by modulation of relative pulse timing. <i>Nature</i> , 2015, 527, 54-58. | 13.7 | 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. | 3.8 | 100 |
| 24 | Profiling the transcriptome with RNA SPOTs. <i>Nature Methods</i> , 2017, 14, 1153-1155. | 9.0 | 93 |
| 25 | Identification of a neural crest stem cell niche by Spatial Genomic Analysis. <i>Nature Communications</i> , 2017, 8, 1830. | 5.8 | 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. | 2.9 | 80 |
| 27 | Imaging cell lineage with a synthetic digital recording system. <i>Science</i> , 2021, 372, . | 6.0 | 78 |
| 28 | Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594. | 6.0 | 74 |
| 29 | Pulsatile Dynamics in the Yeast Proteome. <i>Current Biology</i> , 2014, 24, 2189-2194. | 1.8 | 73 |
| 30 | Multiplexed Dynamic Imaging of Genomic Loci by Combined CRISPR Imaging and DNA Sequential FISH. <i>Biophysical Journal</i> , 2017, 112, 1773-1776. | 0.2 | 70 |
| 31 | Dense transcript profiling in single cells by image correlation decoding. <i>Nature Methods</i> , 2016, 13, 657-660. | 9.0 | 66 |
| 32 | Directed Evolution of a Bright Near-Infrared Fluorescent Rhodopsin Using a Synthetic Chromophore. <i>Cell Chemical Biology</i> , 2017, 24, 415-425. | 2.5 | 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. | 9.4 | 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. | 1.2 | 51 |
| 35 | Noncommutative Biology: Sequential Regulation of Complex Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005089. | 1.5 | 16 |
| 36 | Turning single cells into microarrays by super-resolution barcoding. <i>Briefings in Functional Genomics</i> , 2013, 12, 75-80. | 1.3 | 10 |

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|----|--|-----|-----------|
| 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. | 2.0 | 3 |
| 39 | Single cell biologyâ€™a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97. | 1.8 | 3 |
| 40 | Supplementary Protocol for RNA SPOTs. Protocol Exchange, 0, , . | 0.3 | 1 |
| 41 | RNA seqFISH+ Supplementary Protocol. Protocol Exchange, 0, , . | 0.3 | 1 |