

Rickard Sandberg

List of Publications by Citations

Source: <https://exaly.com/author-pdf/704831/rickard-sandberg-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

103
papers

19,741
citations

49
h-index

119
g-index

119
ext. papers

25,356
ext. citations

19.4
avg, IF

6.86
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 103 | Alternative isoform regulation in human tissue transcriptomes. <i>Nature</i> , 2008 , 456, 470-6 | 50.4 | 3526 |
| 102 | Full-length RNA-seq from single cells using Smart-seq2. <i>Nature Protocols</i> , 2014 , 9, 171-81 | 18.8 | 1981 |
| 101 | Smart-seq2 for sensitive full-length transcriptome profiling in single cells. <i>Nature Methods</i> , 2013 , 10, 1096-8 | 21.6 | 1335 |
| 100 | Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <i>Nature Biotechnology</i> , 2012 , 30, 777-82 | 44.5 | 1045 |
| 99 | Proliferating cells express mRNAs with shortened 3' untranslated regions and fewer microRNA target sites. <i>Science</i> , 2008 , 320, 1643-7 | 33.3 | 984 |
| 98 | Single-cell RNA-seq reveals dynamic, random monoallelic gene expression in mammalian cells. <i>Science</i> , 2014 , 343, 193-6 | 33.3 | 816 |
| 97 | Single-Cell Transcriptome Profiling of Human Pancreatic Islets in Health and Type 2 Diabetes. <i>Cell Metabolism</i> , 2016 , 24, 593-607 | 24.6 | 730 |
| 96 | CTCF-promoted RNA polymerase II pausing links DNA methylation to splicing. <i>Nature</i> , 2011 , 479, 74-9 | 50.4 | 700 |
| 95 | Notch signaling: simplicity in design, versatility in function. <i>Development (Cambridge)</i> , 2011 , 138, 3593-612 | 6.26 | 661 |
| 94 | An abundance of ubiquitously expressed genes revealed by tissue transcriptome sequence data. <i>PLoS Computational Biology</i> , 2009 , 5, e1000598 | 5 | 615 |
| 93 | Single-Cell RNA-Seq Reveals Lineage and X Chromosome Dynamics in Human Preimplantation Embryos. <i>Cell</i> , 2016 , 165, 1012-26 | 56.2 | 475 |
| 92 | Tn5 transposase and tagmentation procedures for massively scaled sequencing projects. <i>Genome Research</i> , 2014 , 24, 2033-40 | 9.7 | 431 |
| 91 | 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, 11038-43 | 11.5 | 420 |
| 90 | Gene expression perturbation in vitro—a growing case for three-dimensional (3D) culture systems. <i>Seminars in Cancer Biology</i> , 2005 , 15, 405-12 | 12.7 | 416 |
| 89 | The heterogeneity of human CD127(+) innate lymphoid cells revealed by single-cell RNA sequencing. <i>Nature Immunology</i> , 2016 , 17, 451-60 | 19.1 | 319 |
| 88 | Electrophysiological, transcriptomic and morphologic profiling of single neurons using Patch-seq. <i>Nature Biotechnology</i> , 2016 , 34, 199-203 | 44.5 | 299 |
| 87 | Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. <i>Rna</i> , 2007 , 13, 1894-918 | 11.8 | 288 |

