

# Richard Simon

## List of Publications by Year in descending order

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81  
papers

26,264  
citations

41258

49  
h-index

79541

73  
g-index

88  
all docs

88  
docs citations

88  
times ranked

27410  
citing authors

#	ARTICLE	IF	CITATIONS
1	Review of Statistical Methods for Biomarker-Driven Clinical Trials. JCO Precision Oncology, 2019, 3, 1-9.	1.5	3
2	Correlation of gene expression and associated mutation profiles of APOBEC3A, APOBEC3B, REV1, UNG, and FHIT with chemosensitivity of cancer cell lines to drug treatment. Human Genomics, 2018, 12, 20.	1.4	11
3	New designs for basket clinical trials in oncology. Journal of Biopharmaceutical Statistics, 2018, 28, 245-255.	0.4	23
4	Development of Prognostic Biomarker Signatures for Survival Using High-Dimensional Data. ICSA Book Series in Statistics, 2018, , 339-351.	0.0	0
5	Critical Review of Umbrella, Basket, and Platform Designs for Oncology Clinical Trials. Clinical Pharmacology and Therapeutics, 2017, 102, 934-941.	2.3	71
6	A computational study of the inhibition mechanisms of P-glycoprotein mediated paclitaxel efflux by kinase inhibitors. BMC Systems Biology, 2017, 11, 108.	3.0	10
7	The Bayesian basket design for genomic variant-driven phase II trials. Seminars in Oncology, 2016, 43, 13-18.	0.8	81
8	Concerted changes in transcriptional regulation of genes involved in DNA methylation, demethylation, and folate-mediated one-carbon metabolism pathways in the NCI-60 cancer cell line panel in response to cancer drug treatment. Clinical Epigenetics, 2016, 8, 73.	1.8	21
9	Two-stage adaptive cutoff design for building and validating a prognostic biomarker signature. Statistics in Medicine, 2014, 33, 5097-5110.	0.8	5
10	Using single cell sequencing data to model the evolutionary history of a tumor. BMC Bioinformatics, 2014, 15, 27.	1.2	58
11	Class probability estimation for medical studies. Biometrical Journal, 2014, 56, 597-600.	0.6	12
12	Clinical trials for precision oncology using next-generation sequencing. Personalized Medicine, 2013, 10, 485-495.	0.8	21
13	Overfitting in prediction models – Is it a problem only in high dimensions?. Contemporary Clinical Trials, 2013, 36, 636-641.	0.8	122
14	Developing and Validating Continuous Genomic Signatures in Randomized Clinical Trials for Predictive Medicine. Clinical Cancer Research, 2012, 18, 6065-6073.	3.2	54
15	Microarray-based cancer prediction using single genes. BMC Bioinformatics, 2011, 12, 391.	1.2	50
16	An evaluation of resampling methods for assessment of survival risk prediction in high-dimensional settings. Statistics in Medicine, 2011, 30, 642-653.	0.8	33
17	Moving from correlative science to predictive oncology. EPMA Journal, 2010, 1, 377-387.	3.3	4
18	Development and Validation of Predictive Indices for a Continuous Outcome Using Gene Expression Profiles. Cancer Informatics, 2010, 9, CIN.S3805.	0.9	13

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19	Gene Expression-Based Prognostic Signatures in Lung Cancer: Ready for Clinical Use?. Journal of the National Cancer Institute, 2010, 102, 464-474.	3.0	324
20	What should physicians look for in evaluating prognostic gene-expression signatures?. Nature Reviews Clinical Oncology, 2010, 7, 327-334.	12.5	104
21	Clinical trial designs for evaluating the medical utility of prognostic and predictive biomarkers in oncology. Personalized Medicine, 2010, 7, 33-47.	0.8	155
22	The Cross-Validated Adaptive Signature Design. Clinical Cancer Research, 2010, 16, 691-698.	3.2	182
23	Drug and Pharmacodiagnostic Co-Development. , 2010, , 185-205.		0
24	Integration of Predictive Biomarker Diagnostics into Clinical Trials for New Drug Development. , 2010, , 18-1-18-14.		0
25	Analysis of DNA microarray expression data. Best Practice and Research in Clinical Haematology, 2009, 22, 271-282.	0.7	37
26	Development and validation of biomarker classifiers for treatment selection. Journal of Statistical Planning and Inference, 2008, 138, 308-320.	0.4	64
27	Microarray-based expression profiling and informatics. Current Opinion in Biotechnology, 2008, 19, 26-29.	3.3	42
28	Predictive Biomarker Classifiers in the Design of Pivotal Clinical Trials. Methods in Pharmacology and Toxicology, 2008, , 229-238.	0.1	0
29	Lost in translation: Problems and pitfalls in translating laboratory observations to clinical utility. European Journal of Cancer, 2008, 44, 2707-2713.	1.3	57
30	Interpretation of Genomic Data: Questions and Answers. Seminars in Hematology, 2008, 45, 196-204.	1.8	11
31	Challenges of Microarray Data and the Evaluation of Gene Expression Profile Signatures. Cancer Investigation, 2008, 26, 327-332.	0.6	12
32	Calculating Confidence Intervals for Prediction Error in Microarray Classification Using Resampling. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article8.	0.2	33
33	The Use of Genomics in Clinical Trial Design. Clinical Cancer Research, 2008, 14, 5984-5993.	3.2	166
34	Identification of Pharmacogenomic Biomarker Classifiers in Cancer Drug Development. , 2008, , 327-338.		1
35	Gene Expression Profiling Reveals a Massive, Aneuploidy-Dependent Transcriptional Deregulation and Distinct Differences between Lymph Node-“Negative and Lymph Node-“Positive Colon Carcinomas. Cancer Research, 2007, 67, 41-56.	0.4	108
36	Resampling Strategies for Model Assessment and Selection. , 2007, , 173-186.		18

