

Joel S Parker

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.

203
papers

51,723
citations

76
h-index

213
g-index

213
ext. papers

64,893
ext. citations

12.6
avg, IF

8.5
L-index

#	Paper	IF	Citations
203	Rapid idiosyncratic mechanisms of clinical resistance to KRAS G12C inhibition.. <i>Journal of Clinical Investigation</i> , 2022 ,	15.9	5
202	Development and validation of the new HER2DX assay for predicting pathological response and survival outcome in early-stage HER2-positive breast cancer.. <i>EBioMedicine</i> , 2022 , 75, 103801	8.8	3
201	A multi-omic single-cell landscape of human gynecologic malignancies. <i>Molecular Cell</i> , 2021 , 81, 4924-4941	11.6	102
200	UNMASC: tumor-only variant calling with unmatched normal controls. <i>NAR Cancer</i> , 2021 , 3, zcab040	5.2	2
199	Cistrome analysis of YY1 uncovers a regulatory axis of YY1:BRD2/4-PFKP during tumorigenesis of advanced prostate cancer. <i>Nucleic Acids Research</i> , 2021 , 49, 4971-4988	20.1	1
198	Genomic heterogeneity and copy number variant burden are associated with poor recurrence-free survival and 11q loss in human papillomavirus-positive squamous cell carcinoma of the oropharynx. <i>Cancer</i> , 2021 , 127, 2788-2800	6.4	2
197	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021 , 372,	33.3	18
196	FOXA1 and adaptive response determinants to HER2 targeted therapy in TBCRC 036. <i>Npj Breast Cancer</i> , 2021 , 7, 51	7.8	4
195	Validation of reference genes for whole blood gene expression analysis in cord blood of preterm and full-term neonates and peripheral blood of healthy adults. <i>BMC Genomics</i> , 2021 , 22, 489	4.5	1
194	CPT1A and fatty acid oxidation are essential for tumor cell growth and survival in hormone receptor-positive breast cancer. <i>NAR Cancer</i> , 2021 , 3, zcab035	5.2	5
193	Subependymal giant cell astrocytomas are characterized by mTORC1 hyperactivation, a very low somatic mutation rate, and a unique gene expression profile. <i>Modern Pathology</i> , 2021 , 34, 264-279	9.8	1
192	Improved T-cell Receptor Diversity Estimates Associate with Survival and Response to Anti-PD-1 Therapy. <i>Cancer Immunology Research</i> , 2021 , 9, 103-112	12.5	1
191	Genomic Analysis of Germline Variation Associated with Survival of Patients with Colorectal Cancer Treated with Chemotherapy Plus Biologics in CALGB/SWOG 80405 (Alliance). <i>Clinical Cancer Research</i> , 2021 , 27, 267-275	12.9	2
190	Epigenomic characterization of latent HIV infection identifies latency regulating transcription factors. <i>PLoS Pathogens</i> , 2021 , 17, e1009346	7.6	6
189	CRTC1/MAML2 directs a PGC-1 β /GF-1 circuit that confers vulnerability to PPAR γ inhibition. <i>Cell Reports</i> , 2021 , 34, 108768	10.6	2
188	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. <i>Science Translational Medicine</i> , 2021 , 13, eabj1578	17.5	10
187	Leveraging gene expression subgroups to classify DLBCL patients and select for clinical benefit from a novel agent. <i>Blood</i> , 2020 , 135, 1008-1018	2.2	7

