

Rickard Sandberg

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

28,590
citations

39113

52
h-index

49824

91
g-index

119
all docs

119
docs citations

119
times ranked

47463
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional kinetics and molecular functions of long noncoding RNAs. <i>Nature Genetics</i> , 2022, 54, 306-317.	9.4	29
2	Molecular spikes: a gold standard for single-cell RNA counting. <i>Nature Methods</i> , 2022, 19, 560-566.	9.0	12
3	Scalable single-cell RNA sequencing from full transcripts with Smart-seq3xpress. <i>Nature Biotechnology</i> , 2022, 40, 1452-1457.	9.4	43
4	Phenotypic variation of transcriptomic cell types in mouse motor cortex. <i>Nature</i> , 2021, 598, 144-150.	13.7	196
5	A DNA-nanoassembly-based approach to map membrane protein nanoenvironments. <i>Nature Nanotechnology</i> , 2021, 16, 85-95.	15.6	24
6	Transcriptional bursts explain autosomal random monoallelic expression and affect allelic imbalance. <i>PLoS Computational Biology</i> , 2021, 17, e1008772.	1.5	20
7	Understanding interactions between risk factors, and assessing the utility of the additive and multiplicative models through simulations. <i>PLoS ONE</i> , 2021, 16, e0250282.	1.1	5
8	Single-cell RNA sequencing reveals the mesangial identity and species diversity of glomerular cell transcriptomes. <i>Nature Communications</i> , 2021, 12, 2141.	5.8	55
9	Divergent clonal differentiation trajectories establish CD8+ memory T cell heterogeneity during acute viral infections in humans. <i>Cell Reports</i> , 2021, 35, 109174.	2.9	9
10	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
11	BAMboozle removes genetic variation from human sequence data for open data sharing. <i>Nature Communications</i> , 2021, 12, 6216.	5.8	11
12	Cell shape determines gene expression: cardiomyocyte morphotypic transcriptomes. <i>Basic Research in Cardiology</i> , 2020, 115, 7.	2.5	14
13	LCM-seq reveals unique transcriptional adaptation mechanisms of resistant neurons and identifies protective pathways in spinal muscular atrophy. <i>Genome Research</i> , 2020, 30, 1083-1096.	2.4	29
14	Single-cell RNA counting at allele and isoform resolution using Smart-seq3. <i>Nature Biotechnology</i> , 2020, 38, 708-714.	9.4	399
15	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	9.4	313
16	The Molecular Anatomy of Mouse Skin during Hair Growth and Rest. <i>Cell Stem Cell</i> , 2020, 26, 441-457.e7.	5.2	198
17	Cell type composition and circuit organization of clonally related excitatory neurons in the juvenile mouse neocortex. <i>ELife</i> , 2020, 9, .	2.8	37
18	NASC-seq monitors RNA synthesis in single cells. <i>Nature Communications</i> , 2019, 10, 3138.	5.8	75

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19	Layer 4 of mouse neocortex differs in cell types and circuit organization between sensory areas. <i>Nature Communications</i> , 2019, 10, 4174.	5.8	101
20	X-chromosome upregulation is driven by increased burst frequency. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 963-969.	3.6	64
21	Intussusceptive Vascular Remodeling Precedes Pathological Neovascularization. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 1402-1418.	1.1	20
22	Disruption of the Extracellular Matrix Progressively Impairs Central Nervous System Vascular Maturation Downstream of β -Catenin Signaling. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 1432-1447.	1.1	14
23	Genomic encoding of transcriptional burst kinetics. <i>Nature</i> , 2019, 565, 251-254.	13.7	403
24	Computational correction of index switching in multiplexed sequencing libraries. <i>Nature Methods</i> , 2018, 15, 305-307.	9.0	67
25	Identification of spatial expression trends in single-cell gene expression data. <i>Nature Methods</i> , 2018, 15, 339-342.	9.0	241
26	Mouse Model of Alagille Syndrome and Mechanisms of Jagged1 Missense Mutations. <i>Gastroenterology</i> , 2018, 154, 1080-1095.	0.6	92
27	Small-seq for single-cell small-RNA sequencing. <i>Nature Protocols</i> , 2018, 13, 2407-2424.	5.5	47
28	Parental haplotype-specific single-cell transcriptomics reveal incomplete epigenetic reprogramming in human female germ cells. <i>Nature Communications</i> , 2018, 9, 1873.	5.8	46
29	Exploring parasite heterogeneity using single-cell RNA-seq reveals a gene signature among sexual stage <i>Plasmodium falciparum</i> parasites. <i>Experimental Cell Research</i> , 2018, 371, 130-138.	1.2	31
30	Reply to "High prevalence of clonal monoallelic expression". <i>Nature Genetics</i> , 2018, 50, 1199-1200.	9.4	13
31	Single-cell transcriptomics uncovers distinct molecular signatures of stem cells in chronic myeloid leukemia. <i>Nature Medicine</i> , 2017, 23, 692-702.	15.2	336
32	A <i>TRPV1</i> secretagogue regulatory axis controls pancreatic β -cell survival by modulating protein turnover. <i>EMBO Journal</i> , 2017, 36, 2107-2125.	3.5	52
33	Sample Moments and Weak Convergence to Multivariate Stochastic Power Integrals. <i>Journal of Time Series Analysis</i> , 2017, 38, 1000-1009.	0.7	0
34	Multimodal profiling of single-cell morphology, electrophysiology, and gene expression using Patch-seq. <i>Nature Protocols</i> , 2017, 12, 2531-2553.	5.5	126
35	Single-Cell Analysis Reveals a Close Relationship between Differentiating Dopamine and Subthalamic Nucleus Neuronal Lineages. <i>Cell Stem Cell</i> , 2017, 20, 29-40.	5.2	127
36	Reading and editing the <i>Pleurodeles waltl</i> genome reveals novel features of tetrapod regeneration. <i>Nature Communications</i> , 2017, 8, 2286.	5.8	123

