

# Christos Hatzis

## List of Publications by Year in descending order

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Version: 2024-02-01

134  
papers

8,398  
citations

76326

40  
h-index

49909

87  
g-index

140  
all docs

140  
docs citations

140  
times ranked

12548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Analysis of Metabolic Isozyme Targets in Cancer. <i>Cancer Research</i> , 2022, 82, 1698-1711.	0.9	4
2	Targeted RNAseq assay incorporating unique molecular identifiers for improved quantification of gene expression signatures and transcribed mutation fraction in fixed tumor samples. <i>BMC Cancer</i> , 2021, 21, 114.	2.6	6
3	Whole-genome sequencing of phenotypically distinct inflammatory breast cancers reveals similar genomic alterations to non-inflammatory breast cancers. <i>Genome Medicine</i> , 2021, 13, 70.	8.2	8
4	Treatment scheduling effects on the evolution of drug resistance in heterogeneous cancer cell populations. <i>Npj Breast Cancer</i> , 2021, 7, 60.	5.2	19
5	Intra- and Interlaboratory Reproducibility of the Sensitivity to Endocrine Therapy Assay for Stage II/III Breast Cancer. <i>Clinical Chemistry</i> , 2021, 67, 1240-1248.	3.2	3
6	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
7	Data augmentation based on waterfall plots to increase value of response data generated by small single arm Phase II trials. <i>Contemporary Clinical Trials</i> , 2021, 110, 106589.	1.8	0
8	Multi-Omics Investigation of Innate Navitoclax Resistance in Triple-Negative Breast Cancer Cells. <i>Cancers</i> , 2020, 12, 2551.	3.7	12
9	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. <i>Nature Communications</i> , 2020, 11, 2438.	12.8	52
10	Analysis of Pre- and Posttreatment Tissues from the SWOG S0800 Trial Reveals an Effect of Neoadjuvant Chemotherapy on the Breast Cancer Genome. <i>Clinical Cancer Research</i> , 2020, 26, 1977-1984.	7.0	9
11	Genomic and Immune Profiling of a Patient With Triple-Negative Breast Cancer That Progressed During Neoadjuvant Chemotherapy Plus PD-L1 Blockade. <i>JCO Precision Oncology</i> , 2019, 3, 1-6.	3.0	3
12	A prospective decision-impact study incorporating Breast Cancer Index into extended endocrine therapy decision-making. <i>Breast Cancer Management</i> , 2019, 8, BMT22.	0.2	8
13	Identification and Validation of a Novel Biologics Target in Triple Negative Breast Cancer. <i>Scientific Reports</i> , 2019, 9, 14934.	3.3	19
14	SETER/PR: a robust 18-gene predictor for sensitivity to endocrine therapy for metastatic breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 16.	5.2	48
15	Examining the cost-effectiveness of baseline left ventricular function assessment among breast cancer patients undergoing anthracycline-based therapy. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 261-270.	2.5	11
16	Immune profiling of pre- and post-treatment breast cancer tissues from the SWOG S0800 neoadjuvant trial. <i>Breast Cancer Research and Treatment</i> , 2019, 7, 88.		51
17	The impact of communication style on patient satisfaction. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 349-356.	2.5	16
18	Immune microenvironment of triple-negative breast cancer in African-American and Caucasian women. <i>Breast Cancer Research and Treatment</i> , 2019, 175, 247-259.	2.5	43

