

# Arjun Raj

## List of Publications by Year in descending order

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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	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
2	Nature, Nurture, or Chance: Stochastic Gene Expression and Its Consequences. <i>Cell</i> , 2008, 135, 216-226.	13.5	2,236
3	Imaging individual mRNA molecules using multiple singly labeled probes. <i>Nature Methods</i> , 2008, 5, 877-879.	9.0	1,770
4	Stochastic mRNA Synthesis in Mammalian Cells. <i>PLoS Biology</i> , 2006, 4, e309.	2.6	1,528
5	Rare cell variability and drug-induced reprogramming as a mode of cancer drug resistance. <i>Nature</i> , 2017, 546, 431-435.	13.7	938
6	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	13.7	810
7	Noise in Gene Expression Determines Cell Fate in <i>Bacillus subtilis</i> . <i>Science</i> , 2007, 317, 526-529.	6.0	622
8	Variability in gene expression underlies incomplete penetrance. <i>Nature</i> , 2010, 463, 913-918.	13.7	607
9	SAVER: gene expression recovery for single-cell RNA sequencing. <i>Nature Methods</i> , 2018, 15, 539-542.	9.0	574
10	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
11	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , 2015, 16, 20.	3.8	565
12	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
13	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
14	Single-Molecule Approaches to Stochastic Gene Expression. <i>Annual Review of Biophysics</i> , 2009, 38, 255-270.	4.5	317
15	Nanoscale imaging of RNA with expansion microscopy. <i>Nature Methods</i> , 2016, 13, 679-684.	9.0	314
16	Enhancer Regulation of Transcriptional Bursting Parameters Revealed by Forced Chromatin Looping. <i>Molecular Cell</i> , 2016, 62, 237-247.	4.5	296
17	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
18	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

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19	The long non-coding RNA Morbid regulates Bim and short-lived myeloid cell lifespan. <i>Nature</i> , 2016, 537, 239-243.	13.7	234
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	Mitotic transcription and waves of gene reactivation during mitotic exit. <i>Science</i> , 2017, 358, 119-122.	6.0	201
22	What'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
23	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. <i>Blood</i> , 2014, 123, 1927-1937.	0.6	169
24	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
25	Single-chromosome transcriptional profiling reveals chromosomal gene expression regulation. <i>Nature Methods</i> , 2013, 10, 246-248.	9.0	147
26	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
27	Global Analysis of RNA Secondary Structure in Two Metazoans. <i>Cell Reports</i> , 2012, 1, 69-82.	2.9	126
28	<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
29	Stochastic NANOG fluctuations allow mouse embryonic stem cells to explore pluripotency. <i>Development (Cambridge)</i> , 2014, 141, 2770-2779.	1.2	120
30	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
31	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
32	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
33	Tumor-associated B-cells induce tumor heterogeneity and therapy resistance. <i>Nature Communications</i> , 2017, 8, 607.	5.8	109
34	LADL: light-activated dynamic looping for endogenous gene expression control. <i>Nature Methods</i> , 2019, 16, 633-639.	9.0	108
35	ClampFISH detects individual nucleic acid molecules using click chemistry-based amplification. <i>Nature Biotechnology</i> , 2019, 37, 84-89.	9.4	106
36	Visualizing SNVs to quantify allele-specific expression in single cells. <i>Nature Methods</i> , 2013, 10, 865-867.	9.0	100

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37	Turbo FISH: A Method for Rapid Single Molecule RNA FISH. PLoS ONE, 2013, 8, e75120.	1.1	98
38	Variability within rare cell states enables multiple paths toward drug resistance. Nature Biotechnology, 2021, 39, 865-876.	9.4	94
39	Gene expression distribution deconvolution in single-cell RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6437-E6446.	3.3	93
40	A hyperactive transcriptional state marks genome reactivation at the mitosis→G1 transition. Genes and Development, 2016, 30, 1423-1439.	2.7	92
41	Wind survey of high-speed bulk flows and field-aligned beams in the near-Earth plasma sheet. Journal of Geophysical Research, 2002, 107, SMP 3-1-SMP 3-17.	3.3	86
42	Intercellular mRNA trafficking via membrane nanotube-like extensions in mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9873-E9882.	3.3	75
43	Dynamic enhancer→gene body contacts during transcription elongation. Genes and Development, 2015, 29, 1992-1997.	2.7	72
44	Visualization of lncRNA by Single-Molecule Fluorescence In Situ Hybridization. Methods in Molecular Biology, 2015, 1262, 3-19.	0.4	68
45	Single Molecule Imaging of RNA In Situ. Methods in Molecular Biology, 2011, 714, 3-13.	0.4	68
46	Genes methylated by DNA methyltransferase 3b are similar in mouse intestine and human colon cancer. Journal of Clinical Investigation, 2011, 121, 1748-1752.	3.9	64
47	Transcriptional Bursting Explains the Noise→Versus→Mean Relationship in mRNA and Protein Levels. PLoS ONE, 2016, 11, e0158298.	1.1	60
48	Tumor endothelial marker 1→specific DNA vaccination targets tumor vasculature. Journal of Clinical Investigation, 2014, 124, 1497-1511.	3.9	59
49	Replication defective viral genomes exploit a cellular pro-survival mechanism to establish paramyxovirus persistence. Nature Communications, 2017, 8, 799.	5.8	58
50	Group 1 Innate Lymphoid Cell Lineage Identity Is Determined by a cis-Regulatory Element Marked by a Long Non-coding RNA. Immunity, 2017, 47, 435-449.e8.	6.6	57
51	Gene Networks with Transcriptional Bursting Recapitulate Rare Transient Coordinated High Expression States in Cancer. Cell Systems, 2020, 10, 363-378.e12.	2.9	54
52	Allele-specific RNA imaging shows that allelic imbalances can arise in tissues through transcriptional bursting. PLoS Genetics, 2019, 15, e1007874.	1.5	52
53	Quanti.us: a tool for rapid, flexible, crowd-based annotation of images. Nature Methods, 2018, 15, 587-590.	9.0	50
54	Identification of a Natural Viral RNA Motif That Optimizes Sensing of Viral RNA by RIG-I. MBio, 2015, 6, e01265-15.	1.8	48