186	A pan-cancer analysis of the frequency of DNA alterations across cell cycle activity levels. <i>Oncogene</i> , 2020 , 39, 5430-5440	9.2	3
185	Human genes differ by their UV sensitivity estimated through analysis of UV-induced silent mutations in melanoma. <i>Human Mutation</i> , 2020 , 41, 1751-1760	4.7	
184	A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. <i>Cell Reports</i> , 2020 , 30, 1385-1399.e7	10.6	11
183	Identifying transcriptional profiles and evaluating prognostic biomarkers of HIV-associated diffuse large B-cell lymphoma from Malawi. <i>Modern Pathology</i> , 2020 , 33, 1482-1491	9.8	3
182	Virus expression detection reveals RNA-sequencing contamination in TCGA. <i>BMC Genomics</i> , 2020 , 21, 79	4.5	6
181	Neoadjuvant pazopanib and molecular analysis of tissue response in renal cell carcinoma. <i>JCI Insight</i> , 2020 , 5,	9.9	4
180	FGFR4 regulates tumor subtype differentiation in luminal breast cancer and metastatic disease. <i>Journal of Clinical Investigation</i> , 2020 , 130, 4871-4887	15.9	15
179	Re-expression of SMARCA4/BRG1 in small cell carcinoma of ovary, hypercalcemic type (SCCOHT) promotes an epithelial-like gene signature through an AP-1-dependent mechanism. <i>ELife</i> , 2020 , 9,	8.9	7
178	Development and validation of a NanoString BASE47 bladder cancer gene classifier. <i>PLoS ONE</i> , 2020 , 15, e0243935	3.7	1
177	Tight Junction Protein Claudin-7 Is Essential for Intestinal Epithelial Stem Cell Self-Renewal and Differentiation. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020 , 9, 641-659	7.9	15
176	PIK3CA Mutation in HPV-Associated OPSCC Patients Receiving Deintensified Chemoradiation. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 855-858	9.7	27
175	Survival, Pathologic Response, and Genomics in CALGB 40601 (Alliance), a Neoadjuvant Phase III Trial of Paclitaxel-Trastuzumab With or Without Lapatinib in HER2-Positive Breast Cancer. <i>Journal of Clinical Oncology</i> , 2020 , 38, 4184-4193	2.2	28
174	A multivariable prognostic score to guide systemic therapy in early-stage HER2-positive breast cancer: a retrospective study with an external evaluation. <i>Lancet Oncology, The</i> , 2020 , 21, 1455-1464	21.7	20
173	A Prognostic Model Based on PAM50 and Clinical Variables (PAM50MET) for Metastatic Hormone Receptor-positive HER2-negative Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 6141-6148	12.9	2
172	HER2-Enriched Subtype and ERBB2 Expression in HER2-Positive Breast Cancer Treated with Dual HER2 Blockade. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 46-54	9.7	48
171	Genetic determinants of cellular addiction to DNA polymerase theta. <i>Nature Communications</i> , 2019 , 10, 4286	17.4	57
170	Genome-Wide RNAi Screen Identifies Regulators of Cardiomyocyte Necrosis. <i>ACS Pharmacology and Translational Science</i> , 2019 , 2, 361-371	5.9	2
169	Histone deacetylase 11 inhibition promotes breast cancer metastasis from lymph nodes. <i>Nature Communications</i> , 2019 , 10, 4192	17.4	27

168	Machine-Learning Prediction of Tumor Antigen Immunogenicity in the Selection of Therapeutic Epitopes. <i>Cancer Immunology Research</i> , 2019 , 7, 1591-1604	12.5	27
167	Cells exhibiting strong promoter activation in vivo display features of senescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 2603-2611	11.5	108
166	Rapid Clearance Profile of Plasma Circulating Tumor HPV Type 16 DNA during Chemoradiotherapy Correlates with Disease Control in HPV-Associated Oropharyngeal Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 4682-4690	12.9	90
165	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 1349-1361	4.3	11
164	I-Boost: an integrative boosting approach for predicting survival time with multiple genomics platforms. <i>Genome Biology</i> , 2019 , 20, 52	18.3	4
163	Dynamic changes in lung responses after single and repeated exposures to cigarette smoke in mice. <i>PLoS ONE</i> , 2019 , 14, e0212866	3.7	5
162	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019 , 21, 36	8.3	21
161	RNA-Sequencing of Umbilical Cord Blood to Investigate Spontaneous Preterm Birth: A Pilot Study. <i>AJP Reports</i> , 2019 , 9, e60-e66	1.2	2
160	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. <i>Cell Systems</i> , 2019 , 9, 24-34.e10	10.6	64
159	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. <i>Cell</i> , 2019 , 179, 1191-1206.e21	56.2	146
158	An Immunocompetent Mouse Model of HPV16(+) Head and Neck Squamous Cell Carcinoma. <i>Cell Reports</i> , 2019 , 29, 1660-1674.e7	10.6	7
157	Genetic determinants of the molecular portraits of epithelial cancers. <i>Nature Communications</i> , 2019 , 10, 5666	17.4	8
156	Interaction between androgen receptor and coregulator SLIRP is regulated by Ack1 tyrosine kinase and androgen. <i>Scientific Reports</i> , 2019 , 9, 18637	4.9	4
155	PAM50 Molecular Intrinsic Subtypes in the Nurses' Health Study Cohorts. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 798-806	4	8
154	Improved indel detection in DNA and RNA via realignment with ABRA2. <i>Bioinformatics</i> , 2019 , 35, 2966-2973	17.3	18
153	Male breast cancer: a disease distinct from female breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019 , 173, 37-48	4.4	85
152	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. <i>Frontiers in Oncology</i> , 2018 , 8, 584	5.3	9
151	The Chromatin Remodeler BPTF Activates a Stemness Gene-Expression Program Essential for the Maintenance of Adult Hematopoietic Stem Cells. <i>Stem Cell Reports</i> , 2018 , 10, 675-683	8	15

