

Alexander van Oudenaarden

List of Publications by Year in descending order

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155
papers

45,227
citations

3531

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all docs

164
docs citations

164
times ranked

51995
citing authors

#	ARTICLE	IF	CITATIONS
1	Spatial transcriptomics unveils ZBTB11 as a regulator of cardiomyocyte degeneration in arrhythmogenic cardiomyopathy. Cardiovascular Research, 2023, 119, 477-491.	3.8	17
2	BMP gradient along the intestinal villus axis controls zonated enterocyte and goblet cell states. Cell Reports, 2022, 38, 110438.	6.4	45
3	Identification of the stress granule transcriptome via RNA-editing in single cells and in vivo. Cell Reports Methods, 2022, 2, 100235.	2.9	5
4	High-throughput total RNA sequencing in single cells using VASA-seq. Nature Biotechnology, 2022, 40, 1780-1793.	17.5	70
5	Strand-specific single-cell methylomics reveals distinct modes of DNA demethylation dynamics during early mammalian development. Nature Communications, 2021, 12, 1286.	12.8	16
6	3D gastruloids: a novel frontier in stem cell-based in vitro modeling of mammalian gastrulation. Trends in Cell Biology, 2021, 31, 747-759.	7.9	63
7	Single-cell Ribo-seq reveals cell cycle-dependent translational pausing. Nature, 2021, 597, 561-565.	27.8	81
8	H3K9me selectively blocks transcription factor activity and ensures differentiated tissue integrity. Nature Cell Biology, 2021, 23, 1163-1175.	10.3	37
9	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
10	Sequencing metabolically labeled transcripts in single cells reveals mRNA turnover strategies. Science, 2020, 367, 1151-1156.	12.6	92
11	Single-cell and spatial transcriptomics reveal somitogenesis in gastruloids. Nature, 2020, 582, 405-409.	27.8	274
12	An in vitro model of early anteroposterior organization during human development. Nature, 2020, 582, 410-415.	27.8	310
13	Unravelling cellular relationships during development and regeneration using genetic lineage tracing. Nature Reviews Molecular Cell Biology, 2019, 20, 753-765.	37.0	124
14	An organoid platform for ovarian cancer captures intra- and interpatient heterogeneity. Nature Medicine, 2019, 25, 838-849.	30.7	486
15	Oral Mucosal Organoids as a Potential Platform for Personalized Cancer Therapy. Cancer Discovery, 2019, 9, 852-871.	9.4	222
16	Ongoing chromosomal instability and karyotype evolution in human colorectal cancer organoids. Nature Genetics, 2019, 51, 824-834.	21.4	162
17	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.	7.1	66
18	Transcription Factor Induction of Ectopic Vascular Blood Stem Cell Niches In Vivo. Blood, 2019, 134, 525-525.	1.4	5

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19	Single-Cell Sequencing of the Healthy and Diseased Heart Reveals Cytoskeleton-Associated Protein 4 as a New Modulator of Fibroblasts Activation. <i>Circulation</i> , 2018, 138, 166-180.	1.6	231
20	Troy+ brain stem cells cycle through quiescence and regulate their number by sensing niche occupancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E610-E619.	7.1	138
21	Blastocyst-like structures generated solely from stem cells. <i>Nature</i> , 2018, 557, 106-111.	27.8	366
22	Expansion of Adult Human Pancreatic Tissue Yields Organoids Harboring Progenitor Cells with Endocrine Differentiation Potential. <i>Stem Cell Reports</i> , 2018, 10, 712-724.	4.8	106
23	Whole-organism clone tracing using single-cell sequencing. <i>Nature</i> , 2018, 556, 108-112.	27.8	345
24	Spatial Transcriptomics of <i>C.Âelegans</i> Males and Hermaphrodites Identifies Sex-Specific Differences in Gene Expression Patterns. <i>Developmental Cell</i> , 2018, 47, 801-813.e6.	7.0	55
25	Mapping the physical network of cellular interactions. <i>Nature Methods</i> , 2018, 15, 547-553.	19.0	121
26	Single-cell transcriptomics reveal the dynamic of haematopoietic stem cell production in the aorta. <i>Nature Communications</i> , 2018, 9, 2517.	12.8	99
27	Tdrd6a Regulates the Aggregation of Buc into Functional Subcellular Compartments that Drive Germ Cell Specification. <i>Developmental Cell</i> , 2018, 46, 285-301.e9.	7.0	68
28	Single-Cell Transcriptomics Meets Lineage Tracing. <i>Cell Stem Cell</i> , 2018, 23, 166-179.	11.1	306
29	A <i>Caenorhabditis elegans</i> protein with a PRDM9-like SET domain localizes to chromatin-associated foci and promotes spermatocyte gene expression, sperm production and fertility. <i>PLoS Genetics</i> , 2018, 14, e1007295.	3.5	14
30	Identity and dynamics of mammary stem cells during branching morphogenesis. <i>Nature</i> , 2017, 542, 313-317.	27.8	157
31	Celebrating 100 years of Developmental Biology at the Hubrecht Institute. <i>Developmental Biology</i> , 2017, 428, 259-260.	2.0	0
32	Circadian networks in human embryonic stem cellâ€derived cardiomyocytes. <i>EMBO Reports</i> , 2017, 18, 1199-1212.	4.5	61
33	Single-cell sequencing reveals dissociation-induced gene expression in tissue subpopulations. <i>Nature Methods</i> , 2017, 14, 935-936.	19.0	752
34	Tomo-Seq Identifies SOX9 as a Key Regulator of Cardiac Fibrosis During Ischemic Injury. <i>Circulation</i> , 2017, 136, 1396-1409.	1.6	81
35	A Single-Cell RNA Sequencing Study Reveals Cellular and Molecular Dynamics of the Hippocampal Neurogenic Niche. <i>Cell Reports</i> , 2017, 21, 3271-3284.	6.4	204
36	Patched Receptors Sense, Interpret, and Establish an Epidermal Hedgehog SignalingÂGradient. <i>Journal of Investigative Dermatology</i> , 2017, 137, 179-186.	0.7	11

