Paul C Boutros

List of Publications by Citations

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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.

341 papers

19,964 citations

64 h-index

134 g-index

390 ext. papers

26,466 ext. citations

10.9 avg, IF 7.85 L-index

#	Paper	IF	Citations
341	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
340	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
339	VennDiagram: a package for the generation of highly-customizable Venn and Euler diagrams in R. <i>BMC Bioinformatics</i> , 2011 , 12, 35	3.6	1098
338	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
337	The c-Myc oncogene directly induces the H19 noncoding RNA by allele-specific binding to potentiate tumorigenesis. <i>Cancer Research</i> , 2006 , 66, 5330-7	10.1	384
336	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14	56.2	342
335	Genomic hallmarks of localized, non-indolent prostate cancer. <i>Nature</i> , 2017 , 541, 359-364	50.4	320
334	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020 , 578, 122-128	50.4	307
333	Spatial genomic heterogeneity within localized, multifocal prostate cancer. <i>Nature Genetics</i> , 2015 , 47, 736-45	36.3	306
332	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	36.3	292
331	Predicting outcomes in radiation oncologymultifactorial decision support systems. <i>Nature Reviews Clinical Oncology</i> , 2013 , 10, 27-40	19.4	270
330	Dysregulation of the mevalonate pathway promotes transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15051-6	11.5	264
329	Aryl hydrocarbon receptor regulates distinct dioxin-dependent and dioxin-independent gene batteries. <i>Molecular Pharmacology</i> , 2006 , 69, 140-53	4.3	263
328	Molecular landmarks of tumor hypoxia across cancer types. <i>Nature Genetics</i> , 2019 , 51, 308-318	36.3	255
327	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015 , 12, 615-621	21.6	235
326	Characterisation of retinoblastomas without RB1 mutations: genomic, gene expression, and clinical studies. <i>Lancet Oncology, The</i> , 2013 , 14, 327-34	21.7	221
325	Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. <i>Lancet Oncology, The</i> , 2014 , 15, 1521-1532	21.7	218

324	Widespread and Functional RNA Circularization in Localized Prostate Cancer. Cell, 2019, 176, 831-843.e	23 6.2	214
323	Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. Laboratory Investigation, 2009 , 89, 597-606	5.9	205
322	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. <i>Nature Methods</i> , 2015 , 12, 623-30	21.6	201
321	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015 , 6, 10001	17.4	199
320	Three-gene prognostic classifier for early-stage non small-cell lung cancer. <i>Journal of Clinical Oncology</i> , 2007 , 25, 5562-9	2.2	195
319	Frequent amplification of a chr19q13.41 microRNA polycistron in aggressive primitive neuroectodermal brain tumors. <i>Cancer Cell</i> , 2009 , 16, 533-46	24.3	178
318	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
317	NanoStringNorm: an extensible R package for the pre-processing of NanoString mRNA and miRNA data. <i>Bioinformatics</i> , 2012 , 28, 1546-8	7.2	168
316	Hypoxia promotes stem cell phenotypes and poor prognosis through epigenetic regulation of DICER. <i>Nature Communications</i> , 2014 , 5, 5203	17.4	164
315	Prognostic gene signatures for non-small-cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2824-8	11.5	159
314	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016 , 48, 1142-50	36.3	158
313	Risk SNP-Mediated Promoter-Enhancer Switching Drives Prostate Cancer through lncRNA PCAT19. <i>Cell</i> , 2018 , 174, 564-575.e18	56.2	154
312	Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. <i>Nature Genetics</i> , 2014 , 46, 1166-9	36.3	150
311	Serine racemase is associated with schizophrenia susceptibility in humans and in a mouse model. <i>Human Molecular Genetics</i> , 2009 , 18, 3227-43	5.6	145
310	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. <i>Journal of Pathology</i> , 2012 , 227, 286-97	9.4	142
309	How do changes in the mtDNA and mitochondrial dysfunction influence cancer and cancer therapy? Challenges, opportunities and models. <i>Mutation Research - Reviews in Mutation Research</i> , 2015 , 764, 16-	-370	132
308	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013 , 10, 723-9	21.6	129
307	Germline BRCA2 mutations drive prostate cancers with distinct evolutionary trajectories. <i>Nature Communications</i> , 2017 , 8, 13671	17.4	128

