

Robert Tibshirani

List of Publications by Citations

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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.

75
papers

50,681
citations

54
h-index

77
g-index

77
ext. papers

59,024
ext. citations

8.8
avg, IF

7.78
L-index

#	Paper	IF	Citations
75	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000 , 403, 503-11	50.4	7592
74	Regression Shrinkage and Selection Via the Lasso. <i>Journal of the Royal Statistical Society Series B: Methodological</i> , 1996 , 58, 267-288		7587
73	Statistical significance for genomewide studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 9440-5	11.5	7380
72	Least angle regression. <i>Annals of Statistics</i> , 2004 , 32, 407	3.2	5029
71	Repeated observation of breast tumor subtypes in independent gene expression data sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8418-23	11.5	4262
70	Additive logistic regression: a statistical view of boosting (With discussion and a rejoinder by the authors). <i>Annals of Statistics</i> , 2000 , 28, 337	3.2	3535
69	Sparse inverse covariance estimation with the graphical lasso. <i>Biostatistics</i> , 2008 , 9, 432-41	3.7	2705
68	Empirical Bayes Analysis of a Microarray Experiment. <i>Journal of the American Statistical Association</i> , 2001 , 96, 1151-1160	2.8	1156
67	Gene expression profiling identifies clinically relevant subtypes of prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 811-6	11.5	1047
66	Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 3738-43	11.5	823
65	Use of gene-expression profiling to identify prognostic subclasses in adult acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2004 , 350, 1605-16	59.2	822
64	Improvements on Cross-Validation: The 632+ Bootstrap Method. <i>Journal of the American Statistical Association</i> , 1997 , 92, 548-560	2.8	760
63	Classification by pairwise coupling. <i>Annals of Statistics</i> , 1998 , 26, 451	3.2	640
62	On the degrees of freedom of the lasso. <i>Annals of Statistics</i> , 2007 , 35, 2173	3.2	500
61	Empirical bayes methods and false discovery rates for microarrays. <i>Genetic Epidemiology</i> , 2002 , 23, 70-86.6		471
60	Semi-supervised methods to predict patient survival from gene expression data. <i>PLoS Biology</i> , 2004 , 2, E108	9.7	457
59	Flexible Discriminant Analysis by Optimal Scoring. <i>Journal of the American Statistical Association</i> , 1994 , 89, 1255-1270	2.8	392

58	Regularized linear discriminant analysis and its application in microarrays. <i>Biostatistics</i> , 2007 , 8, 86-100	3.7	370
57	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000 , 1, RESEARCH0003	18.3	304
56	Finding consistent patterns: a nonparametric approach for identifying differential expression in RNA-Seq data. <i>Statistical Methods in Medical Research</i> , 2013 , 22, 519-36	2.3	287
55	Gene expression patterns in ovarian carcinomas. <i>Molecular Biology of the Cell</i> , 2003 , 14, 4376-86	3.5	273
54	Strong rules for discarding predictors in lasso-type problems. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012 , 74, 245-266	3.9	254
53	Class Prediction by Nearest Shrunken Centroids, with Applications to DNA Microarrays. <i>Statistical Science</i> , 2003 , 18, 104	2.4	252
52	Normalization, testing, and false discovery rate estimation for RNA-sequencing data. <i>Biostatistics</i> , 2012 , 13, 523-38	3.7	217
51	Differentiation stage-specific expression of microRNAs in B lymphocytes and diffuse large B-cell lymphomas. <i>Blood</i> , 2009 , 113, 3754-64	2.2	213
50	Transcriptional profiling of long non-coding RNAs and novel transcribed regions across a diverse panel of archived human cancers. <i>Genome Biology</i> , 2012 , 13, R75	18.3	195
49	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018 , 36, 2845-2853	2.2	164
48	Risk factors of delayed extubation, prolonged length of stay in the intensive care unit, and mortality in patients undergoing coronary artery bypass graft with fast-track cardiac anesthesia: a new cardiac risk score. <i>Anesthesiology</i> , 1999 , 91, 936-44	4.3	152
47	A network model of a cooperative genetic landscape in brain tumors. <i>JAMA - Journal of the American Medical Association</i> , 2009 , 302, 261-75	27.4	144
46	LMO2 protein expression predicts survival in patients with diffuse large B-cell lymphoma treated with anthracycline-based chemotherapy with and without rituximab. <i>Journal of Clinical Oncology</i> , 2008 , 26, 447-54	2.2	143
45	Exact Post-Selection Inference for Sequential Regression Procedures. <i>Journal of the American Statistical Association</i> , 2016 , 111, 600-620	2.8	135
44	Covariance-regularized regression and classification for high-dimensional problems. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2009 , 71, 615-636	3.9	133
43	Flexible Discriminant Analysis by Optimal Scoring		122
42	Supervised harvesting of expression trees. <i>Genome Biology</i> , 2001 , 2, RESEARCH0003	18.3	113
41	3'-end sequencing for expression quantification (3SEQ) from archival tumor samples. <i>PLoS ONE</i> , 2010 , 5, e8768	3.7	108