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37	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
38	De Novo Prediction of Stem Cell Identity using Single-Cell Transcriptome Data. Cell Stem Cell, 2016, 19, 266-277.	11.1	484
39	Viral genome imaging of hepatitis C virus to probe heterogeneous viral infection and responses to antiviral therapies. Virology, 2016, 494, 236-247.	2.4	17
40	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.	7.1	232
41	A Single-Cell Transcriptome Atlas of the Human Pancreas. Cell Systems, 2016, 3, 385-394.e3.	6.2	966
42	Single-cell 5hmC sequencing reveals chromosome-wide cell-to-cell variability and enables lineage reconstruction. Nature Biotechnology, 2016, 34, 852-856.	17.5	144
43	Replacement of Lost Lgr5-Positive Stem Cells through Plasticity of Their Enterocyte-Lineage Daughters. Cell Stem Cell, 2016, 18, 203-213.	11.1	451
44	Spatially Resolved Genome-wide Transcriptional Profiling Identifies BMP Signaling as Essential Regulator of Zebrafish Cardiomyocyte Regeneration. Developmental Cell, 2016, 36, 36-49.	7.0	176
45	Genome-Wide RNA Tomography of the Hematopoietic Stem Cell Niche in Zebrafish Reveals Unexpected Functional Macrophage-Stem Cell Interactions. Blood, 2016, 128, 3882-3882.	1.4	0
46	DAZL regulates Tet1 translation in murine embryonic stem cells. EMBO Reports, 2015, 16, 791-802.	4.5	24
47	Differential Stoichiometry among Core Ribosomal Proteins. Cell Reports, 2015, 13, 865-873.	6.4	178
48	Single-Cell Transcriptomics Enters the Age of Mass Production. Molecular Cell, 2015, 58, 563-564.	9.7	17
49	Studying Lineage Decision-Making In Vitro: Emerging Concepts and Novel Tools. Annual Review of Cell and Developmental Biology, 2015, 31, 317-345.	9.4	41
50	Ascl2 Acts as an R-spondin/Wnt-Responsive Switch to Control Stemness in Intestinal Crypts. Cell Stem Cell, 2015, 16, 158-170.	11.1	217
51	Integrated genome and transcriptome sequencing of the same cell. Nature Biotechnology, 2015, 33, 285-289.	17.5	439
52	Licensing of Primordial Germ Cells for Gametogenesis Depends on Genital Ridge Signaling. PLoS Genetics, 2015, 11, e1005019.	3.5	48
53	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
54	MicroRNA control of protein expression noise. Science, 2015, 348, 128-132.	12.6	337