306	Best practices for benchmarking germline small-variant calls in human genomes. <i>Nature Biotechnology</i> , 2019 , 37, 555-560	44.5	125
305	The Evolutionary Landscape of Localized Prostate Cancers Drives Clinical Aggression. <i>Cell</i> , 2018 , 173, 1003-1013.e15	56.2	115
304	Gene expression profiling in cervical cancer: an exploration of intratumor heterogeneity. <i>Clinical Cancer Research</i> , 2006 , 12, 5632-40	12.9	114
303	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018 , 50, 682-692	36.3	112
302	TMPRSS2-ERG fusion co-opts master transcription factors and activates NOTCH signaling in primary prostate cancer. <i>Nature Genetics</i> , 2017 , 49, 1336-1345	36.3	105
301	Onco-proteogenomics: cancer proteomics joins forces with genomics. <i>Nature Methods</i> , 2014 , 11, 1107-	13 1.6	102
300	Novel PRKD gene rearrangements and variant fusions in cribriform adenocarcinoma of salivary gland origin. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 845-56	5	102
299	A Prostate Cancer "Nimbosus": Genomic Instability and SChLAP1 Dysregulation Underpin Aggression of Intraductal and Cribriform Subpathologies. <i>European Urology</i> , 2017 , 72, 665-674	10.2	98
298	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
297	Toxicological implications of polymorphisms in receptors for xenobiotic chemicals: the case of the aryl hydrocarbon receptor. <i>Toxicology and Applied Pharmacology</i> , 2005 , 207, 43-51	4.6	98
296	The Proteogenomic Landscape of Curable Prostate Cancer. Cancer Cell, 2019, 35, 414-427.e6	24.3	97
295	Aryl hydrocarbon receptor is a transcriptional activator of the human breast cancer resistance protein (BCRP/ABCG2). <i>Molecular Pharmacology</i> , 2010 , 78, 175-85	4.3	89
294	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
293	Two phases of disulfide bond formation have differing requirements for oxygen. <i>Journal of Cell Biology</i> , 2013 , 203, 615-27	7.3	84
292	Nanocall: an open source basecaller for Oxford Nanopore sequencing data. <i>Bioinformatics</i> , 2017 , 33, 49-55	7.2	83
291	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. <i>Nucleic Acids Research</i> , 2005 , 33, 2952-61	20.1	82
290	Unsupervised pattern recognition: an introduction to the whys and wherefores of clustering microarray data. <i>Briefings in Bioinformatics</i> , 2005 , 6, 331-43	13.4	82
289	Dioxin-responsive AHRE-II gene battery: identification by phylogenetic footprinting. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 321, 707-15	3.4	78