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55	Social reprogramming in ants induces longevity-associated glia remodeling. <i>Science Advances</i> , 2020, 6, eaba9869.	4.7	46
56	Spo0A <sup>1/4</sup> 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
57	Single-cell differences in matrix gene expression do not predict matrix deposition. <i>Nature Communications</i> , 2016, 7, 10865.	5.8	43
58	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
59	p53 mediates target gene association with nuclear speckles for amplified RNA expression. <i>Molecular Cell</i> , 2021, 81, 1666-1681.e6.	4.5	41
60	Genetic screening for single-cell variability modulators driving therapy resistance. <i>Nature Genetics</i> , 2021, 53, 76-85.	9.4	41
61	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
62	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
63	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
64	Visualizing adenosine-to-inosine RNA editing in single mammalian cells. <i>Nature Methods</i> , 2017, 14, 801-804.	9.0	33
65	The Finite Element Method on the Sierpinski Gasket. <i>Constructive Approximation</i> , 2001, 17, 561-588.	1.8	32
66	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
67	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
68	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
69	Neutrophils and Ly6Chi monocytes collaborate in generating an optimal cytokine response that protects against pulmonary <i>Legionella pneumophila</i> infection. <i>PLoS Pathogens</i> , 2017, 13, e1006309.	2.1	26
70	Inhibition of intestinal tumor formation by deletion of the DNA methyltransferase 3a. <i>Oncogene</i> , 2015, 34, 1822-1830.	2.6	25
71	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
72	Imaging Single mRNA Molecules in Yeast. <i>Methods in Enzymology</i> , 2010, 470, 429-446.	0.4	23

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73	Multiplexed detection of viral infections using rapid in situ RNA analysis on a chip. Lab on A Chip, 2015, 15, 3170-3182.	3.1	22
74	Heterogeneous lineage marker expression in naive embryonic stem cells is mostly due to spontaneous differentiation. Scientific Reports, 2015, 5, 13339.	1.6	21
75	Half dozen of one, six billion of the other: What can small- and large-scale molecular systems biology learn from one another?. Genome Research, 2015, 25, 1466-1472.	2.4	19
76	lluminating Genomic Dark Matter with RNA Imaging. Cold Spring Harbor Perspectives in Biology, 2019, 11, a032094.	2.3	17
77	Responsiveness to perturbations is a hallmark of transcription factors that maintain cell identity in vitro. Cell Systems, 2021, 12, 885-899.e8.	2.9	17
78	The influence of chromosome flexibility on chromosome transport during anaphase A. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5349-5354.	3.3	15
79	Gene regulation gravitates toward either addition or multiplication when combining the effects of two signals. ELife, 2020, 9, .	2.8	13
80	Cell type determination for cardiac differentiation occurs soon after seeding of human-induced pluripotent stem cells. Genome Biology, 2022, 23, 90.	3.8	13
81	Systematically quantifying morphological features reveals constraints on organoid phenotypes. Cell Systems, 2022, 13, 547-560.e3.	2.9	8
82	RNA sequencing in situ. Nature Biotechnology, 2014, 32, 543-544.	9.4	7
83	Overlapping cell population expression profiling and regulatory inference in C. elegans. BMC Genomics, 2016, 17, 159.	1.2	6
84	Robust hematopoietic progenitor cell commitment in a noisy environment via suppression of a conflicting signal. Journal of Cell Science, 2015, 128, 3009-17.	1.2	3
85	Single cell biology—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	1.8	3
86	Molecular memoirs of a cellular family. Nature, 2017, 541, 38-39.	13.7	2
87	Time-Lapse Transcription. Science, 2011, 332, 431-432.	6.0	1
88	FISHing Out the Details of CRISPR Genome Tracks. Biophysical Journal, 2017, 112, 1045-1046.	0.2	0
89	ç®çš,ç°èfžã®â±€âœ”ã*ââ«é–çä¿,ã,’â€æ™,ã«è¿½/2è·jã¬èf½ã*â^†â. Nature Digest, 2017, 14, 33-35.	0.0	0
90	Hematopoietic Transcriptional Regulation At The Mitosis-G1 Transition. Blood, 2013, 122, 2440-2440.	0.6	0