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55	Design and Analysis of Single-Cell Sequencing Experiments. <i>Cell</i> , 2015, 163, 799-810.	28.9	441
56	Single-cell messenger RNA sequencing reveals rare intestinal cell types. <i>Nature</i> , 2015, 525, 251-255.	27.8	1,091
57	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	28.9	399
58	Genome-wide RNA tomography analysis of the microenvironment promoting hematopoietic stem cell emergence in the embryo aorta. <i>Experimental Hematology</i> , 2015, 43, S104.	0.4	0
59	Spatially resolved transcriptomics and beyond. <i>Nature Reviews Genetics</i> , 2015, 16, 57-66.	16.3	406
60	A Gene Regulatory Program for Meiotic Prophase in the Fetal Ovary. <i>PLoS Genetics</i> , 2015, 11, e1005531.	3.5	93
61	Cell Intrinsic Modulation of Wnt Signaling Controls Neuroblast Migration in <i>C.Âëlegans</i> . <i>Developmental Cell</i> , 2014, 31, 188-201.	7.0	36
62	A Predictive Model of Bifunctional Transcription Factor Signaling during Embryonic Tissue Patterning. <i>Developmental Cell</i> , 2014, 31, 448-460.	7.0	31
63	Global discovery of erythroid long noncoding RNAs reveals novel regulators of red cell maturation. <i>Blood</i> , 2014, 123, 570-581.	1.4	181
64	Inference of Tumor Evolution during Chemotherapy by Computational Modeling and In Situ Analysis of Genetic and Phenotypic Cellular Diversity. <i>Cell Reports</i> , 2014, 6, 514-527.	6.4	239
65	Transcriptional profiling of cells sorted by RNA abundance. <i>Nature Methods</i> , 2014, 11, 549-551.	19.0	34
66	Every Cell Is Special: Genome-wide Studies Add a New Dimension to Single-Cell Biology. <i>Cell</i> , 2014, 157, 8-11.	28.9	177
67	Genetic and Phenotypic Diversity in Breast Tumor Metastases. <i>Cancer Research</i> , 2014, 74, 1338-1348.	0.9	161
68	Genome-wide RNA Tomography in the Zebrafish Embryo. <i>Cell</i> , 2014, 159, 662-675.	28.9	248
69	Validation of noise models for single-cell transcriptomics. <i>Nature Methods</i> , 2014, 11, 637-640.	19.0	685
70	Constant Growth Rate Can Be Supported by Decreasing Energy Flux and Increasing Aerobic Glycolysis. <i>Cell Reports</i> , 2014, 7, 705-714.	6.4	85
71	Allele-specific detection of single mRNA molecules in situ. <i>Nature Methods</i> , 2013, 10, 869-871.	19.0	64
72	Single-molecule mRNA detection and counting in mammalian tissue. <i>Nature Protocols</i> , 2013, 8, 1743-1758.	12.0	187

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73	Robustness and Epistasis in the C.Âlegans Vulval Signaling Network Revealed by Pathway Dosage Modulation. Developmental Cell, 2013, 24, 64-75.	7.0	77
74	Feedback Control of Gene Expression Variability in the Caenorhabditis elegans Wnt Pathway. Cell, 2013, 155, 869-880.	28.9	75
75	Dampening of expression oscillations by synchronous regulation of a microRNA and its target. Nature Genetics, 2013, 45, 1337-1344.	21.4	96
76	Systematic Identification of Signal-Activated Stochastic Gene Regulation. Science, 2013, 339, 584-587.	12.6	250
77	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. Nature Methods, 2013, 10, 122-124.	19.0	66
78	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.	7.1	373
79	Stochastic Cytokine Expression Induces Mixed T Helper Cell States. PLoS Biology, 2013, 11, e1001618.	5.6	56
80	Deconvolving the roles of Wnt ligands and receptors in sensing and amplification. Molecular Systems Biology, 2013, 9, 631.	7.2	4
81	A physical sciences network characterization of non-tumorigenic and metastatic cells. Scientific Reports, 2013, 3, 1449.	3.3	146
82	A Critical Role for the Wnt Effector Tcf4 in Adult Intestinal Homeostatic Self-Renewal. Molecular and Cellular Biology, 2012, 32, 1918-1927.	2.3	216
83	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.	5.9	158
84	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent â€+4â€™ cell markers. EMBO Journal, 2012, 31, 3079-3091.	7.8	634
85	Transcription of Two Long Noncoding RNAs Mediates Mating-Type Control of Gametogenesis in Budding Yeast. Cell, 2012, 150, 1170-1181.	28.9	235
86	Single-Cell Expression Analyses during Cellular Reprogramming Reveal an Early Stochastic and a Late Hierarchic Phase. Cell, 2012, 150, 1209-1222.	28.9	769
87	Dll1+ secretory progenitor cells revert to stem cells upon crypt damage. Nature Cell Biology, 2012, 14, 1099-1104.	10.3	647
88	Single-Cell Analysis Reveals that Noncoding RNAs Contribute to Clonal Heterogeneity by Modulating Transcription Factor Recruitment. Molecular Cell, 2012, 45, 470-482.	9.7	100
89	When Noisy Neighbors Are a Blessing: Analysis of Gene Expression Noise Identifies Coregulated Genes. Molecular Cell, 2012, 45, 437-438.	9.7	4
90	How to Regulate a Gene: To Repress or to Activate?. Molecular Cell, 2012, 46, 551-552.	9.7	0