150	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
149	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
148	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
147	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
146	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
145	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
144	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
143	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
142	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
141	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
140	Gene expression-phenotype associations in adults with eosinophilic esophagitis. <i>Digestive and Liver Disease</i> , 2018 , 50, 804-811	3.3	9
139	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
138	Disease burden and conditioning regimens in ASCT1221, a randomized phase II trial in children with juvenile myelomonocytic leukemia: A Children's Oncology Group study. <i>Pediatric Blood and Cancer</i> , 2018 , 65, e27034	3	17
137	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
136	Integrated Analysis of RNA and DNA from the Phase III Trial CALGB 40601 Identifies Predictors of Response to Trastuzumab-Based Neoadjuvant Chemotherapy in HER2-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 5292-5304	12.9	41
135	Intrinsic molecular subtypes of breast cancers categorized as HER2-positive using an alternative chromosome 17 probe assay. <i>Breast Cancer Research</i> , 2018 , 20, 75	8.3	4
134	VHL substrate transcription factor ZHX2 as an oncogenic driver in clear cell renal cell carcinoma. <i>Science</i> , 2018 , 361, 290-295	33.3	73
133	Haploinsufficiency for Microtubule Methylation Is an Early Driver of Genomic Instability in Renal Cell Carcinoma. <i>Cancer Research</i> , 2018 , 78, 3135-3146	10.1	31

