

Daniel Brewer

List of Publications by Year in descending order

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58
papers

7,478
citations

172457

29
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123424

61
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all docs

64
docs citations

64
times ranked

14548
citing authors

#	ARTICLE	IF	CITATIONS
1	A Model to Detect Significant Prostate Cancer Integrating Urinary Peptide and Extracellular Vesicle RNA Data. <i>Cancers</i> , 2022, 14, 1995.	3.7	5
2	Microbiomes of Urine and the Prostate Are Linked to Human Prostate Cancer Risk Groups. <i>European Urology Oncology</i> , 2022, 5, 412-419.	5.4	21
3	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. <i>European Urology</i> , 2022, 82, 201-211.	1.9	2
4	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. <i>Cancers</i> , 2021, 13, 2102.	3.7	5
5	The Urine Biomarker PUR-4 Is Positively Associated with the Amount of Gleason 4 in Human Prostate Cancers. <i>Life</i> , 2021, 11, 1172.	2.4	1
6	Methodology for the at-home collection of urine samples for prostate cancer detection. <i>BioTechniques</i> , 2020, 68, 65-71.	1.8	11
7	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020, 11, 5070.	12.8	44
8	Convergence of Prognostic Gene Signatures Suggests Underlying Mechanisms of Human Prostate Cancer Progression. <i>Genes</i> , 2020, 11, 802.	2.4	8
9	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> , 2020, 80, 547-558.	2.3	17
10	A novel stratification framework for predicting outcome in patients with prostate cancer. <i>British Journal of Cancer</i> , 2020, 122, 1467-1476.	6.4	9
11	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
12	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , 2020, 52, 320-330.	21.4	261
13	SEPATH: benchmarking the search for pathogens in human tissue whole genome sequence data leads to template pipelines. <i>Genome Biology</i> , 2019, 20, 208.	8.8	11
14	A four-group urine risk classifier for predicting outcomes in patients with prostate cancer. <i>BJU International</i> , 2019, 124, 609-620.	2.5	30
15	epiCaPtur: A Urine DNA Methylation Test for Early Detection of Aggressive Prostate Cancer. <i>JCO Precision Oncology</i> , 2019, 2019, 1-18.	3.0	27
16	Transcriptome-Wide Effects of Sphingosine Kinases Knockdown in Metastatic Prostate and Breast Cancer Cells: Implications for Therapeutic Targeting. <i>Frontiers in Pharmacology</i> , 2019, 10, 303.	3.5	20
17	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. <i>Wellcome Open Research</i> , 2019, 4, 155.	1.8	9
18	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	21.4	182

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19	DESNT: A Poor Prognosis Category of Human Prostate Cancer. <i>European Urology Focus</i> , 2018, 4, 842-850.	3.1	30
20	A urine-based DNA methylation assay, ProCUrE, to identify clinically significant prostate cancer. <i>Clinical Epigenetics</i> , 2018, 10, 147.	4.1	26
21	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. <i>PLoS Genetics</i> , 2017, 13, e1007001.	3.5	34
22	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , 2016, 7, 12605.	12.8	214
23	Prostate Single Nucleotide Polymorphism Provides a Crucial Clue to Cancer Aggression in Active Surveillance Patients. <i>European Urology</i> , 2016, 69, 229-230.	1.9	2
24	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> , 2015, 68, 212-217.	2.0	21
25	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> , 2015, 47, 367-372.	21.4	380
26	HES5 silencing is an early and recurrent change in prostate tumourigenesis. <i>Endocrine-Related Cancer</i> , 2015, 22, 131-144.	3.1	10
27	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	27.8	1,185
28	A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. <i>Leukemia and Lymphoma</i> , 2015, 56, 594-601.	1.3	7
29	Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. <i>EBioMedicine</i> , 2015, 2, 1133-1144.	6.1	260
30	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , 2014, 3, .	6.0	318
31	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. <i>BMC Genomics</i> , 2014, 15, 880.	2.8	44
32	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	12.6	348
33	Focal amplification of the androgen receptor gene in hormone-naive human prostate cancer. <i>British Journal of Cancer</i> , 2014, 110, 1655-1662.	6.4	26
34	Prognostic value of PTEN loss in men with conservatively managed localised prostate cancer. <i>British Journal of Cancer</i> , 2013, 108, 2582-2589.	6.4	91
35	Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , 2013, 162, 348-359.	2.5	53
36	Novel, gross chromosomal alterations involving PTEN cooperate with allelic loss in prostate cancer. <i>Modern Pathology</i> , 2012, 25, 902-910.	5.5	48

