Alexander van Oudenaarden

List of Publications by Year in descending order

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155 papers 45,227 citations

90 h-index 153

164 all docs

164 docs citations

164 times ranked 51995 citing authors

g-index

#	Article	IF	CITATIONS
1	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11667-11672.	3.3	2,709
2	Nature, Nurture, or Chance: Stochastic Gene Expression and Its Consequences. Cell, 2008, 135, 216-226.	13.5	2,236
3	Imaging individual mRNA molecules using multiple singly labeled probes. Nature Methods, 2008, 5, 877-879.	9.0	1,770
4	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710
5	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547
6	Regulation of noise in the expression of a single gene. Nature Genetics, 2002, 31, 69-73.	9.4	1,443
7	Population genomics of domestic and wild yeasts. Nature, 2009, 458, 337-341.	13.7	1,391
8	Single-cell messenger RNA sequencing reveals rare intestinal cell types. Nature, 2015, 525, 251-255.	13.7	1,091
9	A Single-Cell Transcriptome Atlas of the Human Pancreas. Cell Systems, 2016, 3, 385-394.e3.	2.9	966
10	Cellular Decision Making and Biological Noise: From Microbes to Mammals. Cell, 2011, 144, 910-925.	13.5	944
11	Direct cell reprogramming is a stochastic process amenable to acceleration. Nature, 2009, 462, 595-601.	13.7	936
12	Multistability in the lactose utilization network of Escherichia coli. Nature, 2004, 427, 737-740.	13.7	932
13	Slug and Sox9 Cooperatively Determine the Mammary Stem Cell State. Cell, 2012, 148, 1015-1028.	13.5	830
14	Stochastic switching as a survival strategy in fluctuating environments. Nature Genetics, 2008, 40, 471-475.	9.4	789
15	Single-Cell Expression Analyses during Cellular Reprogramming Reveal an Early Stochastic and a Late Hierarchic Phase. Cell, 2012, 150, 1209-1222.	13.5	769
16	Single-cell sequencing reveals dissociation-induced gene expression in tissue subpopulations. Nature Methods, 2017, 14, 935-936.	9.0	752
17	Noise Propagation in Gene Networks. Science, 2005, 307, 1965-1969.	6.0	746
18	Using Gene Expression Noise to Understand Gene Regulation. Science, 2012, 336, 183-187.	6.0	685

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19	Validation of noise models for single-cell transcriptomics. Nature Methods, 2014, 11, 637-640.	9.0	685
20	MicroRNA-Mediated Feedback and Feedforward Loops Are Recurrent Network Motifs in Mammals. Molecular Cell, 2007, 26, 753-767.	4.5	673
21	Dll1+ secretory progenitor cells revert to stem cells upon crypt damage. Nature Cell Biology, 2012, 14, 1099-1104.	4.6	647
22	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent â€~+4' cell markers. EMBO Journal, 2012, 31, 3079-3091.	3.5	634
23	Variability in gene expression underlies incomplete penetrance. Nature, 2010, 463, 913-918.	13.7	607
24	Snowdrift game dynamics and facultative cheating in yeast. Nature, 2009, 459, 253-256.	13.7	594
25	MicroRNAs can generate thresholds in target gene expression. Nature Genetics, 2011, 43, 854-859.	9.4	568
26	Stochastic Gene Expression in Fluctuating Environments. Genetics, 2004, 167, 523-530.	1.2	492
27	An organoid platform for ovarian cancer captures intra- and interpatient heterogeneity. Nature Medicine, 2019, 25, 838-849.	15.2	486
28	De Novo Prediction of Stem Cell Identity using Single-Cell Transcriptome Data. Cell Stem Cell, 2016, 19, 266-277.	5.2	484
29	Enhancement of cellular memory by reducing stochastic transitions. Nature, 2005, 435, 228-232.	13.7	476
30	Replacement of Lost Lgr5-Positive Stem Cells through Plasticity of Their Enterocyte-Lineage Daughters. Cell Stem Cell, 2016, 18, 203-213.	5.2	451
31	Design and Analysis of Single-Cell Sequencing Experiments. Cell, 2015, 163, 799-810.	13.5	441
32	Integrated genome and transcriptome sequencing of the same cell. Nature Biotechnology, 2015, 33, 285-289.	9.4	439
33	Spatially resolved transcriptomics and beyond. Nature Reviews Genetics, 2015, 16, 57-66.	7.7	406
34	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. Cell, 2015, 163, 134-147.	13.5	399
35	Highly expressed loci are vulnerable to misleading ChIP localization of multiple unrelated proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18602-18607.	3.3	373
36	Blastocyst-like structures generated solely from stem cells. Nature, 2018, 557, 106-111.	13.7	366