132	Identification of Clonal Hematopoiesis Mutations in Solid Tumor Patients Undergoing Unpaired Next-Generation Sequencing Assays. <i>Clinical Cancer Research</i> , 2018 , 24, 5918-5924	12.9	50
131	Age-Associated Changes in the Respiratory Epithelial Response to Influenza Infection. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018 , 73, 1643-1650	6.4	11
130	A survey of microRNA single nucleotide polymorphisms identifies novel breast cancer susceptibility loci in a case-control, population-based study of African-American women. <i>Breast Cancer Research</i> , 2018 , 20, 45	8.3	11
129	Endogenous retroviral signatures predict immunotherapy response in clear cell renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2018 , 128, 4804-4820	15.9	116
128	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. <i>Journal of Clinical Investigation</i> , 2018 , 128, 1371-1383	15.9	83
127	Identification of Germline Variants in Tumor Genomic Sequencing Analysis. <i>Journal of Molecular Diagnostics</i> , 2018 , 20, 123-125	5.1	11
126	Enhancing Next-Generation Sequencing-Guided Cancer Care Through Cognitive Computing. <i>Oncologist</i> , 2018 , 23, 179-185	5.7	54
125	ZFX Mediates Non-canonical Oncogenic Functions of the Androgen Receptor Splice Variant 7 in Castrate-Resistant Prostate Cancer. <i>Molecular Cell</i> , 2018 , 72, 341-354.e6	17.6	38
124	Epstein-Barr Virus-Positive Cancers Show Altered B-Cell Clonality. <i>MSystems</i> , 2018 , 3,	7.6	14
123	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
122	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. <i>Melanoma Research</i> , 2018 , 28, 380-389	3.3	12
121	A Monolayer of Primary Colonic Epithelium Generated on a Scaffold with a Gradient of Stiffness for Drug Transport Studies. <i>Analytical Chemistry</i> , 2018 , 90, 13331-13340	7.8	15
120	A Functional riboSNitch in the 3' Untranslated Region of Alters MicroRNA-320a Binding Efficiency and Mediates Vulnerability to Chronic Post-Traumatic Pain. <i>Journal of Neuroscience</i> , 2018 , 38, 8407-8420	6.6	31
119	LCCC 1025: a phase II study of everolimus, trastuzumab, and vinorelbine to treat progressive HER2-positive breast cancer brain metastases. <i>Breast Cancer Research and Treatment</i> , 2018 , 171, 637-648	4.4	22
118	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
117	Tumor-homing cytotoxic human induced neural stem cells for cancer therapy. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	53
116	Enhancer Remodeling during Adaptive Bypass to MEK Inhibition Is Attenuated by Pharmacologic Targeting of the P-TEFb Complex. <i>Cancer Discovery</i> , 2017 , 7, 302-321	24.4	80
115	BRG1 and BRM function antagonistically with c-MYC in adult cardiomyocytes to regulate conduction and contractility. <i>Journal of Molecular and Cellular Cardiology</i> , 2017 , 105, 99-109	5.8	11

114	A Gene Expression Panel is Accurate for Diagnosis and Monitoring Treatment of Eosinophilic Esophagitis in Adults. <i>Clinical and Translational Gastroenterology</i> , 2017 , 8, e74	4.2	20
113	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017 , 162, 439-450	4.4	34
112	Combined kinase inhibitors of MEK1/2 and either PI3K or PDGFR are efficacious in intracranial triple-negative breast cancer. <i>Neuro-Oncology</i> , 2017 , 19, 1481-1493	1	23
111	A PAM50-Based Chemoendocrine Score for Hormone Receptor-Positive Breast Cancer with an Intermediate Risk of Relapse. <i>Clinical Cancer Research</i> , 2017 , 23, 3035-3044	12.9	17
110	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
109	MYC activation cooperates with Vhl and Ink4a/Arf loss to induce clear cell renal cell carcinoma. <i>Nature Communications</i> , 2017 , 8, 15770	17.4	40
108	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. <i>Nature Communications</i> , 2017 , 8, 15290	17.4	109
107	A B-Cell Gene Signature Correlates With the Extent of Gluten-Induced Intestinal Injury in Celiac Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017 , 4, 1-17	7.9	7
106	An Oral Selective Alpha-1A Adrenergic Receptor Agonist Prevents Doxorubicin Cardiotoxicity. <i>JACC Basic To Translational Science</i> , 2017 , 2, 39-53	8.7	25
105	Immunophenotyping and Transcriptomic Outcomes in PDX-Derived TNBC Tissue. <i>Molecular Cancer Research</i> , 2017 , 15, 429-438	6.6	9
104	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017 , 8, 1231	17.4	79
103	Exceptional Chemotherapy Response in Metastatic Colorectal Cancer Associated With Hyper-Indel-Hypermutated Cancer Genome and Comutation of and. <i>JCO Precision Oncology</i> , 2017 , 2017,	3.6	1
102	Comprehensive Molecular Characterization of Urachal Adenocarcinoma Reveals Commonalities With Colorectal Cancer, Including a Hypermutable Phenotype. <i>JCO Precision Oncology</i> , 2017 , 1,	3.6	10
101	SynthEx: a synthetic-normal-based DNA sequencing tool for copy number alteration detection and tumor heterogeneity profiling. <i>Genome Biology</i> , 2017 , 18, 66	18.3	20
100	Molecular and Clinical Characterization of a Claudin-Low Subtype of Gastric Cancer.. <i>JCO Precision Oncology</i> , 2017 , 1, 1-10	3.6	4
99	Treg depletion potentiates checkpoint inhibition in claudin-low breast cancer. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3472-3483	15.9	84
98	Transcriptome Variability in Keratocystic Odontogenic Tumor Suggests Distinct Molecular Subtypes. <i>Scientific Reports</i> , 2016 , 6, 24236	4.9	7
97	Assembly-based inference of B-cell receptor repertoires from short read RNA sequencing data with V@Jer. <i>Bioinformatics</i> , 2016 , 32, 3729-3734	7.2	39

