Daniel Brewer

List of Publications by Year
in descending order

58 papers	7,478 citations	172457 29 h-index	123424 61 g-index
64 all docs	64 docs citations	64 times ranked	14548 citing authors

#	Article	IF	Citations
1	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
2	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
3	A census of amplified and overexpressed human cancer genes. Nature Reviews Cancer, 2010, 10, 59-64.	28.4	480
4	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	21.4	380
5	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
6	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
7	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
8	Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. EBioMedicine, 2015, 2, 1133-1144.	6.1	260
9	Molecular characterisation of ERG, ETV1 and PTEN gene loci identifies patients at low and high risk of death from prostate cancer. British Journal of Cancer, 2010, 102, 678-684.	6.4	234
10	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	12.8	214
11	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	21.4	182
12	Prognostic value of blood mRNA expression signatures in castration-resistant prostate cancer: a prospective, two-stage study. Lancet Oncology, The, 2012, 13, 1114-1124.	10.7	125
13	Time- and concentration-dependent changes in gene expression induced by benzo(a)pyrene in two human cell lines, MCF-7 and HepG2. BMC Genomics, 2006, 7, 260.	2.8	104
14	Ranked prediction of p53 targets using hidden variable dynamic modeling. Genome Biology, 2006, 7, R25.	9.6	102
15	Prognostic value of PTEN loss in men with conservatively managed localised prostate cancer. British Journal of Cancer, 2013, 108, 2582-2589.	6.4	91
16	AHR- and DNA-Damage-Mediated Gene Expression Responses Induced by Benzo(a)pyrene in Human Cell Lines. Chemical Research in Toxicology, 2007, 20, 1797-1810.	3.3	86
17	TEAD1 and c-Cbl are novel prostate basal cell markers that correlate with poor clinical outcome in prostate cancer. British Journal of Cancer, 2008, 99, 1849-1858.	6.4	75
18	Expression profiling of CD133$^+$ and CD133$^-$ epithelial cells from human prostate. Prostate, 2008, 68, 1007-1024.	2.3	64

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19	Integration of *ERG* gene mapping and gene‐expression profiling identifies distinct categories of human prostate cancer. BJU International, 2009, 103, 1256-1269.	2.5	54
20	A HIF-Regulated VHL-PTP1B-Src Signaling Axis Identifies a Therapeutic Target in Renal Cell Carcinoma. Science Translational Medicine, 2011, 3, 85ra47.	12.4	54
21	Improved risk stratification in myeloma using a microRNA‐based classifier. British Journal of Haematology, 2013, 162, 348-359.	2.5	53
22	siRNA Knockdown of Ribosomal Protein Gene RPL19 Abrogates the Aggressive Phenotype of Human Prostate Cancer. PLoS ONE, 2011, 6, e22672.	2.5	50
23	Detection of TMPRSS2-ERG Translocations in Human Prostate Cancer by Expression Profiling Using GeneChip Human Exon 1.0 ST Arrays. Journal of Molecular Diagnostics, 2008, 10, 50-57.	2.8	49
24	Novel, gross chromosomal alterations involving PTEN cooperate with allelic loss in prostate cancer. Modern Pathology, 2012, 25, 902-910.	5.5	48
25	Fitting ordinary differential equations to short time course data. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 519-544.	3.4	47
26	PRKC-Â Expression Promotes the Aggressive Phenotype of Human Prostate Cancer Cells and Is a Novel Target for Therapeutic Intervention. Genes and Cancer, 2010, 1, 444-464.	1.9	46
27	Benzo "Equation missing" <!-- No EquationSource Format="TEX", only image -->pyrene-induced DNA adducts and gene expression profiles in target and non-target organs for carcinogenesis in mice. BMC Genomics, 2014, 15, 880.	2.8	44
28	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. Nature Communications, 2020, 11, 5070.	12.8	44
29	Biopsy tissue microarray study of Ki-67 expression in untreated, localized prostate cancer managed by active surveillance. Prostate Cancer and Prostatic Diseases, 2009, 12, 143-147.	3.9	37
30	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. PLoS Genetics, 2017, 13, e1007001.	3.5	34
31	Interlaboratory and Interplatform Comparison of Microarray Gene Expression Analysis of HepG2 Cells Exposed to Benzo(a)pyrene. OMICS A Journal of Integrative Biology, 2009, 13, 115-125.	2.0	31
32	DESNT: A Poor Prognosis Category of Human Prostate Cancer. European Urology Focus, 2018, 4, 842-850.	3.1	30
33	A four‐group urine risk classifier for predicting outcomes in patients with prostate cancer. BJU International, 2019, 124, 609-620.	2.5	30
34	A Gene Expression‐Based Predictor for Myeloma Patients at High Risk of Developing Bone Disease on Bisphosphonate Treatment. Clinical Cancer Research, 2011, 17, 6347-6355.	7.0	27
35	epiCaPture: A Urine DNA Methylation Test for Early Detection of Aggressive Prostate Cancer. JCO Precision Oncology, 2019, 2019, 1-18.	3.0	27
36	Focal amplification of the androgen receptor gene in hormone-naive human prostate cancer. British Journal of Cancer, 2014, 110, 1655-1662.	6.4	26

