

Arjun Raj

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

19,946
citations

46918

47
h-index

46693

89
g-index

122
all docs

122
docs citations

122
times ranked

25280
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell type determination for cardiac differentiation occurs soon after seeding of human-induced pluripotent stem cells. <i>Genome Biology</i> , 2022, 23, 90.	3.8	13
2	Systematically quantifying morphological features reveals constraints on organoid phenotypes. <i>Cell Systems</i> , 2022, 13, 547-560.e3.	2.9	8
3	Variability within rare cell states enables multiple paths toward drug resistance. <i>Nature Biotechnology</i> , 2021, 39, 865-876.	9.4	94
4	p53 mediates target gene association with nuclear speckles for amplified RNA expression. <i>Molecular Cell</i> , 2021, 81, 1666-1681.e6.	4.5	41
5	Responsiveness to perturbations is a hallmark of transcription factors that maintain cell identity in <i>Àvitro</i> . <i>Cell Systems</i> , 2021, 12, 885-899.e8.	2.9	17
6	Genetic screening for single-cell variability modulators driving therapy resistance. <i>Nature Genetics</i> , 2021, 53, 76-85.	9.4	41
7	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	1.8	3
8	Memory Sequencing Reveals Heritable Single-Cell Gene Expression Programs Associated with Distinct Cellular Behaviors. <i>Cell</i> , 2020, 182, 947-959.e17.	13.5	132
9	Social reprogramming in ants induces longevity-associated glia remodeling. <i>Science Advances</i> , 2020, 6, eaba9869.	4.7	46
10	Gene Networks with Transcriptional Bursting Recapitulate Rare Transient Coordinated High Expression States in Cancer. <i>Cell Systems</i> , 2020, 10, 363-378.e12.	2.9	54
11	Genetic Variation in Type 1 Diabetes Reconfigures the 3D Chromatin Organization of T Cells and Alters Gene Expression. <i>Immunity</i> , 2020, 52, 257-274.e11.	6.6	42
12	Gene regulation gravitates toward either addition or multiplication when combining the effects of two signals. <i>ELife</i> , 2020, 9, .	2.8	13
13	LADL: light-activated dynamic looping for endogenous gene expression control. <i>Nature Methods</i> , 2019, 16, 633-639.	9.0	108
14	lluminating Genomic Dark Matter with RNA Imaging. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032094.	2.3	17
15	ClampFISH detects individual nucleic acid molecules using click chemistryâ€™based amplification. <i>Nature Biotechnology</i> , 2019, 37, 84-89.	9.4	106
16	Allele-specific RNA imaging shows that allelic imbalances can arise in tissues through transcriptional bursting. <i>PLoS Genetics</i> , 2019, 15, e1007874.	1.5	52
17	Transcriptional Burst Initiation and Polymerase Pause Release Are Key Control Points of Transcriptional Regulation. <i>Molecular Cell</i> , 2019, 73, 519-532.e4.	4.5	118
18	Remodeling of the Collagen Matrix in Aging Skin Promotes Melanoma Metastasis and Affects Immune Cell Motility. <i>Cancer Discovery</i> , 2019, 9, 64-81.	7.7	260

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19	Rare Cell Detection by Single-Cell RNA Sequencing as Guided by Single-Molecule RNA FISH. <i>Cell Systems</i> , 2018, 6, 171-179.e5.	2.9	111
20	IL-6 Mediates Cross-Talk between Tumor Cells and Activated Fibroblasts in the Tumor Microenvironment. <i>Cancer Research</i> , 2018, 78, 4957-4970.	0.4	203
21	Gene expression distribution deconvolution in single-cell RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6437-E6446.	3.3	93
22	SAVER: gene expression recovery for single-cell RNA sequencing. <i>Nature Methods</i> , 2018, 15, 539-542.	9.0	574
23	Quanti.us: a tool for rapid, flexible, crowd-based annotation of images. <i>Nature Methods</i> , 2018, 15, 587-590.	9.0	50
24	Rare cell variability and drug-induced reprogramming as a mode of cancer drug resistance. <i>Nature</i> , 2017, 546, 431-435.	13.7	938
25	Visualizing adenosine-to-inosine RNA editing in single mammalian cells. <i>Nature Methods</i> , 2017, 14, 801-804.	9.0	33
26	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. <i>Molecular Cell</i> , 2017, 66, 102-116.e7.	4.5	114
27	FISHing Out the Details of CRISPR Genome Tracks. <i>Biophysical Journal</i> , 2017, 112, 1045-1046.	0.2	0
28	Molecular memoirs of a cellular family. <i>Nature</i> , 2017, 541, 38-39.	13.7	2
29	Intercellular mRNA trafficking via membrane nanotube-like extensions in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9873-E9882.	3.3	75
30	Replication defective viral genomes exploit a cellular pro-survival mechanism to establish paramyxovirus persistence. <i>Nature Communications</i> , 2017, 8, 799.	5.8	58
31	Group 1 Innate Lymphoid Cell Lineage Identity Is Determined by a cis-Regulatory Element Marked by a Long Non-coding RNA. <i>Immunity</i> , 2017, 47, 435-449.e8.	6.6	57
32	Tumor-associated B-cells induce tumor heterogeneity and therapy resistance. <i>Nature Communications</i> , 2017, 8, 607.	5.8	109
33	Mitotic transcription and waves of gene reactivation during mitotic exit. <i>Science</i> , 2017, 358, 119-122.	6.0	201
34	A magnetic micropore chip for rapid (<1 hour) unbiased circulating tumor cell isolation and in situ RNA analysis. <i>Lab on A Chip</i> , 2017, 17, 3086-3096.	3.1	38
35	ç®çš,ç°èfžā®ā±€âœ"ā*ââ«é-Çäj,ā,'âĈæ™,ā«èj½è:jâ~èf½āââ^†â. <i>Nature Digest</i> , 2017, 14, 33-35.	0.0	0
36	Neutrophils and Ly6Chi monocytes collaborate in generating an optimal cytokine response that protects against pulmonary Legionella pneumophila infection. <i>PLoS Pathogens</i> , 2017, 13, e1006309.	2.1	26