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19	Breast Cancer Heterogeneity Investigation: Multiple k-Means Clustering Approach. , 2019, , .		1
20	The impact of RNA extraction method on accurate RNA sequencing from formalin-fixed paraffin-embedded tissues. BMC Cancer, 2019, 19, 1189.	2.6	30
21	Breast cancer patients with brain metastasis undergoing GKRS. Breast Cancer, 2019, 26, 147-153.	2.9	5
22	Long-Term Survival of De Novo Stage IV Human Epidermal Growth Receptor 2 (HER2) Positive Breast Cancers Treated with HER2-Targeted Therapy. Oncologist, 2019, 24, 313-318.	3.7	39
23	Single-arm, neoadjuvant, phase II trial of pertuzumab and trastuzumab administered concomitantly with weekly paclitaxel followed by 5-fluoruracil, epirubicin, and cyclophosphamide (FEC) for stage Iâ€“III HER2-positive breast cancer. Breast Cancer Research and Treatment, 2018, 169, 333-340.	2.5	16
24	Comparison of Residual Riskâ€“Based Eligibility vs Tumor Size and Nodal Status for Power Estimates in Adjuvant Trials of Breast Cancer Therapies. JAMA Oncology, 2018, 4, e175092.	7.1	4
25	Tumor-Infiltrating Lymphocytes and PD-L1 Expression in Pre- and Posttreatment Breast Cancers in the SWOG S0800 Phase II Neoadjuvant Chemotherapy Trial. Molecular Cancer Therapeutics, 2018, 17, 1324-1331.	4.1	65
26	An integrative bioinformatics approach reveals coding and non-coding gene variants associated with gene expression profiles and outcome in breast cancer molecular subtypes. British Journal of Cancer, 2018, 118, 1107-1114.	6.4	26
27	TQuest, A Web-Based Platform to Enable Precision Medicine by Linking a Tumorâ€™s Genetic Defects to Therapeutic Options. JCO Clinical Cancer Informatics, 2018, 2, 1-13.	2.1	1
28	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. Cell Reports, 2018, 25, 1446-1457.	6.4	76
29	Immunological differences between primary and metastatic breast cancer. Annals of Oncology, 2018, 29, 2232-2239.	1.2	238
30	Increased epigenetic age in normal breast tissue from luminal breast cancer patients. Clinical Epigenetics, 2018, 10, 112.	4.1	40
31	Association of T-Cell Receptor Repertoire Use With Response to Combined Trastuzumab-Lapatinib Treatment of HER2-Positive Breast Cancer. JAMA Oncology, 2018, 4, e181564.	7.1	13
32	Long-Term Prognostic Risk After Neoadjuvant Chemotherapy Associated With Residual Cancer Burden and Breast Cancer Subtype. Journal of Clinical Oncology, 2017, 35, 1049-1060.	1.6	478
33	Co-targeting the HER and IGF/insulin receptor axis in breast cancer, with triple targeting with endocrine therapy for hormone-sensitive disease. Breast Cancer Research and Treatment, 2017, 163, 37-50.	2.5	16
34	Immune Gene Expression Is Associated with Genomic Aberrations in Breast Cancer. Cancer Research, 2017, 77, 3317-3324.	0.9	117
35	Is complete response the answer?. Annals of Oncology, 2017, 28, 1681-1683.	1.2	6
36	Combinatorial Screening of Pancreatic Adenocarcinoma Reveals Sensitivity to Drug Combinations Including Bromodomain Inhibitor Plus Neddlylation Inhibitor. Molecular Cancer Therapeutics, 2017, 16, 1041-1053.	4.1	12