| | | | |
|----|--|------|-----|
| 86 | Single-cell transcriptomics uncovers distinct molecular signatures of stem cells in chronic myeloid leukemia. <i>Nature Medicine</i> , 2017 , 23, 692-702 | 50.5 | 226 |
| 85 | Myelodysplastic syndromes are propagated by rare and distinct human cancer stem cells in vivo. <i>Cancer Cell</i> , 2014 , 25, 794-808 | 24.3 | 216 |
| 84 | Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011 , 25, 2453-64 | 12.6 | 216 |
| 83 | Genomic encoding of transcriptional burst kinetics. <i>Nature</i> , 2019 , 565, 251-254 | 50.4 | 201 |
| 82 | Lymphomyeloid contribution of an immune-restricted progenitor emerging prior to definitive hematopoietic stem cells. <i>Cell Stem Cell</i> , 2013 , 13, 535-48 | 18 | 170 |
| 81 | Entering the era of single-cell transcriptomics in biology and medicine. <i>Nature Methods</i> , 2014 , 11, 22-4 | 21.6 | 169 |
| 80 | Laser capture microscopy coupled with Smart-seq2 for precise spatial transcriptomic profiling. <i>Nature Communications</i> , 2016 , 7, 12139 | 17.4 | 164 |
| 79 | The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1367-76 | 17.6 | 157 |
| 78 | Single-cell RNA counting at allele and isoform resolution using Smart-seq3. <i>Nature Biotechnology</i> , 2020 , 38, 708-714 | 44.5 | 151 |
| 77 | Capturing whole-genome characteristics in short sequences using a naïve Bayesian classifier. <i>Genome Research</i> , 2001 , 11, 1404-9 | 9.7 | 150 |
| 76 | Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020 , 38, 747-755 | 44.5 | 142 |
| 75 | Improved precision and accuracy for microarrays using updated probe set definitions. <i>BMC Bioinformatics</i> , 2007 , 8, 48 | 3.6 | 130 |
| 74 | 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, 2052-7 | 11.5 | 127 |
| 73 | Single-cell sequencing of the small-RNA transcriptome. <i>Nature Biotechnology</i> , 2016 , 34, 1264-1266 | 44.5 | 120 |
| 72 | Identification of spatial expression trends in single-cell gene expression data. <i>Nature Methods</i> , 2018 , 15, 339-342 | 21.6 | 119 |
| 71 | BMP signaling and its pSMAD1/5 target genes differentially regulate hair follicle stem cell lineages. <i>Cell Stem Cell</i> , 2014 , 15, 619-33 | 18 | 103 |
| 70 | Random monoallelic expression of autosomal genes: stochastic transcription and allele-level regulation. <i>Nature Reviews Genetics</i> , 2015 , 16, 653-64 | 30.1 | 101 |
| 69 | 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, 2360-5 | 11.5 | 101 |

| | | | |
|----|--|------|----|
| 68 | Analysis of allelic expression patterns in clonal somatic cells by single-cell RNA-seq. <i>Nature Genetics</i> , 2016 , 48, 1430-1435 | 36.3 | 92 |
| 67 | In Vivo Effects of Mesenchymal Stromal Cells in Two Patients With Severe Acute Respiratory Distress Syndrome. <i>Stem Cells Translational Medicine</i> , 2015 , 4, 1199-213 | 6.9 | 90 |
| 66 | Single-Cell Analysis Reveals a Close Relationship between Differentiating Dopamine and Subthalamic Nucleus Neuronal Lineages. <i>Cell Stem Cell</i> , 2017 , 20, 29-40 | 18 | 90 |
| 65 | Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <i>Genome Biology</i> , 2015 , 16, 156 | 18.3 | 89 |
| 64 | Reading and editing the <i>Pleurodeles waltl</i> genome reveals novel features of tetrapod regeneration. <i>Nature Communications</i> , 2017 , 8, 2286 | 17.4 | 83 |
| 63 | The Logic of Life. <i>Genome Research</i> , 2003 , 13, 2375-2376 | 9.7 | 78 |
| 62 | Position- and Hippo signaling-dependent plasticity during lineage segregation in the early mouse embryo. <i>ELife</i> , 2017 , 6, | 8.9 | 76 |
| 61 | The Molecular Anatomy of Mouse Skin during Hair Growth and Rest. <i>Cell Stem Cell</i> , 2020 , 26, 441-457.e718 | | 69 |
| 60 | Multimodal profiling of single-cell morphology, electrophysiology, and gene expression using Patch-seq. <i>Nature Protocols</i> , 2017 , 12, 2531-2553 | 18.8 | 68 |
| 59 | Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. <i>Genome Research</i> , 2016 , 26, 1342-1354 | 9.7 | 64 |
| 58 | Transcription factor-induced lineage selection of stem-cell-derived neural progenitor cells. <i>Cell Stem Cell</i> , 2011 , 8, 663-75 | 18 | 57 |
| 57 | The molecular portrait of in vitro growth by meta-analysis of gene-expression profiles. <i>Genome Biology</i> , 2005 , 6, R65 | 18.3 | 56 |
| 56 | Mouse Model of Alagille Syndrome and Mechanisms of Jagged1 Missense Mutations. <i>Gastroenterology</i> , 2018 , 154, 1080-1095 | 13.3 | 55 |
| 55 | Lack of correct data format and comparability limits future integrative microarray research. <i>Nature Biotechnology</i> , 2006 , 24, 1322-3 | 44.5 | 50 |
| 54 | 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, 7330-5 | 11.5 | 49 |
| 53 | Phenotypic variation of transcriptomic cell types in mouse motor cortex. <i>Nature</i> , 2021 , 598, 144-150 | 50.4 | 49 |
| 52 | Quantifying the species-specificity in genomic signatures, synonymous codon choice, amino acid usage and G+C content. <i>Gene</i> , 2003 , 311, 35-42 | 3.8 | 47 |
| 51 | Comparative microarray analysis. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 381-97 | 3.8 | 46 |

