

# Sandrine Dudoit

## List of Publications by Year in Descending Order

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

84  
papers

26,281  
citations

44  
h-index

94  
g-index

94  
ext. papers

30,753  
ext. citations

9.7  
avg. IF

6.69  
L-index

#	Paper	IF	Citations
84	Klf5 establishes bi-potential cell fate by dual regulation of ICM and TE specification genes. <i>Cell Reports</i> , <b>2021</b> , 37, 109982	10.6	0
83	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , <b>2021</b> , 598, 103-110	10.4	23
82	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , <b>2021</b> , 598, 86-102	10.4	44
81	cvCovEst: Cross-validated covariance matrix estimator selection and evaluation in R. <i>Journal of Open Source Software</i> , <b>2021</b> , 6, 3273	5.2	0
80	Untargeted metabolomics of newborn dried blood spots reveals sex-specific associations with pediatric acute myeloid leukemia. <i>Leukemia Research</i> , <b>2021</b> , 106, 106585	2.7	4
79	Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , <b>2020</b> , 11, 1201	17.4	86
78	scPCA: A toolbox for sparse contrastive principal component analysis in R. <i>Journal of Open Source Software</i> , <b>2020</b> , 5, 2079	5.2	
77	Untargeted adductomics of newborn dried blood spots identifies modifications to human serum albumin associated with childhood leukemia. <i>Leukemia Research</i> , <b>2020</b> , 88, 106268	2.7	9
76	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	514
75	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , <b>2019</b> , 8, 315-328.e8	10.6	66
74	Metabolomics of neonatal blood spots reveal distinct phenotypes of pediatric acute lymphoblastic leukemia and potential effects of early-life nutrition. <i>Cancer Letters</i> , <b>2019</b> , 452, 71-78	9.9	21
73	Untargeted adductomics of Cys34 modifications to human serum albumin in newborn dried blood spots. <i>Analytical and Bioanalytical Chemistry</i> , <b>2019</b> , 411, 2351-2362	4.4	19
72	Cys34 Adductomics Links Colorectal Cancer with the Gut Microbiota and Redox Biology. <i>Cancer Research</i> , <b>2019</b> , 79, 6024-6031	10.1	10
71	A general and flexible method for signal extraction from single-cell RNA-seq data. <i>Nature Communications</i> , <b>2018</b> , 9, 284	17.4	306
70	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , <b>2018</b> , 19, 24	18.3	101
69	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. <i>BMC Genomics</i> , <b>2018</b> , 19, 477	4.5	591
68	Untargeted lipidomic features associated with colorectal cancer in a prospective cohort. <i>BMC Cancer</i> , <b>2018</b> , 18, 996	4.8	13

67	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006378	5	26
66	An untargeted metabolomics method for archived newborn dried blood spots in epidemiologic studies. <i>Metabolomics</i> , <b>2017</b> , 13, 1	4.7	38
65	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , <b>2017</b> , 14, 565-571	21.6	255
64	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 817-830.e8	10.8	104
63	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 775-790.e9	18	42
62	Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. <i>F1000Research</i> , <b>2017</b> , 6, 1158	3.6	11
61	Silencing of odorant receptor genes by G protein signaling ensures the expression of one odorant receptor per olfactory sensory neuron. <i>Neuron</i> , <b>2014</b> , 81, 847-59	13.9	41
60	Normalization of RNA-seq data using factor analysis of control genes or samples. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 896-902	44.5	910
59	Comparing Segmentation Methods for Genome Annotation Based on RNA-Seq Data. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2014</b> , 19, 101-118	1.9	9
58	More power via graph-structured tests for differential expression of gene networks. <i>Annals of Applied Statistics</i> , <b>2012</b> , 6,	2.1	57
57	GC-content normalization for RNA-Seq data. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 480	3.6	458
56	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , <b>2011</b> , 471, 473-9	50.4	1094
55	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , <b>2011</b> , 21, 193-202	9.7	165
54	Polygenic and directional regulatory evolution across pathways in <i>Saccharomyces</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 5058-63	11.5	76
53	Loss-Based Estimation with Evolutionary Algorithms and Cross-Validation. <i>Adaptation, Learning, and Optimization</i> , <b>2010</b> , 453-484	0.7	
52	Identification of functional elements and regulatory circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , <b>2010</b> , 330, 1787-97	33.3	892
51	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e131	20.1	471
50	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 94	3.6	1132