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37	Association Between Genomic Metrics and Immune Infiltration in Triple-Negative Breast Cancer. <i>JAMA Oncology</i> , 2017, 3, 1707.	7.1	129
38	Association of LN Evaluation with Survival in Women Aged 70 Years or Older With Clinically Node-Negative Hormone Receptor Positive Breast Cancer. <i>Annals of Surgical Oncology</i> , 2017, 24, 3073-3081.	1.5	32
39	Functional germline variants as potential co-oncogenes. <i>Npj Breast Cancer</i> , 2017, 3, 46.	5.2	14
40	Intratumor Heterogeneity of Homologous Recombination Deficiency in Primary Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 1193-1199.	7.0	26
41	Testing Violations of the Exponential Assumption in Cancer Clinical Trials with Survival Endpoints. <i>Biometrics</i> , 2017, 73, 687-695.	1.4	6
42	Pathway level alterations rather than mutations in single genes predict response to HER2-targeted therapies in the neo-ALTTO trial. <i>Annals of Oncology</i> , 2017, 28, 128-135.	1.2	54
43	Systematic Drug Screening Identifies Tractable Targeted Combination Therapies in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2017, 77, 566-578.	0.9	38
44	Impacts of Early Guideline-Directed 21-Gene Recurrence Score Testing on Adjuvant Therapy Decision Making. <i>Journal of Oncology Practice</i> , 2017, 13, e1012-e1020.	2.5	6
45	Health economic impact of breast cancer index (BCI) in patients with hormone responsive breast cancer (HRBC) considering extended adjuvant endocrine therapy (EET).. <i>Journal of Clinical Oncology</i> , 2017, 35, 25-25.	1.6	1
46	Chemotherapy for Elderly Ovarian Cancer Patients. <i>Gynecology &amp; Obstetrics (Sunnyvale, Calif )</i> , 2016, 6, .	0.1	3
47	Quantitative assessment of the spatial heterogeneity of tumor-infiltrating lymphocytes in breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 78.	5.0	75
48	T-DM1 Activity in Metastatic Human Epidermal Growth Factor Receptor 2-Positive Breast Cancers That Received Prior Therapy With Trastuzumab and Pertuzumab. <i>Journal of Clinical Oncology</i> , 2016, 34, 3511-3517.	1.6	64
49	Assessing cost-utility of predictive biomarkers in oncology: a streamlined approach. <i>Breast Cancer Research and Treatment</i> , 2016, 155, 223-234.	2.5	3
50	The Neoadjuvant Model and Complete Pathologic Response in Breast Cancer. <i>JAMA Oncology</i> , 2016, 2, 760.	7.1	5
51	Relationship between Complete Pathologic Response to Neoadjuvant Chemotherapy and Survival in Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 26-33.	7.0	49
52	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	1.6	34
53	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016, 5, 2333.	1.6	79
54	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016, 5, 2333.	1.6	51

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55	Predictors of Chemosensitivity in Triple Negative Breast Cancer: An Integrated Genomic Analysis. <i>PLoS Medicine</i> , 2016, 13, e1002193.	8.4	75
56	Mutation based treatment recommendations from next generation sequencing data: a comparison of web tools. <i>Oncotarget</i> , 2016, 7, 22064-22076.	1.8	10
57	Genomic Markers in ER-Negative Breast Cancer. , 2016, , 283-298.		0
58	Association between DNA level aberrations and immune cell infiltration in breast cancer.. <i>Journal of Clinical Oncology</i> , 2016, 34, 3078-3078.	1.6	0
59	Characterization of DNA variants in the human kinome in breast cancer. <i>Scientific Reports</i> , 2015, 5, 14736.	3.3	2
60	Reproducibility of residual cancer burden for prognostic assessment of breast cancer after neoadjuvant chemotherapy. <i>Modern Pathology</i> , 2015, 28, 913-920.	5.5	79
61	Phase 1b study of the mammalian target of rapamycin inhibitor sirolimus in combination with nanoparticle albumin-bound paclitaxel in patients with advanced solid tumors. <i>Cancer</i> , 2015, 121, 1817-1826.	4.1	11
62	Neoadjuvant Model in Cancer Treatment: From Clinical Opportunity to Health-Care Utility. <i>Journal of the National Cancer Institute Monographs</i> , 2015, 2015, 1-3.	2.1	0
63	Prospective assessment of the decision-making impact of the Breast Cancer Index in recommending extended adjuvant endocrine therapy for patients with early-stage ER-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 154, 533-541.	2.5	31
64	Sirolimus and trastuzumab combination therapy for HER2-positive metastatic breast cancer after progression on prior trastuzumab therapy. <i>Breast Cancer Research and Treatment</i> , 2015, 150, 157-167.	2.5	23
65	Multigene prognostic tests in breast cancer: past, present, future. <i>Breast Cancer Research</i> , 2015, 17, 11.	5.0	209
66	Genomic predictor of residual risk of recurrence after adjuvant chemotherapy and endocrine therapy in high risk estrogen receptor-positive breast cancers. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 789-797.	2.5	4
67	A genome-wide approach to link genotype to clinical outcome by utilizing next generation sequencing and gene chip data of 6,697 breast cancer patients. <i>Genome Medicine</i> , 2015, 7, 104.	8.2	65
68	Comprehensive Analysis of Disease-Related Genes in Chronic Lymphocytic Leukemia by Multiplex PCR-Based Next Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0129544.	2.5	23
69	Functional polymorphisms in cancer. <i>Oncoscience</i> , 2015, 2, 73-74.	2.2	1
70	Abstract PD3-2: Broad exonic DNA diversity is associated with resistance to taxane-FAC chemotherapy in triple negative breast cancer. , 2015, , .		0
71	Abstract P2-05-04: Gene expression associated with poor prognosis of young TNBC patients. , 2015, , .		0
72	Abstract P2-03-05: The heterogeneous clinical behavior of luminal breast cancers is associated with different mutational landscapes. , 2015, , .		0