| | | | |
|----|---|------|----|
| 50 | A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021 , 598, 86-102 | 50.4 | 44 |
| 49 | NASC-seq monitors RNA synthesis in single cells. <i>Nature Communications</i> , 2019 , 10, 3138 | 17.4 | 42 |
| 48 | Computational correction of index switching in multiplexed sequencing libraries. <i>Nature Methods</i> , 2018 , 15, 305-307 | 21.6 | 40 |
| 47 | A reference transcriptome and inferred proteome for the salamander <i>Notophthalmus viridescens</i> . <i>Experimental Cell Research</i> , 2013 , 319, 1187-97 | 4.2 | 40 |
| 46 | RNA helicase A is a downstream mediator of KIF1B tumor-suppressor function in neuroblastoma. <i>Cancer Discovery</i> , 2014 , 4, 434-51 | 24.4 | 38 |
| 45 | Layer 4 of mouse neocortex differs in cell types and circuit organization between sensory areas. <i>Nature Communications</i> , 2019 , 10, 4174 | 17.4 | 36 |
| 44 | A TRPV1-to-secretagogue regulatory axis controls pancreatic β cell survival by modulating protein turnover. <i>EMBO Journal</i> , 2017 , 36, 2107-2125 | 13 | 31 |
| 43 | Heterogeneity in mammalian RNA 3' end formation. <i>Experimental Cell Research</i> , 2010 , 316, 1357-64 | 4.2 | 30 |
| 42 | Systems biology is taking off. <i>Genome Research</i> , 2003 , 13, 2377-80 | 9.7 | 30 |
| 41 | Initial seeding of the embryonic thymus by immune-restricted lympho-myeloid progenitors. <i>Nature Immunology</i> , 2016 , 17, 1424-1435 | 19.1 | 29 |
| 40 | Parental haplotype-specific single-cell transcriptomics reveal incomplete epigenetic reprogramming in human female germ cells. <i>Nature Communications</i> , 2018 , 9, 1873 | 17.4 | 29 |
| 39 | Abundance of female-biased and paucity of male-biased somatically expressed genes on the mouse X-chromosome. <i>BMC Genomics</i> , 2012 , 13, 607 | 4.5 | 26 |
| 38 | Small-seq for single-cell small-RNA sequencing. <i>Nature Protocols</i> , 2018 , 13, 2407-2424 | 18.8 | 26 |
| 37 | Efficient and comprehensive representation of uniqueness for next-generation sequencing by minimum unique length analyses. <i>PLoS ONE</i> , 2013 , 8, e53822 | 3.7 | 25 |
| 36 | How to analyze gene expression using RNA-sequencing data. <i>Methods in Molecular Biology</i> , 2012 , 802, 259-74 | 1.4 | 22 |
| 35 | X-chromosome upregulation is driven by increased burst frequency. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 963-969 | 17.6 | 17 |
| 34 | 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 | 4.2 | 16 |
| 33 | Intussusceptive Vascular Remodeling Precedes Pathological Neovascularization. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019 , 39, 1402-1418 | 9.4 | 15 |

