

# Daniel Brewer

## 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.

53  
papers

4,908  
citations

29  
h-index

64  
g-index

64  
ext. papers

6,500  
ext. citations

10.9  
avg, IF

7.08  
L-index

#	Paper	IF	Citations
53	Development of a multivariable risk model integrating urinary cell DNA methylation and cell-free RNA data for the detection of significant prostate cancer. <i>Prostate</i> , <b>2020</b> , 80, 547-558	4.2	8
52	A novel stratification framework for predicting outcome in patients with prostate cancer. <i>British Journal of Cancer</i> , <b>2020</b> , 122, 1467-1476	8.7	3
51	Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93	50.4	840
50	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , <b>2020</b> , 52, 320-330	36.3	113
49	Methodology for the at-home collection of urine samples for prostate cancer detection. <i>BioTechniques</i> , <b>2020</b> , 68, 65-71	2.5	4
48	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , <b>2020</b> , 11, 5070	17.4	18
47	Convergence of Prognostic Gene Signatures Suggests Underlying Mechanisms of Human Prostate Cancer Progression. <i>Genes</i> , <b>2020</b> , 11,	4.2	3
46	A Four-Group Urine Risk Classifier for Predicting Outcome in Prostate Cancer Patients. <i>BJU International</i> , <b>2019</b> , 124, 609	5.6	17
45	epiCaPture: A Urine DNA Methylation Test for Early Detection of Aggressive Prostate Cancer. <i>JCO Precision Oncology</i> , <b>2019</b> , 2019,	3.6	17
44	Transcriptome-Wide Effects of Sphingosine Kinases Knockdown in Metastatic Prostate and Breast Cancer Cells: Implications for Therapeutic Targeting. <i>Frontiers in Pharmacology</i> , <b>2019</b> , 10, 303	5.6	17
43	SEPATH: benchmarking the search for pathogens in human tissue whole genome sequence data leads to template pipelines. <i>Genome Biology</i> , <b>2019</b> , 20, 208	18.3	4
42	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. <i>Wellcome Open Research</i> , <b>2019</b> , 4, 155	4.8	4
41	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , <b>2018</b> , 50, 682-692	36.3	112
40	DESNT: A Poor Prognosis Category of Human Prostate Cancer. <i>European Urology Focus</i> , <b>2018</b> , 4, 842-850	5.1	18
39	A urine-based DNA methylation assay, ProCUrE, to identify clinically significant prostate cancer. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 147	7.7	18
38	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007001	6	20
37	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , <b>2016</b> , 7, 12605	17.4	152

36	Mutation detection in formalin-fixed prostate cancer biopsies taken at the time of diagnosis using next-generation DNA sequencing. <i>Journal of Clinical Pathology</i> , <b>2015</b> , 68, 212-7	3.9	18
35	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. <i>Nature Genetics</i> , <b>2015</b> , 47, 367-372	36.3	292
34	HES5 silencing is an early and recurrent change in prostate tumourigenesis. <i>Endocrine-Related Cancer</i> , <b>2015</b> , 22, 131-44	5.7	8
33	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , <b>2015</b> , 520, 353-357	50.4	857
32	A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. <i>Leukemia and Lymphoma</i> , <b>2015</b> , 56, 594-601	1.9	3
31	Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. <i>EBioMedicine</i> , <b>2015</b> , 2, 1133-44	8.8	143
30	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , <b>2014</b> , 345, 1251343	33.3	250
29	Focal amplification of the androgen receptor gene in hormone-naive human prostate cancer. <i>British Journal of Cancer</i> , <b>2014</b> , 110, 1655-62	8.7	19
28	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , <b>2014</b> , 3,	8.9	229
27	Benzo pyrene-induced DNA adducts and gene expression profiles in target and non-target organs for carcinogenesis in mice. <i>BMC Genomics</i> , <b>2014</b> , 15, 880	4.5	36
26	Prognostic value of PTEN loss in men with conservatively managed localised prostate cancer. <i>British Journal of Cancer</i> , <b>2013</b> , 108, 2582-9	8.7	82
25	Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , <b>2013</b> , 162, 348-59	4.5	44
24	Prognostic value of blood mRNA expression signatures in castration-resistant prostate cancer: a prospective, two-stage study. <i>Lancet Oncology, The</i> , <b>2012</b> , 13, 1114-24	21.7	97
23	Novel, gross chromosomal alterations involving PTEN cooperate with allelic loss in prostate cancer. <i>Modern Pathology</i> , <b>2012</b> , 25, 902-10	9.8	44
22	siRNA knockdown of ribosomal protein gene RPL19 abrogates the aggressive phenotype of human prostate cancer. <i>PLoS ONE</i> , <b>2011</b> , 6, e22672	3.7	37
21	Modelling Transcription Factor Activity <b>2011</b> , 440-450		
20	A gene expression-based predictor for myeloma patients at high risk of developing bone disease on bisphosphonate treatment. <i>Clinical Cancer Research</i> , <b>2011</b> , 17, 6347-55	12.9	25
19	A HIF-regulated VHL-PTP1B-Src signaling axis identifies a therapeutic target in renal cell carcinoma. <i>Science Translational Medicine</i> , <b>2011</b> , 3, 85ra47	17.5	47

