Rickard Sandberg

List of Publications by Year
in descending order

90 papers	28,590 citations	34100 52 h-index	43886 91 g-index
119 all docs	119 docs citations	119 times ranked	42833 citing authors

#	Article	IF	Citations
1	Alternative isoform regulation in human tissue transcriptomes. Nature, 2008, 456, 470-476.	27.8	4,508
2	Full-length RNA-seq from single cells using Smart-seq2. Nature Protocols, 2014, 9, 171-181.	12.0	3,308
3	Smart-seq2 for sensitive full-length transcriptome profiling in single cells. Nature Methods, 2013, 10, 1096-1098.	19.0	2,022
4	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. Nature Biotechnology, 2012, 30, 777-782.	17.5	1,347
5	Proliferating Cells Express mRNAs with Shortened 3' Untranslated Regions and Fewer MicroRNA Target Sites. Science, 2008, 320, 1643-1647.	12.6	1,213
6	Single-Cell Transcriptome Profiling of Human Pancreatic Islets in Health and Type 2 Diabetes. Cell Metabolism, 2016, 24, 593-607.	16.2	1,173
7	Single-Cell RNA-Seq Reveals Dynamic, Random Monoallelic Gene Expression in Mammalian Cells. Science, 2014, 343, 193-196.	12.6	1,164
8	CTCF-promoted RNA polymerase II pausing links DNA methylation to splicing. Nature, 2011, 479, 74-79.	27.8	853
9	Single-Cell RNA-Seq Reveals Lineage and X Chromosome Dynamics in Human Preimplantation Embryos. Cell, 2016, 165, 1012-1026.	28.9	830
10	Notch signaling: simplicity in design, versatility in function. Development (Cambridge), 2011, 138, 3593-3612.	2.5	823
11	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. PLoS Computational Biology, 2009, 5, e1000598.	3.2	777
12	Tn5 transposase and tagmentation procedures for massively scaled sequencing projects. Genome Research, 2014, 24, 2033-2040.	5.5	692
13	Gene expression perturbation in vitroâ€"A growing case for three-dimensional (3D) culture systems. Seminars in Cancer Biology, 2005, 15, 405-412.	9.6	505
14	Electrophysiological, transcriptomic and morphologic profiling of single neurons using Patch-seq. Nature Biotechnology, 2016, 34, 199-203.	17.5	478
15	Regional and strain-specific gene expression mapping in the adult mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 11038-11043.	7.1	463
16	The heterogeneity of human CD127+ innate lymphoid cells revealed by single-cell RNA sequencing. Nature Immunology, 2016, 17, 451-460.	14.5	416
17	Genomic encoding of transcriptional burst kinetics. Nature, 2019, 565, 251-254.	27.8	403
18	Single-cell RNA counting at allele and isoform resolution using Smart-seq3. Nature Biotechnology, 2020, 38, 708-714.	17.5	399

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19	Single-cell transcriptomics uncovers distinct molecular signatures of stem cells in chronic myeloid leukemia. Nature Medicine, 2017, 23, 692-702.	30.7	336
20	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. Rna, 2007, 13, 1894-1910.	3.5	333
21	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
22	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
23	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2014, 25, 794-808.	16.8	272
24	Sequentially acting Sox transcription factors in neural lineage development. Genes and Development, 2011, 25, 2453-2464.	5.9	263
25	Laser capture microscopy coupled with Smart-seq2 for precise spatial transcriptomic profiling. Nature Communications, 2016, 7, 12139.	12.8	246
26	Identification of spatial expression trends in single-cell gene expression data. Nature Methods, 2018, 15, 339-342.	19.0	241
27	Lymphomyeloid Contribution of an Immune-Restricted Progenitor Emerging Prior to Definitive Hematopoietic Stem Cells. Cell Stem Cell, 2013, 13, 535-548.	11.1	225
28	Entering the era of single-cell transcriptomics in biology and medicine. Nature Methods, 2014, 11, 22-24.	19.0	221
29	The human cap-binding complex is functionally connected to the nuclear RNA exosome. Nature Structural and Molecular Biology, 2013, 20, 1367-1376.	8.2	199
30	The Molecular Anatomy of Mouse Skin during Hair Growth and Rest. Cell Stem Cell, 2020, 26, 441-457.e7.	11.1	198
31	Phenotypic variation of transcriptomic cell types in mouse motor cortex. Nature, 2021, 598, 144-150.	27.8	196
32	Capturing Whole-Genome Characteristics in Short Sequences Using a Naive Bayesian Classifier. Genome Research, 2001, 11, 1404-1409.	5.5	184
33	Random monoallelic expression of autosomal genes: stochastic transcription and allele-level regulation. Nature Reviews Genetics, 2015, 16, 653-664.	16.3	174
34	Single-cell sequencing of the small-RNA transcriptome. Nature Biotechnology, 2016, 34, 1264-1266.	17.5	172
35	Assessment of tumor characteristic gene expression in cell lines using a tissue similarity index (TSI). Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2052-2057.	7.1	148
36	Improved precision and accuracy for microarrays using updated probe set definitions. BMC Bioinformatics, 2007, 8, 48.	2.6	145