49	Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in <i>Drosophila</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000525	6	68
48	Diverse transcriptional programs associated with environmental stress and hormones in the <i>Arabidopsis</i> receptor-like kinase gene family. <i>Molecular Plant</i> , <b>2009</b> , 2, 84-107	14.4	71
47	The establishment of gene silencing at single-cell resolution. <i>Nature Genetics</i> , <b>2009</b> , 41, 800-6	36.3	53
46	Novel low abundance and transient RNAs in yeast revealed by tiling microarrays and ultra high-throughput sequencing are not conserved across closely related yeast species. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000299	6	29
45	Resampling-based empirical Bayes multiple testing procedures for controlling generalized tail probability and expected value error rates: focus on the false discovery rate and simulation study. <i>Biometrical Journal</i> , <b>2008</b> , 50, 716-44	1.5	20
44	A deletion/substitution/addition algorithm for classification neural networks, with applications to biomedical data. <i>Journal of Statistical Planning and Inference</i> , <b>2008</b> , 138, 464-488	0.8	7
43	A general framework for statistical performance comparison of evolutionary computation algorithms. <i>Information Sciences</i> , <b>2008</b> , 178, 2870-2879	7.7	71
42	Stage II colon cancer prognosis prediction by tumor gene expression profiling. <i>Journal of Clinical Oncology</i> , <b>2006</b> , 24, 4685-91	2.2	173
41	Oracle inequalities for multi-fold cross validation. <i>Statistics &amp; Risk Modeling</i> , <b>2006</b> , 24, 351-371		66
40	The cross-validated adaptive epsilon-net estimator. <i>Statistics &amp; Risk Modeling</i> , <b>2006</b> , 24, 373-395		52
39	Survival ensembles. <i>Biostatistics</i> , <b>2006</b> , 7, 355-73	3.7	403
38	Multiple testing methods for ChIP-Chip high density oligonucleotide array data. <i>Journal of Computational Biology</i> , <b>2006</b> , 13, 579-613	1.7	34
37	A fine-scale linkage-disequilibrium measure based on length of haplotype sharing. <i>American Journal of Human Genetics</i> , <b>2006</b> , 78, 615-28	11	12
36	Exploration of global gene expression in human liver steatosis by high-density oligonucleotide microarray. <i>Laboratory Investigation</i> , <b>2006</b> , 86, 154-65	5.9	76
35	Colon cancer prognosis prediction by gene expression profiling. <i>Oncogene</i> , <b>2005</b> , 24, 6155-64	9.2	83
34	Asymptotics of cross-validated risk estimation in estimator selection and performance assessment. <i>Statistical Methodology</i> , <b>2005</b> , 2, 131-154		93
33	Gene expression profiling of nonneoplastic mucosa may predict clinical outcome of colon cancer patients. <i>Diseases of the Colon and Rectum</i> , <b>2005</b> , 48, 2238-48	3.1	25
32	Ischemic preconditioning modulates the expression of several genes, leading to the overproduction of IL-1Ra, iNOS, and Bcl-2 in a human model of liver ischemia-reperfusion. <i>FASEB Journal</i> , <b>2005</b> , 19, 1617-26	0.9	60

31	Augmentation procedures for control of the generalized family-wise error rate and tail probabilities for the proportion of false positives. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2004</b> , 3, Article15	1.2	62
30	Tree-based multivariate regression and density estimation with right-censored data. <i>Journal of Multivariate Analysis</i> , <b>2004</b> , 90, 154-177	1.4	45
29	Asymptotic optimality of likelihood-based cross-validation. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2004</b> , 3, Article4	1.2	56
28	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , <b>2004</b> , 5, R80	18.3	9148
27	Asymptotically optimal model selection method with right censored outcomes. <i>Bernoulli</i> , <b>2004</b> , 10, 1011-16	1.6	9
26	Multiple testing. Part I. Single-step procedures for control of general type I error rates. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2004</b> , 3, Article13	1.2	84
25	Multiple testing. Part II. Step-down procedures for control of the family-wise error rate. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2004</b> , 3, Article14	1.2	43
24	Multiple Hypothesis Testing in Microarray Experiments. <i>Statistical Science</i> , <b>2003</b> , 18, 71	2.4	614
23	Loss-based estimation with cross-validation. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery &amp; Data Mining</i> , <b>2003</b> , 5, 56-68	4.6	9
22	Open Source Software for the Analysis of Microarray Data. <i>BioTechniques</i> , <b>2003</b> , 34, S45-S51	2.5	172
21	Resampling-based multiple testing for microarray data analysis. <i>Test</i> , <b>2003</b> , 12, 1-77	1.1	366
20	Bagging to improve the accuracy of a clustering procedure. <i>Bioinformatics</i> , <b>2003</b> , 19, 1090-9	7.2	344
19	Supervised detection of regulatory motifs in DNA sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2003</b> , 2, Article5	1.2	10
18	Diversity, topographic differentiation, and positional memory in human fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 12877-82	11.5	852
17	Stereotyped and specific gene expression programs in human innate immune responses to bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 972-7	11.5	337
16	Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, e15	20.1	2571
15	Comparison of Methods for Image Analysis on cDNA Microarray Data. <i>Journal of Computational and Graphical Statistics</i> , <b>2002</b> , 11, 108-136	1.4	243
14	A prediction-based resampling method for estimating the number of clusters in a dataset. <i>Genome Biology</i> , <b>2002</b> , 3, RESEARCH0036	18.3	384

13	Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. <i>Journal of the American Statistical Association</i> , <b>2002</b> , 97, 77-87	2.8	1778
12	Power and robustness of a score test for linkage analysis of quantitative traits using identity by descent data on sib pairs. <i>Genetic Epidemiology</i> , <b>2001</b> , 20, 415-31	2.6	6
11	Power of a score test for quantitative trait linkage analysis of relative pairs. <i>Genetic Epidemiology</i> , <b>2000</b> , 19 Suppl 1, S85-91	2.6	3
10	A score test for the linkage analysis of qualitative and quantitative traits based on identity by descent data from sib-pairs. <i>Biostatistics</i> , <b>2000</b> , 1, 1-26	3.7	41
9	Microarray Expression Profiling Identifies Genes with Altered Expression in HDL-Deficient Mice. <i>Genome Research</i> , <b>2000</b> , 10, 2022-2029	9.7	12
8	Exploring High-Dimensional Biological Data with Sparse Contrastive Principal Component Analysis		1
7	ZINB-WaVE: A general and flexible method for signal extraction from single-cell RNA-seq data		19
6	Slingshot: Cell lineage and pseudotime inference for single-cell transcriptomics		15
5	An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types		23
4	A multimodal cell census and atlas of the mammalian primary motor cortex		12
3	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-seq		16
2	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets		2
1	Trajectory-based differential expression analysis for single-cell sequencing data		9