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73	Abstract PD3-4: Reliability of whole exome sequencing for assessing intratumor heterogeneity from breast tumor biopsies. , 2015, , .		1
74	Prospective study of the decision-making impact of the Breast Cancer Index in the selection of patients with ER+ breast cancer for extended endocrine therapy.. Journal of Clinical Oncology, 2015, 33, 538-538.	1.6	0
75	A framework to assess the cost effectiveness of predictive biomarkers in oncology: Test Incremental Cost Effectiveness Ratio (TICER).. Journal of Clinical Oncology, 2015, 33, 6621-6621.	1.6	0
76	Mutation-based treatment recommendations from next generation sequencing data: A comparison of web tools.. Journal of Clinical Oncology, 2015, 33, e12564-e12564.	1.6	0
77	Increasing Consistency of Disease Biomarker Prediction Across Datasets. PLoS ONE, 2014, 9, e91272.	2.5	6
78	Common Contaminants in Next-Generation Sequencing That Hinder Discovery of Low-Abundance Microbes. PLoS ONE, 2014, 9, e97876.	2.5	285
79	Both Carboplatin and Bevacizumab Improve Pathological Complete Remission Rate in Neoadjuvant Treatment of Triple Negative Breast Cancer: A Meta-Analysis. PLoS ONE, 2014, 9, e108405.	2.5	29
80	Quantification of Heterogeneity as a Biomarker in Tumor Imaging: A Systematic Review. PLoS ONE, 2014, 9, e110300.	2.5	122
81	Statistical measures of transcriptional diversity capture genomic heterogeneity of cancer. BMC Genomics, 2014, 15, 876.	2.8	29
82	Gene Signatureâ€“Guided Dasatinib Therapy in Metastatic Breast Cancer. Clinical Cancer Research, 2014, 20, 5265-5271.	7.0	28
83	Global gene expression changes induced by prolonged cold ischemic stress and preservation method of breast cancer tissue. Molecular Oncology, 2014, 8, 717-727.	4.6	29
84	Metabolic isoenzyme shifts in cancer as potential novel therapeutic targets. Breast Cancer Research and Treatment, 2014, 148, 477-488.	2.5	5
85	Combined analysis of gene expression, DNA copy number, and mutation profiling data to display biological process anomalies in individual breast cancers. Breast Cancer Research and Treatment, 2014, 144, 561-568.	2.5	4
86	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.9	90
87	Bioinformatics analysis pipeline for exome sequencing data. AACR Education Book, 2014, 2014, 131-134.	0.0	1
88	Cardiac outcomes in women receiving aromatase inhibitors as adjuvant endocrine therapy for breast cancer.. Journal of Clinical Oncology, 2014, 32, e11501-e11501.	1.6	1
89	Randomized Pharmacokinetic Study Comparing Subcutaneous and Intravenous Palonosetron in Cancer Patients Treated with Platinum Based Chemotherapy. PLoS ONE, 2014, 9, e89747.	2.5	8
90	Identification of serum analytes and metabolites associated with aerobic capacity. European Journal of Applied Physiology, 2013, 113, 1311-1320.	2.5	30

