

Sandrine Dudoit

List of Publications by Year in descending order

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78
papers

34,629
citations

38742

50
h-index

66911

78
g-index

94
all docs

94
docs citations

94
times ranked

53911
citing authors

#	ARTICLE	IF	CITATIONS
1	CALDERA: finding all significant de Bruijn subgraphs for bacterial GWAS. <i>Bioinformatics</i> , 2022, 38, i36-i44.	4.1	6
2	cvCovEst: Cross-validated covariance matrix estimator selection and evaluation in R. <i>Journal of Open Source Software</i> , 2021, 6, 3273.	4.6	3
3	Untargeted metabolomics of newborn dried blood spots reveals sex-specific associations with pediatric acute myeloid leukemia. <i>Leukemia Research</i> , 2021, 106, 106585.	0.8	6
4	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
5	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	27.8	316
6	Extending the HSA-Cys34-Adductomics Pipeline to Modifications at Lys525. <i>Chemical Research in Toxicology</i> , 2021, 34, 2549-2557.	3.3	5
7	Klf5 establishes bi-potential cell fate by dual regulation of ICM and TE specification genes. <i>Cell Reports</i> , 2021, 37, 109982.	6.4	13
8	Untargeted adductomics of newborn dried blood spots identifies modifications to human serum albumin associated with childhood leukemia. <i>Leukemia Research</i> , 2020, 88, 106268.	0.8	17
9	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , 2020, 6, .	10.3	865
10	Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , 2020, 11, 1201.	12.8	345
11	scPCA: A toolbox for sparse contrastive principal component analysis in R. <i>Journal of Open Source Software</i> , 2020, 5, 2079.	4.6	0
12	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	6.2	117
13	Metabolomics of neonatal blood spots reveal distinct phenotypes of pediatric acute lymphoblastic leukemia and potential effects of early-life nutrition. <i>Cancer Letters</i> , 2019, 452, 71-78.	7.2	36
14	Untargeted adductomics of Cys34 modifications to human serum albumin in newborn dried blood spots. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 2351-2362.	3.7	23
15	Cys34 Adductomics Links Colorectal Cancer with the Gut Microbiota and Redox Biology. <i>Cancer Research</i> , 2019, 79, 6024-6031.	0.9	23
16	A general and flexible method for signal extraction from single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 284.	12.8	540
17	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24.	8.8	180
18	Untargeted lipidomic features associated with colorectal cancer in a prospective cohort. <i>BMC Cancer</i> , 2018, 18, 996.	2.6	21

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19	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. <i>PLoS Computational Biology</i> , 2018, 14, e1006378.	3.2	48
20	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. <i>BMC Genomics</i> , 2018, 19, 477.	2.8	1,562
21	An untargeted metabolomics method for archived newborn dried blood spots in epidemiologic studies. <i>Metabolomics</i> , 2017, 13, 1.	3.0	58
22	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571.	19.0	405
23	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , 2017, 20, 817-830.e8.	11.1	164
24	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , 2017, 21, 775-790.e9.	11.1	67
25	Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. <i>F1000Research</i> , 2017, 6, 1158.	1.6	13
26	Silencing of Odorant Receptor Genes by G Protein $\beta\gamma$ Signaling Ensures the Expression of One Odorant Receptor per Olfactory Sensory Neuron. <i>Neuron</i> , 2014, 81, 847-859.	8.1	47
27	Normalization of RNA-seq data using factor analysis of control genes or samples. <i>Nature Biotechnology</i> , 2014, 32, 896-902.	17.5	1,570
28	Comparing Segmentation Methods for Genome Annotation Based on RNA-Seq Data. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 101-118.	1.4	9
29	More power via graph-structured tests for differential expression of gene networks. <i>Annals of Applied Statistics</i> , 2012, 6, .	1.1	67
30	GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480.	2.6	712
31	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	27.8	1,379
32	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	5.5	208
33	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.	2.6	1,421
34	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> , 2010, 107, 5058-5063.	7.1	93
35	Loss-Based Estimation with Evolutionary Algorithms and Cross-Validation. <i>Adaptation, Learning, and Optimization</i> , 2010, , 453-484.	0.6	0
36	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124