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37	A urine-based DNA methylation assay, ProCUrE, to identify clinically significant prostate cancer. Clinical Epigenetics, 2018, 10, 147.	4.1	26
38	Reconstructing gene networks: what are the limits?. Biochemical Society Transactions, 2003, 31, 1519-1525.	3.4	25
39	Dissection of a complex transcriptional response using genome‐wide transcriptional modelling. Molecular Systems Biology, 2009, 5, 327.	7.2	22
40	Mutation detection in formalin-fixed prostate cancer biopsies taken at the time of diagnosis using next-generation DNA sequencing. Journal of Clinical Pathology, 2015, 68, 212-217.	2.0	21
41	Microbiomes of Urine and the Prostate Are Linked to Human Prostate Cancer Risk Groups. European Urology Oncology, 2022, 5, 412-419.	5.4	21
42	Transcriptome-Wide Effects of Sphingosine Kinases Knockdown in Metastatic Prostate and Breast Cancer Cells: Implications for Therapeutic Targeting. Frontiers in Pharmacology, 2019, 10, 303.	3.5	20
43	Development of a multivariable risk model integrating urinary cell DNA methylation and cell‐free RNA data for the detection of significant prostate cancer. Prostate, 2020, 80, 547-558.	2.3	17
44	SEPATH: benchmarking the search for pathogens in human tissue whole genome sequence data leads to template pipelines. Genome Biology, 2019, 20, 208.	8.8	11
45	Methodology for the at-home collection of urine samples for prostate cancer detection. BioTechniques, 2020, 68, 65-71.	1.8	11
46	HES5 silencing is an early and recurrent change in prostate tumourigenesis. Endocrine-Related Cancer, 2015, 22, 131-144.	3.1	10
47	A novel stratification framework for predicting outcome in patients with prostate cancer. British Journal of Cancer, 2020, 122, 1467-1476.	6.4	9
48	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. Wellcome Open Research, 2019, 4, 155.	1.8	9
49	rHVDM: an R package to predict the activity and targets of a transcription factor. Bioinformatics, 2009, 25, 419-420.	4.1	8
50	Convergence of Prognostic Gene Signatures Suggests Underlying Mechanisms of Human Prostate Cancer Progression. Genes, 2020, 11, 802.	2.4	8
51	Correction of scaling mismatches in oligonucleotide microarray data. BMC Bioinformatics, 2006, 7, 251.	2.6	7
52	A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. Leukemia and Lymphoma, 2015, 56, 594-601.	1.3	7
53	Integration of Urinary EN2 Protein & Cell-Free RNA Data in the Development of a Multivariable Risk Model for the Detection of Prostate Cancer Prior to Biopsy. Cancers, 2021, 13, 2102.	3.7	5
54	A Model to Detect Significant Prostate Cancer Integrating Urinary Peptide and Extracellular Vesicle RNA Data. Cancers, 2022, 14, 1995.	3.7	5

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55	rHVDM â€" a fast and user-friendly R package to predict transcription factor targets from microarray time series data. BMC Systems Biology, 2007, 1, .	3.0	4
56	Prostate Single Nucleotide Polymorphism Provides a Crucial Clue to Cancer Aggression in Active Surveillance Patients. European Urology, 2016, 69, 229-230.	1.9	2
57	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. European Urology, 2022, 82, 201-211.	1.9	2
58	The Urine Biomarker PUR-4 Is Positively Associated with the Amount of Gleason 4 in Human Prostate Cancers. Life, 2021, 11, 1172.	2.4	1