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37	Nanoscale imaging of RNA with expansion microscopy. <i>Nature Methods</i> , 2016, 13, 679-684.	9.0	314
38	Single-cell differences in matrix gene expression do not predict matrix deposition. <i>Nature Communications</i> , 2016, 7, 10865.	5.8	43
39	Enhancer Regulation of Transcriptional Bursting Parameters Revealed by Forced Chromatin Looping. <i>Molecular Cell</i> , 2016, 62, 237-247.	4.5	296
40	The long non-coding RNA Morrbid regulates Bim and short-lived myeloid cell lifespan. <i>Nature</i> , 2016, 537, 239-243.	13.7	234
41	A hyperactive transcriptional state marks genome reactivation at the mitosisâ€“G1 transition. <i>Genes and Development</i> , 2016, 30, 1423-1439.	2.7	92
42	Whatâ€™s Luck Got to Do with It: Single Cells, Multiple Fates, and Biological Nondeterminism. <i>Molecular Cell</i> , 2016, 62, 788-802.	4.5	179
43	Overlapping cell population expression profiling and regulatory inference in <i>C. elegans</i> . <i>BMC Genomics</i> , 2016, 17, 159.	1.2	6
44	Visualizing allele-specific expression in single cells reveals epigenetic mosaicism in an <i>H19</i> loss-of-imprinting mutant. <i>Genes and Development</i> , 2016, 30, 567-578.	2.7	38
45	Transcriptional Bursting Explains the Noiseâ€“Versusâ€“Mean Relationship in mRNA and Protein Levels. <i>PLoS ONE</i> , 2016, 11, e0158298.	1.1	60
46	Heterogeneous lineage marker expression in naive embryonic stem cells is mostly due to spontaneous differentiation. <i>Scientific Reports</i> , 2015, 5, 13339.	1.6	21
47	Visualization of lncRNA by Single-Molecule Fluorescence In Situ Hybridization. <i>Methods in Molecular Biology</i> , 2015, 1262, 3-19.	0.4	68
48	The Bicoid Class Homeodomain Factors <i>ceh-36/OTX</i> and <i>unc-30/PITX</i> Cooperate in <i>C. elegans</i> Embryonic Progenitor Cells to Regulate Robust Development. <i>PLoS Genetics</i> , 2015, 11, e1005003.	1.5	29
49	Multiplexed detection of viral infections using rapid in situ RNA analysis on a chip. <i>Lab on A Chip</i> , 2015, 15, 3170-3182.	3.1	22
50	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , 2015, 16, 20.	3.8	565
51	Single Mammalian Cells Compensate for Differences in Cellular Volume and DNA Copy Number through Independent Global Transcriptional Mechanisms. <i>Molecular Cell</i> , 2015, 58, 339-352.	4.5	429
52	Half dozen of one, six billion of the other: What can small- and large-scale molecular systems biology learn from one another?. <i>Genome Research</i> , 2015, 25, 1466-1472.	2.4	19
53	Dynamic enhancerâ€“gene body contacts during transcription elongation. <i>Genes and Development</i> , 2015, 29, 1992-1997.	2.7	72
54	Identification of a Natural Viral RNA Motif That Optimizes Sensing of Viral RNA by RIG-I. <i>MBio</i> , 2015, 6, e01265-15.	1.8	48