288	ONECUT2 is a driver of neuroendocrine prostate cancer. <i>Nature Communications</i> , 2019 , 10, 278	17.4	7 ²
287	Role of Nek2 on centrosome duplication and aneuploidy in breast cancer cells. <i>Oncogene</i> , 2014 , 33, 237	'5 ₉ 8 <u>2</u> 4	72
286	microRNAs in adult rodent liver are refractory to dioxin treatment. <i>Toxicological Sciences</i> , 2007 , 99, 470)-8474	72
285	Exploiting the mevalonate pathway to distinguish statin-sensitive multiple myeloma. <i>Blood</i> , 2010 , 115, 4787-97	2.2	71
284	The DNA methylation landscape of advanced prostate cancer. <i>Nature Genetics</i> , 2020 , 52, 778-789	36.3	71
283	Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. <i>Genome Medicine</i> , 2013 , 5, 29	14.4	70
282	Transcriptomic responses to 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) in liver: comparison of rat and mouse. <i>BMC Genomics</i> , 2008 , 9, 419	4.5	68
281	Development and Validation of a 28-gene Hypoxia-related Prognostic Signature for Localized Prostate Cancer. <i>EBioMedicine</i> , 2018 , 31, 182-189	8.8	67
280	novoBreak: local assembly for breakpoint detection in cancer genomes. <i>Nature Methods</i> , 2017 , 14, 65-6	5721.6	67
279	Mitochondrial mutations drive prostate cancer aggression. <i>Nature Communications</i> , 2017 , 8, 656	17.4	66
278	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. <i>Nature Communications</i> , 2019 , 10, 5251	17.4	66
277	The Immune Microenvironment, Genome-wide Copy Number Aberrations, and Survival in Mesothelioma. <i>Journal of Thoracic Oncology</i> , 2017 , 12, 850-859	8.9	64
276	In-depth proteomics of ovarian cancer ascites: combining shotgun proteomics and selected reaction monitoring mass spectrometry. <i>Journal of Proteome Research</i> , 2011 , 10, 2286-99	5.6	63
275	Identification of differentially expressed proteins in direct expressed prostatic secretions of men with organ-confined versus extracapsular prostate cancer. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1870-84	7.6	62
274	MYC Protein Interactome Profiling Reveals Functionally Distinct Regions that Cooperate to Drive Tumorigenesis. <i>Molecular Cell</i> , 2018 , 72, 836-848.e7	17.6	62
273	Systematic evaluation of medium-throughput mRNA abundance platforms. <i>Rna</i> , 2013 , 19, 51-62	5.8	61
272	The parameter sensitivity of random forests. <i>BMC Bioinformatics</i> , 2016 , 17, 331	3.6	60
271	Targeted proteomics identifies liquid-biopsy signatures for extracapsular prostate cancer. <i>Nature Communications</i> , 2016 , 7, 11906	17.4	59

270	Long non-coding RNA urothelial carcinoma associated 1 (UCA1) mediates radiation response in prostate cancer. <i>Oncotarget</i> , 2017 , 8, 4668-4689	3.3	58
269	Crowdsourced estimation of cognitive decline and resilience in Alzheimerß disease. <i>Alzheimerjs and Dementia</i> , 2016 , 12, 645-53	1.2	58
268	Sex Differences in Cancer Driver Genes and Biomarkers. <i>Cancer Research</i> , 2018 , 78, 5527-5537	10.1	58
267	Haploinsufficiency of an RB-E2F1-Condensin II complex leads to aberrant replication and aneuploidy. <i>Cancer Discovery</i> , 2014 , 4, 840-53	24.4	57
266	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
265	Cribriform and intraductal prostate cancer are associated with increased genomic instability and distinct genomic alterations. <i>BMC Cancer</i> , 2018 , 18, 8	4.8	54
264	Determinants of sensitivity to lovastatin-induced apoptosis in multiple myeloma. <i>Molecular Cancer Therapeutics</i> , 2007 , 6, 1886-97	6.1	54
263	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
262	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. <i>Cancer Research</i> , 2017 , 77, 5479-5490	10.1	53
261	PD-L1 and Tumor Infiltrating Lymphocytes as Prognostic Markers in Resected NSCLC. <i>PLoS ONE</i> , 2016 , 11, e0153954	3.7	53
260	Single-cell analysis reveals transcriptomic remodellings in distinct cell types that contribute to human prostate cancer progression. <i>Nature Cell Biology</i> , 2021 , 23, 87-98	23.4	53
259	MicroRNA-196b regulates the homeobox B7-vascular endothelial growth factor axis in cervical cancer. <i>PLoS ONE</i> , 2013 , 8, e67846	3.7	52
258	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , 2018 , 34, 579-595.e8	24.3	52
257	Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer. <i>Journal of Pathology</i> , 2012 , 227, 53-61	9.4	51
256	Role of Pirh2 in mediating the regulation of p53 and c-Myc. <i>PLoS Genetics</i> , 2011 , 7, e1002360	6	51
255	Evaluation of various housekeeping genes for their applicability for normalization of mRNA expression in dioxin-treated rats. <i>Chemico-Biological Interactions</i> , 2006 , 160, 134-49	5	51
254	Differential expression profiling of the hepatic proteome in a rat model of dioxin resistance: correlation with genomic and transcriptomic analyses. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 882-94	4 ^{7.6}	48
253	Divergent mutational processes distinguish hypoxic and normoxic tumours. <i>Nature Communications</i> , 2020 , 11, 737	17.4	46