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37	BMP Signaling and Its pSMAD1/5 Target Genes Differentially Regulate Hair Follicle Stem Cell Lineages. Cell Stem Cell, 2014, 15, 619-633.	11.1	145
38	Transcription factor Nurr1 maintains fiber integrity and nuclear-encoded mitochondrial gene expression in dopamine neurons. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2360-2365.	7.1	143
39	Analysis of allelic expression patterns in clonal somatic cells by single-cell RNAâ€"seq. Nature Genetics, 2016, 48, 1430-1435.	21.4	142
40	In Vivo Effects of Mesenchymal Stromal Cells in Two Patients With Severe Acute Respiratory Distress Syndrome. Stem Cells Translational Medicine, 2015, 4, 1199-1213.	3.3	131
41	Single-Cell Analysis Reveals a Close Relationship between Differentiating Dopamine and Subthalamic Nucleus Neuronal Lineages. Cell Stem Cell, 2017, 20, 29-40.	11.1	127
42	Multimodal profiling of single-cell morphology, electrophysiology, and gene expression using Patch-seq. Nature Protocols, 2017, 12, 2531-2553.	12.0	126
43	Reading and editing the Pleurodeles waltl genome reveals novel features of tetrapod regeneration. Nature Communications, 2017, 8, 2286.	12.8	123
44	Position- and Hippo signaling-dependent plasticity during lineage segregation in the early mouse embryo. ELife, 2017, 6, .	6.0	117
45	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. Genome Biology, 2015, 16, 156.	8.8	108
46	Layer 4 of mouse neocortex differs in cell types and circuit organization between sensory areas. Nature Communications, 2019, 10, 4174.	12.8	101
47	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. Genome Research, 2016, 26, 1342-1354.	5.5	93
48	Mouse Model of Alagille Syndrome and Mechanisms of Jagged1 Missense Mutations. Gastroenterology, 2018, 154, 1080-1095.	1.3	92
49	NASC-seq monitors RNA synthesis in single cells. Nature Communications, 2019, 10, 3138.	12.8	75
50	The molecular portrait of in vitro growth by meta-analysis of gene-expression profiles. Genome Biology, 2005, 6, R65.	9.6	68
51	Computational correction of index switching in multiplexed sequencing libraries. Nature Methods, 2018, 15, 305-307.	19.0	67
52	Transcription Factor-Induced Lineage Selection of Stem-Cell-Derived Neural Progenitor Cells. Cell Stem Cell, 2011, 8, 663-675.	11.1	65
53	X-chromosome upregulation is driven by increased burst frequency. Nature Structural and Molecular Biology, 2019, 26, 963-969.	8.2	64
54	Comparative Microarray Analysis. OMICS A Journal of Integrative Biology, 2006, 10, 381-397.	2.0	56