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91	Optimality in the Development of Intestinal Crypts. <i>Cell</i> , 2012, 148, 608-619.	28.9	142
92	Slug and Sox9 Cooperatively Determine the Mammary Stem Cell State. <i>Cell</i> , 2012, 148, 1015-1028.	28.9	830
93	Identifying the Stem Cell of the Intestinal Crypt: Strategies and Pitfalls. <i>Cell Stem Cell</i> , 2012, 11, 452-460.	11.1	278
94	Using Gene Expression Noise to Understand Gene Regulation. <i>Science</i> , 2012, 336, 183-187.	12.6	685
95	The thrombospondin repeat containing protein MIG-21 controls a leftâ€‘right asymmetric Wnt signaling response in migrating <i>C. elegans</i> neuroblasts. <i>Developmental Biology</i> , 2012, 361, 338-348.	2.0	33
96	MicroRNAs can generate thresholds in target gene expression. <i>Nature Genetics</i> , 2011, 43, 854-859.	21.4	568
97	Cellular Decision Making and Biological Noise: From Microbes to Mammals. <i>Cell</i> , 2011, 144, 910-925.	28.9	944
98	Validating transcripts with probes and imaging technology. <i>Nature Methods</i> , 2011, 8, S12-S19.	19.0	199
99	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	7.2	265
100	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.	8.2	64
101	<i>Caenorhabditis elegans</i> <i>aristaless/Arx</i> gene <i>alr-1</i> restricts variable gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4063-4068.	7.1	40
102	A Novel Sperm-Delivered Toxin Causes Late-Stage Embryo Lethality and Transmission Ratio Distortion in <i>C. elegans</i> . <i>PLoS Biology</i> , 2011, 9, e1001115.	5.6	158
103	The <i>Caenorhabditis elegans</i> Synthetic Multivulva Genes Prevent Ras Pathway Activation by Tightly Repressing Global Ectopic Expression of <i>lin-3</i> EGF. <i>PLoS Genetics</i> , 2011, 7, e1002418.	3.5	38
104	Transcript counting in single cells reveals dynamics of rDNA transcription. <i>Molecular Systems Biology</i> , 2010, 6, 358.	7.2	45
105	Variability in gene expression underlies incomplete penetrance. <i>Nature</i> , 2010, 463, 913-918.	27.8	607
106	Altruistic defence. <i>Nature</i> , 2010, 467, 34-35.	27.8	10
107	A General Mechanism for Network-Dosage Compensation in Gene Circuits. <i>Science</i> , 2010, 329, 1656-1660.	12.6	87
108	Circadian Gating of the Cell Cycle Revealed in Single Cyanobacterial Cells. <i>Science</i> , 2010, 327, 1522-1526.	12.6	152

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109	Imaging Single mRNA Molecules in Yeast. <i>Methods in Enzymology</i> , 2010, 470, 429-446.	1.0	23
110	Genome-wide Dissection of MicroRNA Functions and Cotargeting Networks Using Gene Set Signatures. <i>Molecular Cell</i> , 2010, 38, 140-153.	9.7	212
111	Coupling cellular oscillatorsâ€™ circadian and cell division cycles in cyanobacteria. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 613-618.	3.3	14
112	Elevated ATPase Activity of KaiC Applies a Circadian Checkpoint on Cell Division in <i>Synechococcus elongatus</i> . <i>Cell</i> , 2010, 140, 529-539.	28.9	136
113	Repetitive sequence variation and dynamics in the ribosomal DNA array of <i>Saccharomyces cerevisiae</i> as revealed by whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 626-635.	5.5	82
114	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
115	Snowdrift game dynamics and facultative cheating in yeast. <i>Nature</i> , 2009, 459, 253-256.	27.8	594
116	Direct cell reprogramming is a stochastic process amenable to acceleration. <i>Nature</i> , 2009, 462, 595-601.	27.8	936
117	Growth landscape formed by perception and import of glucose in yeast. <i>Nature</i> , 2009, 462, 875-879.	27.8	80
118	The yin and yang of nature. <i>Nature</i> , 2009, 457, 271-272.	27.8	29
119	Synthetic biology: understanding biological design from synthetic circuits. <i>Nature Reviews Genetics</i> , 2009, 10, 859-871.	16.3	201
120	Quantitative Time-Lapse Fluorescence Microscopy in Single Cells. <i>Annual Review of Cell and Developmental Biology</i> , 2009, 25, 301-327.	9.4	152
121	Single-Molecule Approaches to Stochastic Gene Expression. <i>Annual Review of Biophysics</i> , 2009, 38, 255-270.	10.0	317
122	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.	7.1	2,709
123	A Systems-Level Analysis of Perfect Adaptation in Yeast Osmoregulation. <i>Cell</i> , 2009, 138, 160-171.	28.9	336
124	Stochastic switching as a survival strategy in fluctuating environments. <i>Nature Genetics</i> , 2008, 40, 471-475.	21.4	789
125	Imaging individual mRNA molecules using multiple singly labeled probes. <i>Nature Methods</i> , 2008, 5, 877-879.	19.0	1,770
126	Nature, Nurture, or Chance: Stochastic Gene Expression and Its Consequences. <i>Cell</i> , 2008, 135, 216-226.	28.9	2,236