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37	Analysis of Gene Expression Data Using BRB-Array Tools. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	470
38	Appropriateness of some resampling-based inference procedures for assessing performance of prognostic classifiers derived from microarray data. <i>Statistics in Medicine</i> , 2007, 26, 1102-1113.	0.8	15
39	An investigation of two multivariate permutation methods for controlling the false discovery proportion. <i>Statistics in Medicine</i> , 2007, 26, 4428-4440.	0.8	32
40	A comparison of bootstrap methods and an adjusted bootstrap approach for estimating the prediction error in microarray classification. <i>Statistics in Medicine</i> , 2007, 26, 5320-5334.	0.8	81
41	Challenges of Microarray Data and the Evaluation of Gene Expression Profile Signatures. <i>Translational Medicine Series</i> , 2007, , 27-36.	0.0	0
42	Analysis of gene expression data using BRB-ArrayTools. <i>Cancer Informatics</i> , 2007, 3, 11-7.	0.9	461
43	Validation of pharmacogenomic biomarker classifiers for treatment selection. <i>Cancer Biomarkers</i> , 2006, 2, 89-96.	0.8	21
44	Bias in error estimation when using cross-validation for model selection. <i>BMC Bioinformatics</i> , 2006, 7, 91.	1.2	1,174
45	Development and Evaluation of Therapeutically Relevant Predictive Classifiers Using Gene Expression Profiling. <i>Journal of the National Cancer Institute</i> , 2006, 98, 1169-1171.	3.0	76
46	Molecular Diagnosis of Burkitt's Lymphoma. <i>New England Journal of Medicine</i> , 2006, 354, 2431-2442.	13.9	824
47	Development and Validation of Therapeutically Relevant Multi-Gene Biomarker Classifiers. <i>Journal of the National Cancer Institute</i> , 2005, 97, 866-867.	3.0	95
48	Sample size determination in microarray experiments for class comparison and prognostic classification. <i>Biostatistics</i> , 2005, 6, 27-38.	0.9	151
49	Diffuse large B-cell lymphoma subgroups have distinct genetic profiles that influence tumor biology and improve gene-expression-based survival prediction. <i>Blood</i> , 2005, 106, 3183-3190.	0.6	348
50	Effectiveness of Gene Expression Profiling for Response Prediction of Rectal Adenocarcinomas to Preoperative Chemoradiotherapy. <i>Journal of Clinical Oncology</i> , 2005, 23, 1826-1838.	0.8	325
51	Roadmap for Developing and Validating Therapeutically Relevant Genomic Classifiers. <i>Journal of Clinical Oncology</i> , 2005, 23, 7332-7341.	0.8	361
52	Prediction error estimation: a comparison of resampling methods. <i>Bioinformatics</i> , 2005, 21, 3301-3307.	1.8	1,045
53	Clinical Trial Designs for Therapeutic Cancer Vaccines. <i>Cancer Treatment and Research</i> , 2005, 123, 339-350.	0.2	8
54	Evaluating the Efficiency of Targeted Designs for Randomized Clinical Trials. <i>Clinical Cancer Research</i> , 2004, 10, 6759-6763.	3.2	308