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37	Whole-organism clone tracing using single-cell sequencing. Nature, 2018, 556, 108-112.	13.7	345
38	MicroRNA control of protein expression noise. Science, 2015, 348, 128-132.	6.0	337
39	A Systems-Level Analysis of Perfect Adaptation in Yeast Osmoregulation. Cell, 2009, 138, 160-171.	13.5	336
40	The Frequency Dependence of Osmo-Adaptation in <i>Saccharomyces cerevisiae</i> . Science, 2008, 319, 482-484.	6.0	320
41	Single-Molecule Approaches to Stochastic Gene Expression. Annual Review of Biophysics, 2009, 38, 255-270.	4.5	317
42	An in vitro model of early anteroposterior organization during human development. Nature, 2020, 582, 410-415.	13.7	310
43	Single-Cell Transcriptomics Meets Lineage Tracing. Cell Stem Cell, 2018, 23, 166-179.	5.2	306
44	Contributions of low molecule number and chromosomal positioning to stochastic gene expression. Nature Genetics, 2005, 37, 937-944.	9.4	291
45	Identifying the Stem Cell of the Intestinal Crypt: Strategies and Pitfalls. Cell Stem Cell, 2012, 11, 452-460.	5 . 2	278
46	Single-cell and spatial transcriptomics reveal somitogenesis in gastruloids. Nature, 2020, 582, 405-409.	13.7	274
47	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. Molecular Systems Biology, 2011, 7, 497.	3.2	265
48	Systematic Identification of Signal-Activated Stochastic Gene Regulation. Science, 2013, 339, 584-587.	6.0	250
49	Genome-wide RNA Tomography in the Zebrafish Embryo. Cell, 2014, 159, 662-675.	13.5	248
50	Inference of Tumor Evolution during Chemotherapy by Computational Modeling and In Situ Analysis of Genetic and Phenotypic Cellular Diversity. Cell Reports, 2014, 6, 514-527.	2.9	239
51	Transcription of Two Long Noncoding RNAs Mediates Mating-Type Control of Gametogenesis in Budding Yeast. Cell, 2012, 150, 1170-1181.	13.5	235
52	Reg4 ⁺ deep crypt secretory cells function as epithelial niche for Lgr5 ⁺ stem cells in colon. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5399-407.	3.3	232
53	Single-Cell Sequencing of the Healthy and Diseased Heart Reveals Cytoskeleton-Associated Protein 4 as a New Modulator of Fibroblasts Activation. Circulation, 2018, 138, 166-180.	1.6	231
54	Oral Mucosal Organoids as a Potential Platform for Personalized Cancer Therapy. Cancer Discovery, 2019, 9, 852-871.	7.7	222

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55	Attenuation of Noise in Ultrasensitive Signaling Cascades. Biophysical Journal, 2002, 82, 2943-2950.	0.2	220
56	Ascl2 Acts as an R-spondin/Wnt-Responsive Switch to Control Stemness in Intestinal Crypts. Cell Stem Cell, 2015, 16, 158-170.	5.2	217
57	A Critical Role for the Wnt Effector Tcf4 in Adult Intestinal Homeostatic Self-Renewal. Molecular and Cellular Biology, 2012, 32, 1918-1927.	1.1	216
58	Genome-wide Dissection of MicroRNA Functions and Cotargeting Networks Using Gene Set Signatures. Molecular Cell, 2010, 38, 140-153.	4.5	212
59	A Single-Cell RNA Sequencing Study Reveals Cellular and Molecular Dynamics of the Hippocampal Neurogenic Niche. Cell Reports, 2017, 21, 3271-3284.	2.9	204
60	Synthetic biology: understanding biological design from synthetic circuits. Nature Reviews Genetics, 2009, 10, 859-871.	7.7	201
61	Validating transcripts with probes and imaging technology. Nature Methods, 2011, 8, S12-S19.	9.0	199
62	Single-molecule mRNA detection and counting in mammalian tissue. Nature Protocols, 2013, 8, 1743-1758.	5.5	187
63	Global discovery of erythroid long noncoding RNAs reveals novel regulators of red cell maturation. Blood, 2014, 123, 570-581.	0.6	181
64	Differential Stoichiometry among Core Ribosomal Proteins. Cell Reports, 2015, 13, 865-873.	2.9	178
65	Every Cell Is Special: Genome-wide Studies Add a New Dimension to Single-Cell Biology. Cell, 2014, 157, 8-11.	13.5	177
66	Probing polymerization forces by using actin-propelled lipid vesicles. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4521-4526.	3.3	176
67	Spatially Resolved Genome-wide Transcriptional Profiling Identifies BMP Signaling as Essential Regulator of Zebrafish Cardiomyocyte Regeneration. Developmental Cell, 2016, 36, 36-49.	3.1	176
68	Ongoing chromosomal instability and karyotype evolution in human colorectal cancer organoids. Nature Genetics, 2019, 51, 824-834.	9.4	162
69	Genetic and Phenotypic Diversity in Breast Tumor Metastases. Cancer Research, 2014, 74, 1338-1348.	0.4	161
70	A Novel Sperm-Delivered Toxin Causes Late-Stage Embryo Lethality and Transmission Ratio Distortion in C. elegans. PLoS Biology, 2011, 9, e1001115.	2.6	158
71	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes and Development, 2012, 26, 2802-2816.	2.7	158
72	Identity and dynamics of mammary stem cells during branching morphogenesis. Nature, 2017, 542, 313-317.	13.7	157