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91	Reproducibility of research and preclinical validation: problems and solutions. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 720-724.	27.6	83
92	Annual Review of Biophysics. <i>Medical Physics</i> , 2013, 40, 077303.	3.0	0
93	Estrogen Receptor (ER) mRNA and ER-Related Gene Expression in Breast Cancers That Are 1% to 10% ER-Positive by Immunohistochemistry. <i>Journal of Clinical Oncology</i> , 2012, 30, 729-734.	1.6	231
94	A Genomic Predictor of Response and Survival Following Taxane-Anthracycline Chemotherapy for Invasive Breast Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2011, 305, 1873.	7.4	531
95	Effects of Tissue Handling on RNA Integrity and Microarray Measurements From Resected Breast Cancers. <i>Journal of the National Cancer Institute</i> , 2011, 103, 1871-1883.	6.3	104
96	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
97	Development of Candidate Genomic Markers to Select Breast Cancer Patients for Dasatinib Therapy. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 1120-1127.	4.1	28
98	Molecular Anatomy of Breast Cancer Stroma and Its Prognostic Value in Estrogen Receptor-Positive and -Negative Cancers. <i>Journal of Clinical Oncology</i> , 2010, 28, 4316-4323.	1.6	193
99	Genomic Index of Sensitivity to Endocrine Therapy for Breast Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 4111-4119.	1.6	235
100	Effect of training-sample size and classification difficulty on the accuracy of genomic predictors. <i>Breast Cancer Research</i> , 2010, 12, R5.	5.0	169
101	Genomic Grade Index Is Associated With Response to Chemotherapy in Patients With Breast Cancer. <i>Journal of Clinical Oncology</i> , 2009, 27, 3185-3191.	1.6	173
102	Analysis and modeling of growing budding yeast populations at the single cell level. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009, 75A, 114-120.	1.5	37
103	Hormone receptor status and pathologic response of HER2-positive breast cancer treated with neoadjuvant chemotherapy and trastuzumab. <i>Annals of Oncology</i> , 2008, 19, 2020-2025.	1.2	41
104	Commercialized Multigene Predictors of Clinical Outcome for Breast Cancer. <i>Oncologist</i> , 2008, 13, 477-493.	3.7	235
105	Large-scale identification of novel transcripts in the human genome. <i>Genome Research</i> , 2007, 17, 287-292.	5.5	15
106	Microtubule-Associated Protein-tau is a Bifunctional Predictor of Endocrine Sensitivity and Chemotherapy Resistance in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 2061-2067.	7.0	115
107	Thirty-Gene Pharmacogenomic Test Correlates with Residual Cancer Burden after Preoperative Chemotherapy for Breast Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 4078-4082.	7.0	26
108	CtIP Silencing as a Novel Mechanism of Tamoxifen Resistance in Breast Cancer. <i>Molecular Cancer Research</i> , 2007, 5, 1285-1295.	3.4	28