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55	SoxB1-driven transcriptional network underlies neural-specific interpretation of morphogen signals. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7330-7335.	7.1	56
56	Single-cell RNA sequencing reveals the mesangial identity and species diversity of glomerular cell transcriptomes. Nature Communications, 2021, 12, 2141.	12.8	55
57	Lack of correct data format and comparability limits future integrative microarray research. Nature Biotechnology, 2006, 24, 1322-1323.	17.5	54
58	A <scp>TRPV</scp> 1â€toâ€secretagogin regulatory axis controls pancreatic Î²â€cell survival by modulating protein turnover. EMBO Journal, 2017, 36, 2107-2125.	7.8	52
59	Quantifying the species-specificity in genomic signatures, synonymous codon choice, amino acid usage and G+C content. Gene, 2003, 311, 35-42.	2.2	50
60	A reference transcriptome and inferred proteome for the salamander Notophthalmus viridescens. Experimental Cell Research, 2013, 319, 1187-1197.	2.6	49
61	Initial seeding of the embryonic thymus by immune-restricted lympho-myeloid progenitors. Nature Immunology, 2016, 17, 1424-1435.	14.5	49
62	RNA Helicase A Is a Downstream Mediator of KIF1BÎ² Tumor-Suppressor Function in Neuroblastoma. Cancer Discovery, 2014, 4, 434-451.	9.4	48
63	Small-seq for single-cell small-RNA sequencing. Nature Protocols, 2018, 13, 2407-2424.	12.0	47
64	Parental haplotype-specific single-cell transcriptomics reveal incomplete epigenetic reprogramming in human female germ cells. Nature Communications, 2018, 9, 1873.	12.8	46
65	Scalable single-cell RNA sequencing from full transcripts with Smart-seq3xpress. Nature Biotechnology, 2022, 40, 1452-1457.	17.5	43
66	Cell type composition and circuit organization of clonally related excitatory neurons in the juvenile mouse neocortex. ELife, 2020, 9, .	6.0	37
67	Systems Biology Is Taking Off. Genome Research, 2003, 13, 2377-2380.	5.5	36
68	Heterogeneity in mammalian RNA 3â€² end formation. Experimental Cell Research, 2010, 316, 1357-1364.	2.6	35
69	Abundance of female-biased and paucity of male-biased somatically expressed genes on the mouse X-chromosome. BMC Genomics, 2012, 13, 607.	2.8	32
70	Exploring parasite heterogeneity using single-cell RNA-seq reveals a gene signature among sexual stage Plasmodium falciparum parasites. Experimental Cell Research, 2018, 371, 130-138.	2.6	31
71	Efficient and Comprehensive Representation of Uniqueness for Next-Generation Sequencing by Minimum Unique Length Analyses. PLoS ONE, 2013, 8, e53822.	2.5	29
72	LCM-seq reveals unique transcriptional adaptation mechanisms of resistant neurons and identifies protective pathways in spinal muscular atrophy. Genome Research, 2020, 30, 1083-1096.	5.5	29

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73	Transcriptional kinetics and molecular functions of long noncoding RNAs. Nature Genetics, 2022, 54, 306-317.	21.4	29
74	A DNA-nanoassembly-based approach to map membrane protein nanoenvironments. Nature Nanotechnology, 2021, 16, 85-95.	31.5	24
75	How to Analyze Gene Expression Using RNA-Sequencing Data. Methods in Molecular Biology, 2012, 802, 259-274.	0.9	23
76	scphaser: haplotype inference using single-cell RNA-seq data. Bioinformatics, 2016, 32, 3038-3040.	4.1	20
77	Intussusceptive Vascular Remodeling Precedes Pathological Neovascularization. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1402-1418.	2.4	20
78	Transcriptional bursts explain autosomal random monoallelic expression and affect allelic imbalance. PLoS Computational Biology, 2021, 17, e1008772.	3.2	20
79	Q&A: using Patch-seq to profile single cells. BMC Biology, 2017, 15, 58.	3.8	16
80	Disruption of the Extracellular Matrix Progressively Impairs Central Nervous System Vascular Maturation Downstream of Î²-Catenin Signaling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1432-1447.	2.4	14
81	Cell shape determines gene expression: cardiomyocyte morphotypic transcriptomes. Basic Research in Cardiology, 2020, 115, 7.	5.9	14
82	Reply to â€˜High prevalence of clonal monoallelic expressionâ€™. Nature Genetics, 2018, 50, 1199-1200.	21.4	13
83	Molecular spikes: a gold standard for single-cell RNA counting. Nature Methods, 2022, 19, 560-566.	19.0	12
84	Decoding breast cancer tissueâ€“stroma interactions using species-specific sequencing. Breast Cancer Research, 2015, 17, 109.	5.0	11
85	BAMboozle removes genetic variation from human sequence data for open data sharing. Nature Communications, 2021, 12, 6216.	12.8	11
86	Divergent clonal differentiation trajectories establish CD8+ memory TÂcell heterogeneity during acute viral infections in humans. Cell Reports, 2021, 35, 109174.	6.4	9
87	Understanding interactions between risk factors, and assessing the utility of the additive and multiplicative models through simulations. PLoS ONE, 2021, 16, e0250282.	2.5	5
88	Putting cells in their place. Nature Biotechnology, 2015, 33, 490-491.	17.5	4
89	The Logic of Life. Genome Research, 2003, 13, 2375-2376.	5.5	0
90	Sample Moments and Weak Convergence to Multivariate Stochastic Power Integrals. Journal of Time Series Analysis, 2017, 38, 1000-1009.	1.2	0