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73	Stochastic gene expression: from single molecules to the proteome. Current Opinion in Genetics and Development, 2007, 17, 107-112.	1.5	156
74	Predicting stochastic gene expression dynamics in single cells. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7304-7309.	3.3	152
75	Quantitative Time-Lapse Fluorescence Microscopy in Single Cells. Annual Review of Cell and Developmental Biology, 2009, 25, 301-327.	4.0	152
76	Circadian Gating of the Cell Cycle Revealed in Single Cyanobacterial Cells. Science, 2010, 327, 1522-1526.	6.0	152
77	A physical sciences network characterization of non-tumorigenic and metastatic cells. Scientific Reports, 2013, 3, 1449.	1.6	146
78	Single-cell 5hmC sequencing reveals chromosome-wide cell-to-cell variability and enables lineage reconstruction. Nature Biotechnology, 2016, 34, 852-856.	9.4	144
79	Optimality in the Development of Intestinal Crypts. Cell, 2012, 148, 608-619.	13.5	142
80	Motility of Escherichia coli cells in clusters formed by chemotactic aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13259-13263.	3.3	138
81	Troy+ brain stem cells cycle through quiescence and regulate their number by sensing niche occupancy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E610-E619.	3.3	138
82	Elevated ATPase Activity of KaiC Applies a Circadian Checkpoint on Cell Division in Synechococcus elongatus. Cell, 2010, 140, 529-539.	13.5	136
83	A System of Counteracting Feedback Loops Regulates Cdc42p Activity during Spontaneous Cell Polarization. Developmental Cell, 2005, 9, 565-571.	3.1	131
84	Cooperative symmetry-breaking by actin polymerization in a model for cell motility. Nature Cell Biology, 1999, 1, 493-499.	4.6	124
85	Unravelling cellular relationships during development and regeneration using genetic lineage tracing. Nature Reviews Molecular Cell Biology, 2019, 20, 753-765.	16.1	124
86	Mapping the physical network of cellular interactions. Nature Methods, 2018, 15, 547-553.	9.0	121
87	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
88	Expansion of Adult Human Pancreatic Tissue Yields Organoids Harboring Progenitor Cells with Endocrine Differentiation Potential. Stem Cell Reports, 2018, 10, 712-724.	2.3	106
89	Heritable Stochastic Switching Revealed by Single-Cell Genealogy. PLoS Biology, 2007, 5, e239.	2.6	105
90	Single-Cell Analysis Reveals that Noncoding RNAs Contribute to Clonal Heterogeneity by Modulating Transcription Factor Recruitment. Molecular Cell, 2012, 45, 470-482.	4.5	100