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37	Q&A: using Patch-seq to profile single cells. BMC Biology, 2017, 15, 58.	1.7	16
38	Position- and Hippo signaling-dependent plasticity during lineage segregation in the early mouse embryo. ELife, 2017, 6, .	2.8	117
39	Single-Cell RNA-Seq Reveals Lineage and X Chromosome Dynamics in Human Preimplantation Embryos. Cell, 2016, 165, 1012-1026.	13.5	830
40	Analysis of allelic expression patterns in clonal somatic cells by single-cell RNA-seq. Nature Genetics, 2016, 48, 1430-1435.	9.4	142
41	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. Genome Research, 2016, 26, 1342-1354.	2.4	93
42	Initial seeding of the embryonic thymus by immune-restricted lympho-myeloid progenitors. Nature Immunology, 2016, 17, 1424-1435.	7.0	49
43	Single-Cell Transcriptome Profiling of Human Pancreatic Islets in Health and Type 2 Diabetes. Cell Metabolism, 2016, 24, 593-607.	7.2	1,173
44	scphaser: haplotype inference using single-cell RNA-seq data. Bioinformatics, 2016, 32, 3038-3040.	1.8	20
45	Laser capture microscopy coupled with Smart-seq2 for precise spatial transcriptomic profiling. Nature Communications, 2016, 7, 12139.	5.8	246
46	Single-cell sequencing of the small-RNA transcriptome. Nature Biotechnology, 2016, 34, 1264-1266.	9.4	172
47	The heterogeneity of human CD127+ innate lymphoid cells revealed by single-cell RNA sequencing. Nature Immunology, 2016, 17, 451-460.	7.0	416
48	Electrophysiological, transcriptomic and morphologic profiling of single neurons using Patch-seq. Nature Biotechnology, 2016, 34, 199-203.	9.4	478
49	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. Genome Biology, 2015, 16, 156.	3.8	108
50	Putting cells in their place. Nature Biotechnology, 2015, 33, 490-491.	9.4	4
51	Random monoallelic expression of autosomal genes: stochastic transcription and allele-level regulation. Nature Reviews Genetics, 2015, 16, 653-664.	7.7	174
52	Decoding breast cancer tissue-stroma interactions using species-specific sequencing. Breast Cancer Research, 2015, 17, 109.	2.2	11
53	In Vivo Effects of Mesenchymal Stromal Cells in Two Patients With Severe Acute Respiratory Distress Syndrome. Stem Cells Translational Medicine, 2015, 4, 1199-1213.	1.6	131
54	RNA Helicase A Is a Downstream Mediator of KIF1B ² Tumor-Suppressor Function in Neuroblastoma. Cancer Discovery, 2014, 4, 434-451.	7.7	48