(2019-2008)

252	Inhibition of the sodium/potassium ATPase impairs N-glycan expression and function. <i>Cancer Research</i> , 2008 , 68, 6688-97	10.1	46	
251	Dioxin-dependent and dioxin-independent gene batteries: comparison of liver and kidney in AHR-null mice. <i>Toxicological Sciences</i> , 2009 , 112, 245-56	4.4	45	
250	CUL7 is a novel antiapoptotic oncogene. <i>Cancer Research</i> , 2007 , 67, 9616-22	10.1	45	
249	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. <i>International Journal of Cancer</i> , 2017 , 140, 662-673	7.5	44	
248	Identifying molecular features that distinguish fluvastatin-sensitive breast tumor cells. <i>Breast Cancer Research and Treatment</i> , 2014 , 143, 301-12	4.4	43	
247	Differential interactions between statins and P-glycoprotein: implications for exploiting statins as anticancer agents. <i>International Journal of Cancer</i> , 2010 , 127, 2936-48	7.5	43	
246	ShatterProof: operational detection and quantification of chromothripsis. <i>BMC Bioinformatics</i> , 2014 , 15, 78	3.6	42	
245	Epigenetic markers of prostate cancer in plasma circulating DNA. <i>Human Molecular Genetics</i> , 2012 , 21, 3619-31	5.6	42	
244	Aryl hydrocarbon receptor (AHR)-regulated transcriptomic changes in rats sensitive or resistant to major dioxin toxicities. <i>BMC Genomics</i> , 2010 , 11, 263	4.5	40	
243	Identification of a microRNA signature associated with risk of distant metastasis in nasopharyngeal carcinoma. <i>Oncotarget</i> , 2015 , 6, 4537-50	3.3	40	
242	Precision Radiotherapy: Reduction in Radiation for Oropharyngeal Cancer in the 30 ROC Trial. Journal of the National Cancer Institute, 2021 , 113, 742-751	9.7	39	
241	Hepatic transcriptomic responses to TCDD in dioxin-sensitive and dioxin-resistant rats during the onset of toxicity. <i>Toxicology and Applied Pharmacology</i> , 2011 , 251, 119-29	4.6	38	
240	Aryl hydrocarbon receptor-dependent induction of flavin-containing monooxygenase mRNAs in mouse liver. <i>Drug Metabolism and Disposition</i> , 2008 , 36, 2499-505	4	38	
239	Microarray analysis of the developing cortex. <i>Journal of Neurobiology</i> , 2006 , 66, 1646-58		38	
238	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633	36.3	38	
237	Risk factors for voriconazole hepatotoxicity at 12 weeks in lung transplant recipients. <i>American Journal of Transplantation</i> , 2012 , 12, 1929-35	8.7	37	
236	The prognostic value of temporal in vitro and in vivo derived hypoxia gene-expression signatures in breast cancer. <i>Radiotherapy and Oncology</i> , 2012 , 102, 436-43	5.3	37	
235	The influence of BRCA2 mutation on localized prostate cancer. <i>Nature Reviews Urology</i> , 2019 , 16, 281-29	9 9.5	36	