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91	Single-cell transcriptomics reveal the dynamic of haematopoietic stem cell production in the aorta. Nature Communications, 2018, 9, 2517.	5. 8	99
92	Magneto-electric Aharonov–Bohm effect in metal rings. Nature, 1998, 391, 768-770.	13.7	98
93	A multistep epigenetic switch enables the stable inheritance of DNA methylation states. Nature Genetics, 2007, 39, 269-275.	9.4	98
94	Stochastic gene expression out-of-steady-state in the cyanobacterial circadian clock. Nature, 2007, 450, 1249-1252.	13.7	97
95	Dampening of expression oscillations by synchronous regulation of a microRNA and its target. Nature Genetics, 2013, 45, 1337-1344.	9.4	96
96	A Gene Regulatory Program for Meiotic Prophase in the Fetal Ovary. PLoS Genetics, 2015, 11, e1005531.	1.5	93
97	Sequencing metabolically labeled transcripts in single cells reveals mRNA turnover strategies. Science, 2020, 367, 1151-1156.	6.0	92
98	A General Mechanism for Network-Dosage Compensation in Gene Circuits. Science, 2010, 329, 1656-1660.	6.0	87
99	Constant Growth Rate Can Be Supported by Decreasing Energy Flux and Increasing Aerobic Glycolysis. Cell Reports, 2014, 7, 705-714.	2.9	85
100	One-Dimensional Mott Insulator Formed by Quantum Vortices in Josephson Junction Arrays. Physical Review Letters, 1996, 76, 4947-4950.	2.9	83
101	Repetitive sequence variation and dynamics in the ribosomal DNA array of Saccharomyces cerevisiae as revealed by whole-genome resequencing. Genome Research, 2009, 19, 626-635.	2.4	82
102	Tomo-Seq Identifies SOX9 as a Key Regulator of Cardiac Fibrosis During Ischemic Injury. Circulation, 2017, 136, 1396-1409.	1.6	81
103	Single-cell Ribo-seq reveals cell cycle-dependent translational pausing. Nature, 2021, 597, 561-565.	13.7	81
104	Growth landscape formed by perception and import of glucose in yeast. Nature, 2009, 462, 875-879.	13.7	80
105	Robustness and Epistasis in the C.Âelegans Vulval Signaling Network Revealed by Pathway Dosage Modulation. Developmental Cell, 2013, 24, 64-75.	3.1	77
106	Feedback Control of Gene Expression Variability in the Caenorhabditis elegans Wnt Pathway. Cell, 2013, 155, 869-880.	13.5	75
107	Cellular asymmetry and individuality in directional sensing. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11549-11554.	3.3	72
108	High-throughput total RNA sequencing in single cells using VASA-seq. Nature Biotechnology, 2022, 40, 1780-1793.	9.4	70

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109	Tdrd6a Regulates the Aggregation of Buc into Functional Subcellular Compartments that Drive Germ Cell Specification. Developmental Cell, 2018, 46, 285-301.e9.	3.1	68
110	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. Nature Methods, 2013, 10, 122-124.	9.0	66
111	Enteroendocrine and tuft cells support Lgr5 stem cells on Paneth cell depletion. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26599-26605.	3.3	66
112	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
113	Allele-specific detection of single mRNA molecules in situ. Nature Methods, 2013, 10, 869-871.	9.0	64
114	Biomimetic Systems for Studying Actin-Based Motility. Current Biology, 2003, 13, R734-R744.	1.8	63
115	3D gastruloids: a novel frontier in stem cell-based in vitro modeling of mammalian gastrulation. Trends in Cell Biology, 2021, 31, 747-759.	3.6	63
116	Circadian networks in human embryonic stem cellâ€derived cardiomyocytes. EMBO Reports, 2017, 18, 1199-1212.	2.0	61
117	Stochastic Cytokine Expression Induces Mixed T Helper Cell States. PLoS Biology, 2013, 11, e1001618.	2.6	56
118	Spatial Transcriptomics of C.Âelegans Males and Hermaphrodites Identifies Sex-Specific Differences in Gene Expression Patterns. Developmental Cell, 2018, 47, 801-813.e6.	3.1	55
119	Licensing of Primordial Germ Cells for Gametogenesis Depends on Genital Ridge Signaling. PLoS Genetics, 2015, 11, e1005019.	1.5	48
120	Transcript counting in single cells reveals dynamics of rDNA transcription. Molecular Systems Biology, 2010, 6, 358.	3.2	45
121	BMP gradient along the intestinal villus axis controls zonated enterocyte and goblet cell states. Cell Reports, 2022, 38, 110438.	2.9	45
122	Studying Lineage Decision-Making In Vitro: Emerging Concepts and Novel Tools. Annual Review of Cell and Developmental Biology, 2015, 31, 317-345.	4.0	41
123	<i>Caenorhabditis elegans aristaless/Arx</i> gene <i>alr-1</i> restricts variable gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4063-4068.	3.3	40
124	The Caenorhabditis elegans Synthetic Multivulva Genes Prevent Ras Pathway Activation by Tightly Repressing Global Ectopic Expression of lin-3 EGF. PLoS Genetics, 2011, 7, e1002418.	1.5	38
125	H3K9me selectively blocks transcription factor activity and ensures differentiated tissue integrity. Nature Cell Biology, 2021, 23, 1163-1175.	4.6	37
126	Cell Intrinsic Modulation of Wnt Signaling Controls Neuroblast Migration in C.Âelegans. Developmental Cell, 2014, 31, 188-201.	3.1	36