| | | | |
|----|--|------|----|
| 32 | Cell type composition and circuit organization of clonally related excitatory neurons in the juvenile mouse neocortex. <i>ELife</i> , 2020 , 9, | 8.9 | 15 |
| 31 | Phenotypic variation within and across transcriptomic cell types in mouse motor cortex | | 15 |
| 30 | Benchmarking Single-Cell RNA Sequencing Protocols for Cell Atlas Projects | | 13 |
| 29 | Single-cell RNA sequencing reveals the mesangial identity and species diversity of glomerular cell transcriptomes. <i>Nature Communications</i> , 2021 , 12, 2141 | 17.4 | 13 |
| 28 | A multimodal cell census and atlas of the mammalian primary motor cortex | | 12 |
| 27 | scphaser: haplotype inference using single-cell RNA-seq data. <i>Bioinformatics</i> , 2016 , 32, 3038-40 | 7.2 | 11 |
| 26 | A DNA-nanoassembly-based approach to map membrane protein nanoenvironments. <i>Nature Nanotechnology</i> , 2021 , 16, 85-95 | 28.7 | 11 |
| 25 | Reply to SHigh prevalence of clonal monoallelic expressionS <i>Nature Genetics</i> , 2018 , 50, 1199-1200 | 36.3 | 8 |
| 24 | Disruption of the Extracellular Matrix Progressively Impairs Central Nervous System Vascular Maturation Downstream of E-Catenin Signaling. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019 , 39, 1432-1447 | 9.4 | 7 |
| 23 | Decoding breast cancer tissue-stroma interactions using species-specific sequencing. <i>Breast Cancer Research</i> , 2015 , 17, 109 | 8.3 | 7 |
| 22 | Single-cell RNA counting at allele- and isoform-resolution using Smart-seq3 | | 7 |
| 21 | Q&A: using Patch-seq to profile single cells. <i>BMC Biology</i> , 2017 , 15, 58 | 7.3 | 6 |
| 20 | Cell shape determines gene expression: cardiomyocyte morphotypic transcriptomes. <i>Basic Research in Cardiology</i> , 2019 , 115, 7 | 11.8 | 6 |
| 19 | 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 | 9.7 | 6 |
| 18 | Putting cells in their place. <i>Nature Biotechnology</i> , 2015 , 33, 490-1 | 44.5 | 4 |
| 17 | Computational correction of cross-contamination due to exclusion amplification barcode spreading | | 4 |
| 16 | Scalable full-transcript coverage single cell RNA sequencing with Smart-seq3xpress | | 4 |
| 15 | Transcriptional kinetics and molecular functions of long noncoding RNAs.. <i>Nature Genetics</i> , 2022 , | 36.3 | 4 |

| | | | |
|----|--|------|---|
| 14 | Transcriptional kinetics and molecular functions of long non-coding RNAs | | 3 |
| 13 | Neocortical layer 4 in adult mouse differs in major cell types and circuit organization between primary sensory areas | | 3 |
| 12 | Transcriptional bursts explain autosomal random monoallelic expression and affect allelic imbalance. <i>PLoS Computational Biology</i> , 2021 , 17, e1008772 | 5 | 3 |
| 11 | Divergent clonal differentiation trajectories establish CD8 memory T cell heterogeneity during acute viral infections in humans. <i>Cell Reports</i> , 2021 , 35, 109174 | 10.6 | 3 |
| 10 | Cell type composition and circuit organization of neocortical radial clones | | 2 |
| 9 | Understanding interactions between risk factors, and assessing the utility of the additive and multiplicative models through simulations. <i>PLoS ONE</i> , 2021 , 16, e0250282 | 3.7 | 2 |
| 8 | Transcriptional bursts explain autosomal random monoallelic expression and affect allelic imbalance | | 1 |
| 7 | Clonally distinct differentiation trajectories shape CD8+ memory T cell heterogeneity after acute viral infections in humans | | 1 |
| 6 | BAMboozle removes genetic variation from human sequence data for open data sharing. <i>Nature Communications</i> , 2021 , 12, 6216 | 17.4 | 1 |
| 5 | Transcriptional kinetics of X-chromosome upregulation | | 1 |
| 4 | Understanding interactions between risk factors, and assessing the utility of the additive and multiplicative models through simulations | | 1 |
| 3 | The molecular anatomy of mouse skin during hair growth and rest | | 1 |
| 2 | Molecular spikes: a gold standard for single-cell RNA counting | | 1 |
| 1 | Sample Moments and Weak Convergence to Multivariate Stochastic Power Integrals. <i>Journal of Time Series Analysis</i> , 2017 , 38, 1000-1009 | 0.8 | |