234	Epigenetics in radiotherapy: where are we heading?. Radiotherapy and Oncology, 2014, 111, 168-77	5.3	36
233	Global optimization of somatic variant identification in cancer genomes with a global community challenge. <i>Nature Genetics</i> , 2014 , 46, 318-319	36.3	36
232	Identifying gene locus associations with promyelocytic leukemia nuclear bodies using immuno-TRAP. <i>Journal of Cell Biology</i> , 2013 , 201, 325-35	7.3	35
231	dbZach: A MIAME-compliant toxicogenomic supportive relational database. <i>Toxicological Sciences</i> , 2006 , 90, 558-68	4.4	35
230	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020 , 38, 97-107	44.5	35
229	TMPRSS2-ERG status is not prognostic following prostate cancer radiotherapy: implications for fusion status and DSB repair. <i>Clinical Cancer Research</i> , 2013 , 19, 5202-9	12.9	34
228	A robust benchmark for germline structural variant detection		34
227	C-Terminal region of teneurin-1 co-localizes with dystroglycan and modulates cytoskeletal organization through an extracellular signal-regulated kinase-dependent stathmin- and filamin A-mediated mechanism in hippocampal cells. <i>Neuroscience</i> , 2012 , 219, 255-70	3.9	33
226	Patterns of dioxin-altered mRNA expression in livers of dioxin-sensitive versus dioxin-resistant rats. <i>Archives of Toxicology</i> , 2008 , 82, 809-30	5.8	33
225	Reasons for Discontinuing Active Surveillance: Assessment of 21 Centres in 12 Countries in the Movember GAP3 Consortium. <i>European Urology</i> , 2019 , 75, 523-531	10.2	33
224	BPG: Seamless, automated and interactive visualization of scientific data. <i>BMC Bioinformatics</i> , 2019 , 20, 42	3.6	31
223	Molecular Hallmarks of Multiparametric Magnetic Resonance Imaging Visibility in Prostate Cancer. <i>European Urology</i> , 2019 , 76, 18-23	10.2	30
222	Detecting protein variants by mass spectrometry: a comprehensive study in cancer cell-lines. <i>Genome Medicine</i> , 2017 , 9, 62	14.4	30
221	Genome-wide gene expression profiling of stress response in a spinal cord clip compression injury model. <i>BMC Genomics</i> , 2013 , 14, 583	4.5	30
220	TCDD dysregulation of 13 AHR-target genes in rat liver. <i>Toxicology and Applied Pharmacology</i> , 2014 , 274, 445-54	4.6	30
219	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. <i>Stem Cell Reports</i> , 2015 , 4, 313-322	8	29
218	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. <i>Cell Cycle</i> , 2016 , 15, 1693-705	4.7	29
217	Toward better benchmarking: challenge-based methods assessment in cancer genomics. <i>Genome Biology</i> , 2014 , 15, 462	18.3	29

(2018-2011)