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55	Tn5 transposase and tagmentation procedures for massively scaled sequencing projects. <i>Genome Research</i> , 2014, 24, 2033-2040.	2.4	692
56	Entering the era of single-cell transcriptomics in biology and medicine. <i>Nature Methods</i> , 2014, 11, 22-24.	9.0	221
57	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. <i>Cancer Cell</i> , 2014, 25, 794-808.	7.7	272
58	Full-length RNA-seq from single cells using Smart-seq2. <i>Nature Protocols</i> , 2014, 9, 171-181.	5.5	3,308
59	Single-Cell RNA-Seq Reveals Dynamic, Random Monoallelic Gene Expression in Mammalian Cells. <i>Science</i> , 2014, 343, 193-196.	6.0	1,164
60	BMP Signaling and Its pSMAD1/5 Target Genes Differentially Regulate Hair Follicle Stem Cell Lineages. <i>Cell Stem Cell</i> , 2014, 15, 619-633.	5.2	145
61	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1367-1376.	3.6	199
62	Lymphomyeloid Contribution of an Immune-Restricted Progenitor Emerging Prior to Definitive Hematopoietic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 535-548.	5.2	225
63	Smart-seq2 for sensitive full-length transcriptome profiling in single cells. <i>Nature Methods</i> , 2013, 10, 1096-1098.	9.0	2,022
64	Transcription factor Nurr1 maintains fiber integrity and nuclear-encoded mitochondrial gene expression in dopamine neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2360-2365.	3.3	143
65	A reference transcriptome and inferred proteome for the salamander <i>Notophthalmus viridescens</i> . <i>Experimental Cell Research</i> , 2013, 319, 1187-1197.	1.2	49
66	SoxB1-driven transcriptional network underlies neural-specific interpretation of morphogen signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7330-7335.	3.3	56
67	Efficient and Comprehensive Representation of Uniqueness for Next-Generation Sequencing by Minimum Unique Length Analyses. <i>PLoS ONE</i> , 2013, 8, e53822.	1.1	29
68	How to Analyze Gene Expression Using RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 802, 259-274.	0.4	23
69	Abundance of female-biased and paucity of male-biased somatically expressed genes on the mouse X-chromosome. <i>BMC Genomics</i> , 2012, 13, 607.	1.2	32
70	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <i>Nature Biotechnology</i> , 2012, 30, 777-782.	9.4	1,347
71	Notch signaling: simplicity in design, versatility in function. <i>Development (Cambridge)</i> , 2011, 138, 3593-3612.	1.2	823
72	CTCF-promoted RNA polymerase II pausing links DNA methylation to splicing. <i>Nature</i> , 2011, 479, 74-79.	13.7	853

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73	Transcription Factor-Induced Lineage Selection of Stem-Cell-Derived Neural Progenitor Cells. <i>Cell Stem Cell</i> , 2011, 8, 663-675.	5.2	65
74	Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011, 25, 2453-2464.	2.7	263
75	Heterogeneity in mammalian RNA 3' end formation. <i>Experimental Cell Research</i> , 2010, 316, 1357-1364.	1.2	35
76	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	1.5	777
77	Alternative isoform regulation in human tissue transcriptomes. <i>Nature</i> , 2008, 456, 470-476.	13.7	4,508
78	Proliferating Cells Express mRNAs with Shortened 3' Untranslated Regions and Fewer MicroRNA Target Sites. <i>Science</i> , 2008, 320, 1643-1647.	6.0	1,213
79	Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. <i>Rna</i> , 2007, 13, 1894-1910.	1.6	333
80	Improved precision and accuracy for microarrays using updated probe set definitions. <i>BMC Bioinformatics</i> , 2007, 8, 48.	1.2	145
81	Lack of correct data format and comparability limits future integrative microarray research. <i>Nature Biotechnology</i> , 2006, 24, 1322-1323.	9.4	54
82	Comparative Microarray Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 381-397.	1.0	56
83	Gene expression perturbation in vitro – A growing case for three-dimensional (3D) culture systems. <i>Seminars in Cancer Biology</i> , 2005, 15, 405-412.	4.3	505
84	Assessment of tumor characteristic gene expression in cell lines using a tissue similarity index (TSI). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2052-2057.	3.3	148
85	The molecular portrait of in vitro growth by meta-analysis of gene-expression profiles. <i>Genome Biology</i> , 2005, 6, R65.	13.9	68
86	Quantifying the species-specificity in genomic signatures, synonymous codon choice, amino acid usage and G+C content. <i>Gene</i> , 2003, 311, 35-42.	1.0	50
87	Systems Biology Is Taking Off. <i>Genome Research</i> , 2003, 13, 2377-2380.	2.4	36
88	The Logic of Life. <i>Genome Research</i> , 2003, 13, 2375-2376.	2.4	0
89	Capturing Whole-Genome Characteristics in Short Sequences Using a Naive Bayesian Classifier. <i>Genome Research</i> , 2001, 11, 1404-1409.	2.4	184
90	Regional and strain-specific gene expression mapping in the adult mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11038-11043.	3.3	463