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55	When is a genomic classifier ready for prime time?. <i>Nature Clinical Practice Oncology</i> , 2004, 1, 4-5.	4.3	21
56	Iterative class discovery and feature selection using Minimal Spanning Trees. <i>BMC Bioinformatics</i> , 2004, 5, 126.	1.2	23
57	Prediction of Survival in Follicular Lymphoma Based on Molecular Features of Tumor-Infiltrating Immune Cells. <i>New England Journal of Medicine</i> , 2004, 351, 2159-2169.	13.9	1,293
58	Clinical Trial Designs for Therapeutic Vaccine Studies. , 2004, , 519-525.		1
59	The proliferation gene expression signature is a quantitative integrator of oncogenic events that predicts survival in mantle cell lymphoma. <i>Cancer Cell</i> , 2003, 3, 185-197.	7.7	848
60	Predicting hepatitis B virusâ€“positive metastatic hepatocellular carcinomas using gene expression profiling and supervised machine learning. <i>Nature Medicine</i> , 2003, 9, 416-423.	15.2	805
61	Molecular Diagnosis of Primary Mediastinal B Cell Lymphoma Identifies a Clinically Favorable Subgroup of Diffuse Large B Cell Lymphoma Related to Hodgkin Lymphoma. <i>Journal of Experimental Medicine</i> , 2003, 198, 851-862.	4.2	1,002
62	Pitfalls in the Use of DNA Microarray Data for Diagnostic and Prognostic Classification. <i>Journal of the National Cancer Institute</i> , 2003, 95, 14-18.	3.0	943
63	Questions and Answers on Design of Dual-Label Microarrays for Identifying Differentially Expressed Genes. <i>Journal of the National Cancer Institute</i> , 2003, 95, 1362-1369.	3.0	81
64	Supervised analysis when the number of candidate features (p) greatly exceeds the number of cases (n). <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery &amp; Data Mining</i> , 2003, 5, 31-36.	3.2	63
65	Using DNA microarrays for diagnostic and prognostic prediction. <i>Expert Review of Molecular Diagnostics</i> , 2003, 3, 587-595.	1.5	36
66	A Paradigm for Class Prediction Using Gene Expression Profiles. <i>Journal of Computational Biology</i> , 2002, 9, 505-511.	0.8	268
67	Initiating oncogenic event determines gene-expression patterns of human breast cancer models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6967-6972.	3.3	192
68	The Use of Molecular Profiling to Predict Survival after Chemotherapy for Diffuse Large-B-Cell Lymphoma. <i>New England Journal of Medicine</i> , 2002, 346, 1937-1947.	13.9	3,474
69	Design of studies using DNA microarrays. <i>Genetic Epidemiology</i> , 2002, 23, 21-36.	0.6	183
70	Gene-Expression Profiles in Hereditary Breast Cancer. <i>New England Journal of Medicine</i> , 2001, 344, 539-548.	13.9	1,669
71	Clinical Trial Designs for Cytostatic Agents: Are New Approaches Needed?. <i>Journal of Clinical Oncology</i> , 2001, 19, 265-272.	0.8	324
72	Relation of Gene Expression Phenotype to Immunoglobulin Mutation Genotype in B Cell Chronic Lymphocytic Leukemia. <i>Journal of Experimental Medicine</i> , 2001, 194, 1639-1648.	4.2	978

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73	Twenty Years of Phase III Trials for Patients With Extensive-Stage Small-Cell Lung Cancer: Perceptible Progress. <i>Journal of Clinical Oncology</i> , 1999, 17, 1794-1794.	0.8	340
74	A Bayesian approach to establishing sample size and monitoring criteria for phase II clinical trials. <i>Contemporary Clinical Trials</i> , 1994, 15, 463-481.	2.0	66
75	Practical Bayesian Guidelines for Phase IIB Clinical Trials. <i>Biometrics</i> , 1994, 50, 337.	0.8	197
76	A decade of progress in statistical methodology for clinical trials. <i>Statistics in Medicine</i> , 1991, 10, 1789-1817.	0.8	60
77	Flexible regression models with cubic splines. <i>Statistics in Medicine</i> , 1989, 8, 551-561.	0.8	2,142
78	Optimal two-stage designs for phase II clinical trials. <i>Contemporary Clinical Trials</i> , 1989, 10, 1-10.	2.0	3,264
79	Prognostic factors in Burkitt's lymphoma importance of total tumor burden. <i>Cancer</i> , 1980, 45, 1507-1515.	2.0	112
80	Combination chemotherapy of advanced lung cancer. A randomized trial. <i>Cancer</i> , 1976, 38, 2201-2207.	2.0	85
81	A staging system for hepatocellular carcinoma: Prognostic factors in Ugandan patients. <i>Cancer</i> , 1975, 35, 1357-1364.	2.0	92