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109	Towards understanding of the complex structure of growing yeast populations. Journal of Biotechnology, 2007, 128, 393-402.	3.8	38
110	Measurement of Residual Breast Cancer Burden to Predict Survival After Neoadjuvant Chemotherapy. Journal of Clinical Oncology, 2007, 25, 4414-4422.	1.6	1,243
111	Morphologically-structured models of growing budding yeast populations. Journal of Biotechnology, 2006, 124, 420-438.	3.8	32
112	Ambient Particulate Matter Exhibits Direct Inhibitory Effects on Oxidative Stress Enzymes. Environmental Science & Technology, 2006, 40, 2805-2811.	10.0	47
113	KDD Cup 2001 report. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2002, 3, 47-64.	4.0	72
114	Biochemical Engineering Analysis of Critical Process Factors in the Biomass-to-Ethanol Technology. Biotechnology Progress, 1997, 13, 222-231.	2.6	61
115	Identification of inhibitory components toxic toward zymomonas mobilis CP4(pZB5) xylose fermentation. Applied Biochemistry and Biotechnology, 1997, 67, 185-198.	2.9	119
116	Session 3 bioprocessing research. Applied Biochemistry and Biotechnology, 1997, 63-65, 349-349.	2.9	0
117	Cell-Cycle Analysis in Phagotrophic Microorganisms from Flow Cytometric Histograms. Journal of Theoretical Biology, 1997, 186, 131-144.	1.7	9
118	Bioprocessing Research. , 1997, 63-65, 349-349.		0
119	Optimization of reverse-flow, two-temperature, dilute-acid pretreatment to enhance biomass conversion to ethanol. Applied Biochemistry and Biotechnology, 1996, 57-58, 85-101.	2.9	60
120	Measurement of the inhibitory potential and detoxification of biomass pretreatment hydrolysate for ethanol production. Applied Biochemistry and Biotechnology, 1996, 57-58, 183-191.	2.9	29
121	Detailed material balance and ethanol yield calculations for the biomass-to-ethanol conversion process. Applied Biochemistry and Biotechnology, 1996, 57-58, 443-459.	2.9	29
122	Development of an epi-fluorescence assay for monitoring yeast viability and pretreatment hydrolysate toxicity in the presence of lignocellulosic solids. Applied Biochemistry and Biotechnology, 1996, 57-58, 649-657.	2.9	5
123	Measurement of the Inhibitory Potential and Detoxification of Biomass Pretreatment Hydrolysate for Ethanol Production. , 1996, , 183-191.		2
124	Detailed Material Balance and Ethanol Yield Calculations for the Biomass-to-Ethanol Conversion Process. , 1996, , 443-459.		4
125	Optimization of Reverse-Flow, Two-Temperature, Dilute-Acid Pretreatment to Enhance Biomass Conversion to Ethanol. , 1996, , 85-101.		1
126	Development of an Epi-Fluorescence Assay for Monitoring Yeast Viability and Pretreatment Hydrolysate Toxicity in the Presence of Lignocellulosic Solids. , 1996, , 649-657.		0



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127	Multistaged corpuscular models of microbial growth: Monte Carlo simulations. <i>BioSystems</i> , 1995, 36, 19-35.	2.0	46
128	Feeding heterogeneity in ciliate populations: Effects of culture age and nutritional state. <i>Biotechnology and Bioengineering</i> , 1994, 43, 371-380.	3.3	20
129	Determination of cellular rate distributions in microbial cell populations: Feeding rates of ciliated protozoa. <i>Biotechnology and Bioengineering</i> , 1993, 42, 284-294.	3.3	6
130	Optimal Design in Nonlinear Multiresponse Estimation: Poisson Model for Filter Feeding. <i>Biometrics</i> , 1992, 48, 1235.	1.4	8
131	A statistical analysis of flow cytometric determinations of phagocytosis rates. <i>Cytometry</i> , 1992, 13, 423-431.	1.8	14
132	Size Effects on the Uptake of Particles by Populations of <i>Tetrahymena pyriformis</i> Cells. <i>Journal of Protozoology</i> , 1990, 37, 157-163.	0.8	25
133	A discrete, stochastic model for microbial filter feeding: a model for feeding of ciliated protists on spatially uniform, nondepletable suspensions. <i>Mathematical Biosciences</i> , 1990, 102, 127-181.	1.9	7
134	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 0, 5, 2333.	1.6	8