216	Teneurin C-terminal associated peptide (TCAP)-1 modulates dendritic morphology in hippocampal neurons and decreases anxiety-like behaviors in rats. <i>Physiology and Behavior</i> , 2011 , 104, 199-204	3.5	29
215	Expression profiling during mammary epithelial cell three-dimensional morphogenesis identifies PTPRO as a novel regulator of morphogenesis and ErbB2-mediated transformation. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3913-24	4.8	29
214	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. <i>Genome Biology</i> , 2018 , 19, 188	18.3	29
213	miRNA-106a and prostate cancer radioresistance: a novel role for LITAF in ATM regulation. <i>Molecular Oncology</i> , 2018 , 12, 1324-1341	7.9	29
212	PI3K/AKT/mTOR inhibition in combination with doxorubicin is an effective therapy for leiomyosarcoma. <i>Journal of Translational Medicine</i> , 2016 , 14, 67	8.5	28
211	Translating a Prognostic DNA Genomic Classifier into the Clinic: Retrospective Validation in 563 Localized Prostate Tumors. <i>European Urology</i> , 2017 , 72, 22-31	10.2	28
210	Anti-nucleosome antibodies outperform traditional biomarkers as longitudinal indicators of disease activity in systemic lupus erythematosus. <i>Rheumatology</i> , 2015 , 54, 449-57	3.9	28
209	Identification of genes expressed by immune cells of the colon that are regulated by colorectal cancer-associated variants. <i>International Journal of Cancer</i> , 2014 , 134, 2330-41	7.5	28
208	A Pilot Study Comparing HPV-Positive and HPV-Negative Head and Neck Squamous Cell Carcinomas by Whole Exome Sequencing. <i>ISRN Oncology</i> , 2012 , 2012, 809370		28
207	The evolutionary history of 2,658 cancers		28
206	VennDIS: a JavaFX-based Venn and Euler diagram software to generate publication quality figures. <i>Proteomics</i> , 2015 , 15, 1239-44	4.8	27
205	miR-620 promotes tumor radioresistance by targeting 15-hydroxyprostaglandin dehydrogenase (HPGD). <i>Oncotarget</i> , 2015 , 6, 22439-51	3.3	27
204	The path to routine use of genomic biomarkers in the cancer clinic. <i>Genome Research</i> , 2015 , 25, 1508-13	9.7	26
203	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. <i>Nucleic Acids Research</i> , 2008 , 36, e144	20.1	26
202	Polymorphisms of human nuclear receptors that control expression of drug-metabolizing enzymes. <i>Pharmacogenetics and Genomics</i> , 2005 , 15, 371-9	1.9	26
201	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019 , 25, 1615-1626	50.5	25
200	Male and female mice show significant differences in hepatic transcriptomic response to 2,3,7,8-tetrachlorodibenzo-p-dioxin. <i>BMC Genomics</i> , 2015 , 16, 625	4.5	25
199	Identification of a neutrophil-related gene expression signature that is enriched in adult systemic lupus erythematosus patients with active nephritis: Clinical/pathologic associations and etiologic mechanisms. PLoS ONE 2018, 13, e0196117	3.7	25

198	Inter-strain heterogeneity in rat hepatic transcriptomic responses to 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). <i>Toxicology and Applied Pharmacology</i> , 2012 , 260, 135-45	4.6	25
197	The role of Cancer-Testis antigens as predictive and prognostic markers in non-small cell lung cancer. <i>PLoS ONE</i> , 2013 , 8, e67876	3.7	25
196	NBN gain is predictive for adverse outcome following image-guided radiotherapy for localized prostate cancer. <i>Oncotarget</i> , 2014 , 5, 11081-90	3.3	25
195	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
194	A practical guide to cancer subclonal reconstruction from DNA sequencing. <i>Nature Methods</i> , 2021 , 18, 144-155	21.6	25
193	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021 , 597, 119-125	50.4	25
192	Developing a prognostic micro-RNA signature for human cervical carcinoma. <i>PLoS ONE</i> , 2015 , 10, e0123	3946	24
191	PUNS: transcriptomic- and genomic-in silico PCR for enhanced primer design. <i>Bioinformatics</i> , 2004 , 20, 2399-400	7.2	23
190	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
189	MYC dephosphorylation by the PP1/PNUTS phosphatase complex regulates chromatin binding and protein stability. <i>Nature Communications</i> , 2018 , 9, 3502	17.4	23
188	MYC phosphorylation at novel regulatory regions suppresses transforming activity. <i>Cancer Research</i> , 2013 , 73, 6504-15	10.1	22
187	Comparison of toxicity and outcomes of concurrent radiotherapy with carboplatin/paclitaxel or cisplatin/etoposide in stage III non-small cell lung cancer. <i>Cancer Medicine</i> , 2013 , 2, 916-24	4.8	22
186	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. <i>Nature Communications</i> , 2020 , 11, 441	17.4	21
185	Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. <i>Cancer Cell</i> , 2019 , 36, 674-689.e6	24.3	21
184	ISOpureR: an R implementation of a computational purification algorithm of mixed tumour profiles. <i>BMC Bioinformatics</i> , 2015 , 16, 156	3.6	21
183	Exploiting high-throughput cell line drug screening studies to identify candidate therapeutic agents in head and neck cancer. <i>BMC Pharmacology & Docicology</i> , 2014 , 15, 66	2.6	21
182	Prophylactic valproic acid treatment prevents schizophrenia-related behaviour in Disc1-L100P mutant mice. <i>PLoS ONE</i> , 2012 , 7, e51562	3.7	21
181	Molecular markers of injury in kidney biopsy specimens of patients with lupus nephritis. <i>Journal of Molecular Diagnostics</i> , 2011 , 13, 143-51	5.1	21