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127	The Frequency Dependence of Osmo-Adaptation in <i>Saccharomyces cerevisiae</i> . Science, 2008, 319, 482-484.	12.6	320
128	Necessary Noise. Science, 2007, 317, 463-464.	12.6	32
129	Heritable Stochastic Switching Revealed by Single-Cell Genealogy. PLoS Biology, 2007, 5, e239.	5.6	105
130	Stochastic gene expression: from single molecules to the proteome. Current Opinion in Genetics and Development, 2007, 17, 107-112.	3.3	156
131	MicroRNA-Mediated Feedback and Feedforward Loops Are Recurrent Network Motifs in Mammals. Molecular Cell, 2007, 26, 753-767.	9.7	673
132	A multistep epigenetic switch enables the stable inheritance of DNA methylation states. Nature Genetics, 2007, 39, 269-275.	21.4	98
133	Stochastic gene expression out-of-steady-state in the cyanobacterial circadian clock. Nature, 2007, 450, 1249-1252.	27.8	97
134	When It Comes to Decisions, Myeloid Progenitors Crave Positive Feedback. Cell, 2006, 126, 650-652.	28.9	14
135	Cellular asymmetry and individuality in directional sensing. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11549-11554.	7.1	72
136	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.	7.1	152
137	Contributions of low molecule number and chromosomal positioning to stochastic gene expression. Nature Genetics, 2005, 37, 937-944.	21.4	291
138	Enhancement of cellular memory by reducing stochastic transitions. Nature, 2005, 435, 228-232.	27.8	476
139	Noise Propagation in Gene Networks. Science, 2005, 307, 1965-1969.	12.6	746
140	A System of Counteracting Feedback Loops Regulates Cdc42p Activity during Spontaneous Cell Polarization. Developmental Cell, 2005, 9, 565-571.	7.0	131
141	Stochastic Gene Expression in Fluctuating Environments. Genetics, 2004, 167, 523-530.	2.9	492
142	Amplitude control of cell-cycle waves by nuclear import. Nature Cell Biology, 2004, 6, 451-457.	10.3	17
143	Multistability in the lactose utilization network of Escherichia coli. Nature, 2004, 427, 737-740.	27.8	932
144	Actin Polymerization: Forcing Flat Faces Forward. Current Biology, 2004, 14, R467-R469.	3.9	11

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145	Elastic Instability in Growing Yeast Colonies. Biophysical Journal, 2004, 86, 2740-2747.	0.5	28
146	Biomimetic Systems for Studying Actin-Based Motility. Current Biology, 2003, 13, R734-R744.	3.9	63
147	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.	7.1	138
148	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.	7.1	176
149	Attenuation of Noise in Ultrasensitive Signaling Cascades. Biophysical Journal, 2002, 82, 2943-2950.	0.5	220
150	Regulation of noise in the expression of a single gene. Nature Genetics, 2002, 31, 69-73.	21.4	1,443
151	Cooperative symmetry-breaking by actin polymerization in a model for cell motility. Nature Cell Biology, 1999, 1, 493-499.	10.3	124
152	Magneto-electric Aharonovâ€“Bohm effect in metal rings. Nature, 1998, 391, 768-770.	27.8	98
153	One-Dimensional Mott Insulator Formed by Quantum Vortices in Josephson Junction Arrays. Physical Review Letters, 1996, 76, 4947-4950.	7.8	83
154	Bloch vortices in one-dimensional Josephson junction arrays. European Physical Journal D, 1996, 46, 707-708.	0.4	4
155	One-Dimensional Localization of Quantum Vortices in Disordered Josephson Junction Arrays. Physical Review Letters, 1996, 77, 4257-4260.	7.8	30