18	Molecular characterisation of ERG, ETV1 and PTEN gene loci identifies patients at low and high risk of death from prostate cancer. <i>British Journal of Cancer</i> , <b>2010</b> , 102, 678-84	8.7	217
17	A census of amplified and overexpressed human cancer genes. <i>Nature Reviews Cancer</i> , <b>2010</b> , 10, 59-64	31.3	415
16	PRKCI Expression Promotes the Aggressive Phenotype of Human Prostate Cancer Cells and Is a Novel Target for Therapeutic Intervention. <i>Genes and Cancer</i> , <b>2010</b> , 1, 444-64	2.9	37
15	Dissection of a complex transcriptional response using genome-wide transcriptional modelling. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 327	12.2	20
14	rHVDM: an R package to predict the activity and targets of a transcription factor. <i>Bioinformatics</i> , <b>2009</b> , 25, 419-20	7.2	5
13	Integration of ERG gene mapping and gene-expression profiling identifies distinct categories of human prostate cancer. <i>BJU International</i> , <b>2009</b> , 103, 1256-69	5.6	52
12	Biopsy tissue microarray study of Ki-67 expression in untreated, localized prostate cancer managed by active surveillance. <i>Prostate Cancer and Prostatic Diseases</i> , <b>2009</b> , 12, 143-7	6.2	34
11	Interlaboratory and interplatform comparison of microarray gene expression analysis of HepG2 cells exposed to benzo(a)pyrene. <i>OMICS A Journal of Integrative Biology</i> , <b>2009</b> , 13, 115-25	3.8	29
10	TEAD1 and c-Cbl are novel prostate basal cell markers that correlate with poor clinical outcome in prostate cancer. <i>British Journal of Cancer</i> , <b>2008</b> , 99, 1849-58	8.7	66
9	Detection of TMPRSS2-ERG translocations in human prostate cancer by expression profiling using GeneChip Human Exon 1.0 ST arrays. <i>Journal of Molecular Diagnostics</i> , <b>2008</b> , 10, 50-7	5.1	45
8	Fitting ordinary differential equations to short time course data. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , <b>2008</b> , 366, 519-44	3	40
7	Expression profiling of CD133+ and CD133- epithelial cells from human prostate. <i>Prostate</i> , <b>2008</b> , 68, 1007-24	4.2	60
6	AHR- and DNA-damage-mediated gene expression responses induced by benzo(a)pyrene in human cell lines. <i>Chemical Research in Toxicology</i> , <b>2007</b> , 20, 1797-810	4	72
5	Correction of scaling mismatches in oligonucleotide microarray data. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 251	3.6	6
4	Time- and concentration-dependent changes in gene expression induced by benzo(a)pyrene in two human cell lines, MCF-7 and HepG2. <i>BMC Genomics</i> , <b>2006</b> , 7, 260	4.5	89
3	Ranked prediction of p53 targets using hidden variable dynamic modeling. <i>Genome Biology</i> , <b>2006</b> , 7, R2518.3		86
2	Reconstructing gene networks: what are the limits?. <i>Biochemical Society Transactions</i> , <b>2003</b> , 31, 1519-25	5.1	18
1	The landscape of viral associations in human cancers		6