180	A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. <i>PLoS Computational Biology</i> , 2016 , 12, e1004890	5	21
179	Local Failure and Survival After Definitive Radiotherapy for Aggressive Prostate Cancer: An Individual Patient-level Meta-analysis of Six Randomized Trials. <i>European Urology</i> , 2020 , 77, 201-208	10.2	21
178	Mining Human Prostate Cancer Datasets: The "camcAPP" Shiny App. EBioMedicine, 2017, 17, 5-6	8.8	20
177	PDGFRBtromal adipocyte progenitors transition into epithelial cells during lobulo-alveologenesis in the murine mammary gland. <i>Nature Communications</i> , 2019 , 10, 1760	17.4	20
176	Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. <i>Molecular Cell</i> , 2020 , 77, 1307-1321.e10	17.6	20
175	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. Journal of Cell Biology, 2018 , 217, 2951-2974	7.3	20
174	Genomic Classifier for Guiding Treatment of Intermediate-Risk Prostate Cancers to Dose-Escalated Image Guided Radiation Therapy Without Hormone Therapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2019 , 103, 84-91	4	20
173	Deregulation of the spindle assembly checkpoint is associated with paclitaxel resistance in ovarian cancer. <i>Journal of Ovarian Research</i> , 2018 , 11, 27	5.5	19
172	A three-gene DNA methylation biomarker accurately classifies early stage prostate cancer. <i>Prostate</i> , 2019 , 79, 1705-1714	4.2	19
171	Ensemble analyses improve signatures of tumour hypoxia and reveal inter-platform differences. <i>BMC Bioinformatics</i> , 2014 , 15, 170	3.6	19
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	Copy Number Profiles of Prostate Cancer in Men of Middle Eastern Ancestry. <i>Cancers</i> , 2021 , 13,		1
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8 7 6	Web-based resources for clinical bioinformatics. <i>Methods in Molecular Medicine</i> , 2008 , 141, 309-29 Microarray-Based Investigations in Cancer 2014 , 87-106 Health Economic Evidence for Liquid- and Tissue-based Molecular Tests that Inform Decisions on Prostate Biopsies and Treatment of Localised Prostate Cancer: A Systematic Review. <i>European Urology Open Science</i> , 2021 , 27, 77-87 Comparative survival analysis of multiparametric tests-when molecular tests disagree-A TEAM	
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8 7 6 5 4	Web-based resources for clinical bioinformatics. <i>Methods in Molecular Medicine</i> , 2008 , 141, 309-29 Microarray-Based Investigations in Cancer 2014 , 87-106 Health Economic Evidence for Liquid- and Tissue-based Molecular Tests that Inform Decisions on Prostate Biopsies and Treatment of Localised Prostate Cancer: A Systematic Review. <i>European Urology Open Science</i> , 2021 , 27, 77-87 Comparative survival analysis of multiparametric tests-when molecular tests disagree-A TEAM Pathology study. <i>Npj Breast Cancer</i> , 2021 , 7, 90 Identification of Distinct Prognostic Groups: Implications for Patient Selection to Targeted Therapies Among Anti-Endocrine Therapy-Resistant Early Breast Cancers <i>JCO Precision Oncology</i> , 2019 , 3, 1-13 Data-driven identification of inherent features of eukaryotic stress-responsive genes <i>NAR</i>	7.8 3.6