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37	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	14.5	573
38	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2009, 5, e1000525.	3.5	87
39	Diverse Transcriptional Programs Associated with Environmental Stress and Hormones in the Arabidopsis Receptor-Like Kinase Gene Family. <i>Molecular Plant</i> , 2009, 2, 84-107.	8.3	88
40	The establishment of gene silencing at single-cell resolution. <i>Nature Genetics</i> , 2009, 41, 800-806.	21.4	71
41	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> , 2008, 50, 716-744.	1.0	25
42	A deletion/substitution/addition algorithm for classification neural networks, with applications to biomedical data. <i>Journal of Statistical Planning and Inference</i> , 2008, 138, 464-488.	0.6	8
43	A general framework for statistical performance comparison of evolutionary computation algorithms. <i>Information Sciences</i> , 2008, 178, 2870-2879.	6.9	93
44	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> , 2008, 4, e1000299.	3.5	31
45	Multiple Testing Methods For ChIP-Chip High Density Oligonucleotide Array Data. <i>Journal of Computational Biology</i> , 2006, 13, 579-613.	1.6	44
46	A Fine-Scale Linkage-Disequilibrium Measure Based on Length of Haplotype Sharing. <i>American Journal of Human Genetics</i> , 2006, 78, 615-628.	6.2	13
47	Exploration of global gene expression in human liver steatosis by high-density oligonucleotide microarray. <i>Laboratory Investigation</i> , 2006, 86, 154-165.	3.7	89
48	Stage II Colon Cancer Prognosis Prediction by Tumor Gene Expression Profiling. <i>Journal of Clinical Oncology</i> , 2006, 24, 4685-4691.	1.6	189
49	Oracle inequalities for multi-fold cross validation. <i>Statistics & Risk Modeling</i> , 2006, 24, 351-371.	0.3	88
50	The cross-validated adaptive epsilon-net estimator. <i>Statistics & Risk Modeling</i> , 2006, 24, 373-395.	0.3	73
51	Colon cancer prognosis prediction by gene expression profiling. <i>Oncogene</i> , 2005, 24, 6155-6164.	5.9	92
52	Asymptotics of cross-validated risk estimation in estimator selection and performance assessment. <i>Statistical Methodology</i> , 2005, 2, 131-154.	0.5	115
53	Gene Expression Profiling of Nonneoplastic Mucosa May Predict Clinical Outcome of Colon Cancer Patients. <i>Diseases of the Colon and Rectum</i> , 2005, 48, 2238-2248.	1.3	29
54	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> , 2005, 19, 1617-1626.	0.5	65

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55	Survival ensembles. <i>Biostatistics</i> , 2005, 7, 355-373.	1.5	529
56	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> , 2004, 3, 1-25.	0.6	102
57	Tree-based multivariate regression and density estimation with right-censored data. <i>Journal of Multivariate Analysis</i> , 2004, 90, 154-177.	1.0	52
58	Asymptotic Optimality of Likelihood-Based Cross-Validation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-23.	0.6	75
59	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.	9.6	10,796
60	Asymptotically optimal model selection method with right censored outcomes. <i>Bernoulli</i> , 2004, 10, 1011.	1.3	10
61	Multiple Testing. Part I. Single-Step Procedures for Control of General Type I Error Rates. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-69.	0.6	115
62	Multiple Testing. Part II. Step-Down Procedures for Control of the Family-Wise Error Rate. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-33.	0.6	63
63	Resampling-based multiple testing for microarray data analysis. <i>Test</i> , 2003, 12, 1-77.	1.1	416
64	Bagging to improve the accuracy of a clustering procedure. <i>Bioinformatics</i> , 2003, 19, 1090-1099.	4.1	445
65	Supervised Detection of Regulatory Motifs in DNA Sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article5.	0.6	15
66	Multiple Hypothesis Testing in Microarray Experiments. <i>Statistical Science</i> , 2003, 18, 71.	2.8	786
67	Loss-based estimation with cross-validation. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003, 5, 56-68.	4.0	9
68	Open Source Software for the Analysis of Microarray Data. <i>BioTechniques</i> , 2003, 34, S45-S51.	1.8	223
69	Diversity, topographic differentiation, and positional memory in human fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12877-12882.	7.1	983
70	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> , 2002, 99, 972-977.	7.1	371
71	Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. <i>Nucleic Acids Research</i> , 2002, 30, 15e-15.	14.5	2,946
72	Comparison of Methods for Image Analysis on cDNA Microarray Data. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 108-136.	1.7	341

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73	A prediction-based resampling method for estimating the number of clusters in a dataset. <i>Genome Biology</i> , 2002, 3, research0036.1.	9.6	509
74	Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. <i>Journal of the American Statistical Association</i> , 2002, 97, 77-87.	3.1	2,177
75	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> , 2001, 20, 415-431.	1.3	9
76	Power of a score test for quantitative trait linkage analysis of relative pairs. <i>Genetic Epidemiology</i> , 2000, 19, S85-S91.	1.3	4
77	A score test for the linkage analysis of qualitative and quantitative traits based on identity by descent data from sib-pairs. <i>Biostatistics</i> , 2000, 1, 1-26.	1.5	54
78	Microarray Expression Profiling Identifies Genes with Altered Expression in HDL-Deficient Mice. <i>Genome Research</i> , 2000, 10, 2022-2029.	5.5	22