40	Expression and prognostic significance of a panel of tissue hypoxia markers in head-and-neck squamous cell carcinomas. <i>International Journal of Radiation Oncology Biology Physics</i> , 2007 , 69, 167-75	4	102
39	Averaged gene expressions for regression. <i>Biostatistics</i> , 2007 , 8, 212-27	3.7	101
38	Gene expression profiles at diagnosis in de novo childhood AML patients identify FLT3 mutations with good clinical outcomes. <i>Blood</i> , 2004 , 104, 2646-54	2.2	95
37	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3707-12	11.5	91
36	Survival analysis with high-dimensional covariates. <i>Statistical Methods in Medical Research</i> , 2010 , 19, 29-51	3	90
35	Disease signatures are robust across tissues and experiments. <i>Molecular Systems Biology</i> , 2009 , 5, 307	12.2	90
34	Quantitative SD-OCT imaging biomarkers as indicators of age-related macular degeneration progression 2014 , 55, 7093-103		85
33	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. <i>Cell</i> , 2019 , 178, 699-713.e19	56.2	84
32	HGAL is a novel interleukin-4-inducible gene that strongly predicts survival in diffuse large B-cell lymphoma. <i>Blood</i> , 2003 , 101, 433-40	2.2	79
31	Boolean implication networks derived from large scale, whole genome microarray datasets. <i>Genome Biology</i> , 2008 , 9, R157	18.3	75
30	Single-cell developmental classification of B cell precursor acute lymphoblastic leukemia at diagnosis reveals predictors of relapse. <i>Nature Medicine</i> , 2018 , 24, 474-483	50.5	68
29	The use of plasma surface-enhanced laser desorption/ionization time-of-flight mass spectrometry proteomic patterns for detection of head and neck squamous cell cancers. <i>Clinical Cancer Research</i> , 2004 , 10, 4806-12	12.9	66
28	TRANSPOSABLE REGULARIZED COVARIANCE MODELS WITH AN APPLICATION TO MISSING DATA IMPUTATION. <i>Annals of Applied Statistics</i> , 2010 , 4, 764-790	2.1	64
27	Preconditioning for feature selection and regression in high-dimensional problems. <i>Annals of Statistics</i> , 2008 , 36,	3.2	64
26	Childhood leukemia and personal monitoring of residential exposures to electric and magnetic fields in Ontario, Canada. <i>Cancer Causes and Control</i> , 1999 , 10, 233-43	2.8	63
25	A tail strength measure for assessing the overall univariate significance in a dataset. <i>Biostatistics</i> , 2006 , 7, 167-81	3.7	61
24	Active idiotypic vaccination versus control immunotherapy for follicular lymphoma. <i>Journal of Clinical Oncology</i> , 2014 , 32, 1797-803	2.2	59
23	Sequential selection procedures and false discovery rate control. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2016 , 78, 423-444	3.9	57

22	A multicentre study of primary breast diffuse large B-cell lymphoma in the rituximab era. <i>British Journal of Haematology</i> , 2014 , 165, 358-63	4.5	54
21	The 'miss rate' for the analysis of gene expression data. <i>Biostatistics</i> , 2005 , 6, 111-7	3.7	54
20	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. <i>Nature Genetics</i> , 2017 , 49, 377-386	36.3	52
19	Post-Selection Inference for ℓ_1 -Penalized Likelihood Models. <i>Canadian Journal of Statistics</i> , 2018 , 46, 41-61	10.4	50
18	Cardiolipins Are Biomarkers of Mitochondria-Rich Thyroid Oncocytic Tumors. <i>Cancer Research</i> , 2016 , 76, 6588-6597	10.1	49
17	Estimation of Sparse Binary Pairwise Markov Networks using Pseudo-likelihoods. <i>Journal of Machine Learning Research</i> , 2009 , 10, 883-906	28.6	43
16	Adaptive index models for marker-based risk stratification. <i>Biostatistics</i> , 2011 , 12, 68-86	3.7	32
15	DR-Integrator: a new analytic tool for integrating DNA copy number and gene expression data. <i>Bioinformatics</i> , 2010 , 26, 414-6	7.2	29
14	CD81 protein is expressed at high levels in normal germinal center B cells and in subtypes of human lymphomas. <i>Human Pathology</i> , 2010 , 41, 271-80	3.7	25
13	Inference with Transposable Data: Modeling the Effects of Row and Column Correlations. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012 , 74, 721-743	3.9	22
12	Machine learning methods applied to DNA microarray data can improve the diagnosis of cancer. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003 , 5, 48-55	4.6	19
11	A study of pre-validation. <i>Annals of Applied Statistics</i> , 2008 , 2,	2.1	18
10	Best Subset, Forward Stepwise or Lasso? Analysis and Recommendations Based on Extensive Comparisons. <i>Statistical Science</i> , 2020 , 35,	2.4	16
9	C-C chemokine receptor 1 expression in human hematolymphoid neoplasia. <i>American Journal of Clinical Pathology</i> , 2010 , 133, 473-83	1.9	15
8	Alteration of gene expression signatures of cortical differentiation and wound response in lethal clear cell renal cell carcinomas. <i>PLoS ONE</i> , 2009 , 4, e6039	3.7	13
7	Monotone Shrinkage of Trees. <i>Journal of Computational and Graphical Statistics</i> , 1998 , 7, 417-433	1.4	12
6	Rejoinder: Linear Smoothers and Additive Models. <i>Annals of Statistics</i> , 1989 , 17, 543	3.2	11
5	Pathophysiological significance and therapeutic targeting of germinal center kinase in diffuse large B-cell lymphoma. <i>Blood</i> , 2016 , 128, 239-48	2.2	10

- 4 Local false discovery rate facilitates comparison of different microarray experiments. *Nucleic Acids Research*, **2009**, 37, 7483-97 20.1 9
- 3 A Pliable Lasso. *Journal of Computational and Graphical Statistics*, **2020**, 29, 215-225 1.4 8
- 2 Coaching variables for regression and classification. *Statistics and Computing*, **1998**, 8, 25-33 1.8 7
- 1 Genomic Feature Selection by Coverage Design Optimization. *Journal of Applied Statistics*, **2018**, 45, 2658-2676 1.8 7