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127	Transcriptional profiling of cells sorted by RNA abundance. Nature Methods, 2014, 11, 549-551.	9.0	34
128	The thrombospondin repeat containing protein MIG-21 controls a left–right asymmetric Wnt signaling response in migrating C. elegans neuroblasts. Developmental Biology, 2012, 361, 338-348.	0.9	33
129	Necessary Noise. Science, 2007, 317, 463-464.	6.0	32
130	A Predictive Model of Bifunctional Transcription Factor Signaling during Embryonic Tissue Patterning. Developmental Cell, 2014, 31, 448-460.	3.1	31
131	One-Dimensional Localization of Quantum Vortices in Disordered Josephson Junction Arrays. Physical Review Letters, 1996, 77, 4257-4260.	2.9	30
132	The yin and yang of nature. Nature, 2009, 457, 271-272.	13.7	29
133	Elastic Instability in Growing Yeast Colonies. Biophysical Journal, 2004, 86, 2740-2747.	0.2	28
134	DAZL regulates Tet1 translation in murine embryonic stem cells. EMBO Reports, 2015, 16, 791-802.	2.0	24
135	Imaging Single mRNA Molecules in Yeast. Methods in Enzymology, 2010, 470, 429-446.	0.4	23
136	Amplitude control of cell-cycle waves by nuclear import. Nature Cell Biology, 2004, 6, 451-457.	4.6	17
137	Single-Cell Transcriptomics Enters the Age of Mass Production. Molecular Cell, 2015, 58, 563-564.	4.5	17
138	Viral genome imaging of hepatitis C virus to probe heterogeneous viral infection and responses to antiviral therapies. Virology, 2016, 494, 236-247.	1.1	17
139	Spatial transcriptomics unveils ZBTB11 as a regulator of cardiomyocyte degeneration in arrhythmogenic cardiomyopathy. Cardiovascular Research, 2023, 119, 477-491.	1.8	17
140	Strand-specific single-cell methylomics reveals distinct modes of DNA demethylation dynamics during early mammalian development. Nature Communications, 2021, 12, 1286.	5.8	16
141	When It Comes to Decisions, Myeloid Progenitors Crave Positive Feedback. Cell, 2006, 126, 650-652.	13.5	14
142	Coupling cellular oscillators—circadian and cell division cycles in cyanobacteria. Current Opinion in Genetics and Development, 2010, 20, 613-618.	1.5	14
143	A Caenorhabditis elegans protein with a PRDM9-like SET domain localizes to chromatin-associated foci and promotes spermatocyte gene expression, sperm production and fertility. PLoS Genetics, 2018, 14, e1007295.	1.5	14
144	Actin Polymerization: Forcing Flat Faces Forward. Current Biology, 2004, 14, R467-R469.	1.8	11

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145	Patched Receptors Sense, Interpret, and Establish an Epidermal Hedgehog SignalingÂGradient. Journal of Investigative Dermatology, 2017, 137, 179-186.	0.3	11
146	Altruistic defence. Nature, 2010, 467, 34-35.	13.7	10
147	Transcription Factor Induction of Ectopic Vascular Blood Stem Cell Niches In Vivo. Blood, 2019, 134, 525-525.	0.6	5
148	Identification of the stress granule transcriptome via RNA-editing in single cells and inÂvivo. Cell Reports Methods, 2022, 2, 100235.	1.4	5
149	Bloch vortices in one-dimensional Josephson junction arrays. European Physical Journal D, 1996, 46, 707-708.	0.4	4
150	When Noisy Neighbors Are a Blessing: Analysis of Gene Expression Noise Identifies Coregulated Genes. Molecular Cell, 2012, 45, 437-438.	4.5	4
151	Deconvolving the roles of Wnt ligands and receptors in sensing and amplification. Molecular Systems Biology, 2013, 9, 631.	3.2	4
152	How to Regulate a Gene: To Repress or to Activate?. Molecular Cell, 2012, 46, 551-552.	4.5	0
153	Genome-wide RNA tomography analysis of the microenvironment promoting hematopoietic stem cell emergence in the embryo aorta. Experimental Hematology, 2015, 43, S104.	0.2	0
154	Celebrating 100 years of Developmental Biology at the Hubrecht Institute. Developmental Biology, 2017, 428, 259-260.	0.9	0
155	Genome-Wide RNA Tomography of the Hematopoietic Stem Cell Niche in Zebrafish Reveals Unexpected Functional Macrophage-Stem Cell Interactions. Blood, 2016, 128, 3882-3882.	0.6	O