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55	Robust hematopoietic progenitor cell commitment in a noisy environment via suppression of a conflicting signal. <i>Journal of Cell Science</i> , 2015, 128, 3009-17.	1.2	3
56	Inhibition of intestinal tumor formation by deletion of the DNA methyltransferase 3a. <i>Oncogene</i> , 2015, 34, 1822-1830.	2.6	25
57	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 198-206.	3.6	565
58	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. <i>Blood</i> , 2014, 123, 1927-1937.	0.6	169
59	Stochastic NANOG fluctuations allow mouse embryonic stem cells to explore pluripotency. <i>Development (Cambridge)</i> , 2014, 141, 2770-2779.	1.2	120
60	Nup98 promotes antiviral gene expression to restrict RNA viral infection in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3890-9.	3.3	39
61	RNA sequencing in situ. <i>Nature Biotechnology</i> , 2014, 32, 543-544.	9.4	7
62	LincRNA-p21 Activates p21 In cis to Promote Polycomb Target Gene Expression and to Enforce the G1/S Checkpoint. <i>Molecular Cell</i> , 2014, 54, 777-790.	4.5	412
63	Tumor endothelial marker 1-specific DNA vaccination targets tumor vasculature. <i>Journal of Clinical Investigation</i> , 2014, 124, 1497-1511.	3.9	59
64	Visualizing SNVs to quantify allele-specific expression in single cells. <i>Nature Methods</i> , 2013, 10, 865-867.	9.0	100
65	Using variability in gene expression as a tool for studying gene regulation. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 751-759.	6.6	26
66	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	13.7	810
67	Single-chromosome transcriptional profiling reveals chromosomal gene expression regulation. <i>Nature Methods</i> , 2013, 10, 246-248.	9.0	147
68	Gene transcription is coordinated with, but not dependent on, cell divisions during <i>C. elegans</i> embryonic fate specification. <i>Development (Cambridge)</i> , 2013, 140, 3385-3394.	1.2	31
69	<i>linc-HOXA1</i> is a noncoding RNA that represses <i>Hoxa1</i> transcription in <i>cis</i> . <i>Genes and Development</i> , 2013, 27, 1260-1271.	2.7	120
70	Quantitative assessment of ratiometric bimolecular beacons as a tool for imaging single engineered RNA transcripts and measuring gene expression in living cells. <i>Nucleic Acids Research</i> , 2013, 41, e152-e152.	6.5	24
71	Turbo FISH: A Method for Rapid Single Molecule RNA FISH. <i>PLoS ONE</i> , 2013, 8, e75120.	1.1	98
72	Hematopoietic Transcriptional Regulation At The Mitosis-G1 Transition. <i>Blood</i> , 2013, 122, 2440-2440.	0.6	0

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73	Spo0A ^{1/4} P Imposes a Temporal Gate for the Bimodal Expression of Competence in <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2012, 8, e1002586.	1.5	44
74	Global Analysis of RNA Secondary Structure in Two Metazoans. <i>Cell Reports</i> , 2012, 1, 69-82.	2.9	126
75	Time-Lapse Transcription. <i>Science</i> , 2011, 332, 431-432.	6.0	1
76	Genes methylated by DNA methyltransferase 3b are similar in mouse intestine and human colon cancer. <i>Journal of Clinical Investigation</i> , 2011, 121, 1748-1752.	3.9	64
77	Single Molecule Imaging of RNA In Situ. <i>Methods in Molecular Biology</i> , 2011, 714, 3-13.	0.4	68
78	Variability in gene expression underlies incomplete penetrance. <i>Nature</i> , 2010, 463, 913-918.	13.7	607
79	Imaging Single mRNA Molecules in Yeast. <i>Methods in Enzymology</i> , 2010, 470, 429-446.	0.4	23
80	Detection of Individual Endogenous RNA Transcripts In Situ Using Multiple Singly Labeled Probes. <i>Methods in Enzymology</i> , 2010, 472, 365-386.	0.4	164
81	Single-Molecule Approaches to Stochastic Gene Expression. <i>Annual Review of Biophysics</i> , 2009, 38, 255-270.	4.5	317
82	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	3.3	2,709
83	Imaging individual mRNA molecules using multiple singly labeled probes. <i>Nature Methods</i> , 2008, 5, 877-879.	9.0	1,770
84	Nature, Nurture, or Chance: Stochastic Gene Expression and Its Consequences. <i>Cell</i> , 2008, 135, 216-226.	13.5	2,236
85	Noise in Gene Expression Determines Cell Fate in <i>Bacillus subtilis</i> . <i>Science</i> , 2007, 317, 526-529.	6.0	622
86	The influence of chromosome flexibility on chromosome transport during anaphase A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5349-5354.	3.3	15
87	Stochastic mRNA Synthesis in Mammalian Cells. <i>PLoS Biology</i> , 2006, 4, e309.	2.6	1,528
88	Mechanism of mRNA transport in the nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17008-17013.	3.3	242
89	Wind survey of high-speed bulk flows and field-aligned beams in the near-Earth plasma sheet. <i>Journal of Geophysical Research</i> , 2002, 107, SMP 3-1-SMP 3-17.	3.3	86
90	The Finite Element Method on the Sierpinski Gasket. <i>Constructive Approximation</i> , 2001, 17, 561-588.	1.8	32