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37	Prognostic value of blood mRNA expression signatures in castration-resistant prostate cancer: a prospective, two-stage study. <i>Lancet Oncology</i> , The, 2012, 13, 1114-1124.	10.7	125
38	siRNA Knockdown of Ribosomal Protein Gene RPL19 Abrogates the Aggressive Phenotype of Human Prostate Cancer. <i>PLoS ONE</i> , 2011, 6, e22672.	2.5	50
39	A Gene Expression-Based Predictor for Myeloma Patients at High Risk of Developing Bone Disease on Bisphosphonate Treatment. <i>Clinical Cancer Research</i> , 2011, 17, 6347-6355.	7.0	27
40	A HIF-Regulated VHL-PTP1B-Src Signaling Axis Identifies a Therapeutic Target in Renal Cell Carcinoma. <i>Science Translational Medicine</i> , 2011, 3, 85ra47.	12.4	54
41	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> , 2010, 102, 678-684.	6.4	234
42	A census of amplified and overexpressed human cancer genes. <i>Nature Reviews Cancer</i> , 2010, 10, 59-64.	28.4	480
43	PRKC- Δ Expression Promotes the Aggressive Phenotype of Human Prostate Cancer Cells and Is a Novel Target for Therapeutic Intervention. <i>Genes and Cancer</i> , 2010, 1, 444-464.	1.9	46
44	Dissection of a complex transcriptional response using genome-wide transcriptional modelling. <i>Molecular Systems Biology</i> , 2009, 5, 327.	7.2	22
45	rHVDM: an R package to predict the activity and targets of a transcription factor. <i>Bioinformatics</i> , 2009, 25, 419-420.	4.1	8
46	Integration of <i>ERG</i> gene mapping and gene expression profiling identifies distinct categories of human prostate cancer. <i>BJU International</i> , 2009, 103, 1256-1269.	2.5	54
47	Biopsy tissue microarray study of Ki-67 expression in untreated, localized prostate cancer managed by active surveillance. <i>Prostate Cancer and Prostatic Diseases</i> , 2009, 12, 143-147.	3.9	37
48	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> , 2009, 13, 115-125.	2.0	31
49	Expression profiling of CD133 ⁺ and CD133 ⁻ epithelial cells from human prostate. <i>Prostate</i> , 2008, 68, 1007-1024.	2.3	64
50	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> , 2008, 99, 1849-1858.	6.4	75
51	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> , 2008, 10, 50-57.	2.8	49
52	Fitting ordinary differential equations to short time course data. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 519-544.	3.4	47
53	AHR- and DNA-Damage-Mediated Gene Expression Responses Induced by Benzo(a)pyrene in Human Cell Lines. <i>Chemical Research in Toxicology</i> , 2007, 20, 1797-1810.	3.3	86
54	rHVDM - a fast and user-friendly R package to predict transcription factor targets from microarray time series data. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	4

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55	Ranked prediction of p53 targets using hidden variable dynamic modeling. <i>Genome Biology</i> , 2006, 7, R25.	9.6	102
56	Correction of scaling mismatches in oligonucleotide microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 251.	2.6	7
57	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> , 2006, 7, 260.	2.8	104
58	Reconstructing gene networks: what are the limits?. <i>Biochemical Society Transactions</i> , 2003, 31, 1519-1525.	3.4	25