96	ATR maintains chromosomal integrity during postnatal cerebellar neurogenesis and is required for medulloblastoma formation. <i>Development (Cambridge)</i> , 2016 , 143, 4038-4052	6.6	30
95	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	187
94	Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016 , 17, 181	4.5	19
93	Heterogeneity in global gene expression profiles between biopsy specimens taken peri-surgically from primary ER-positive breast carcinomas. <i>Breast Cancer Research</i> , 2016 , 18, 39	8.3	17
92	Alternate Metabolic Programs Define Regional Variation of Relevant Biological Features in Renal Cell Carcinoma Progression. <i>Clinical Cancer Research</i> , 2016 , 22, 2950-9	12.9	16
91	GeneFu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. <i>Bioinformatics</i> , 2016 , 32, 1097-9	7.2	150
90	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
89	Claudin-low bladder tumors are immune infiltrated and actively immune suppressed. <i>JCI Insight</i> , 2016 , 1, e85902	9.9	117
88	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. <i>JCI Insight</i> , 2016 , 1, e88755	9.9	37
87	G Protein Coupled Receptor Kinase 3 Regulates Breast Cancer Migration, Invasion, and Metastasis. <i>PLoS ONE</i> , 2016 , 11, e0152856	3.7	34
86	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. <i>PLoS Medicine</i> , 2016 , 13, e1002174	11.6	62
85	Identification of Human Papillomavirus Infection in Cancer Tissue by Targeted Next-generation Sequencing. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2016 , 24, 490-5	1.9	10
84	Prospective assessment of serum periostin as a biomarker for diagnosis and monitoring of eosinophilic oesophagitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2016 , 44, 189-97	6.1	16
83	Ameloblastoma Phenotypes Reflected in Distinct Transcriptome Profiles. <i>Scientific Reports</i> , 2016 , 6, 30867	4.9	6
82	Germline Analysis from Tumor-Germline Sequencing Dyads to Identify Clinically Actionable Secondary Findings. <i>Clinical Cancer Research</i> , 2016 , 22, 4087-4094	12.9	48
81	Gene expression profile of pulpitis. <i>Genes and Immunity</i> , 2016 , 17, 239-43	4.4	16
80	An oncogenic Ezh2 mutation induces tumors through global redistribution of histone 3 lysine 27 trimethylation. <i>Nature Medicine</i> , 2016 , 22, 632-40	50.5	122
79	Chemotherapy and Stem Cell Transplantation Increase p16 Expression, a Biomarker of T-cell Aging. <i>EBioMedicine</i> , 2016 , 11, 227-238	8.8	38

78	Defining breast cancer intrinsic subtypes by quantitative receptor expression. <i>Oncologist</i> , 2015 , 20, 474-87	10.2	102
77	Inhibition of Lapatinib-Induced Kinome Reprogramming in ERBB2-Positive Breast Cancer by Targeting BET Family Bromodomains. <i>Cell Reports</i> , 2015 , 11, 390-404	10.6	210
76	Spatially distinct neutrophil responses within the inflammatory lesions of pneumonic plague. <i>MBio</i> , 2015 , 6, e01530-15	7.8	22
75	Tumor Heterogeneity: Focus on the Leaves, the Trees, or the Forest?. <i>Cancer Cell</i> , 2015 , 28, 149-50	24.3	16
74	Cross-species DNA copy number analyses identifies multiple 1q21-q23 subtype-specific driver genes for breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015 , 152, 347-56	4.4	37
73	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. <i>BMC Medical Genomics</i> , 2015 , 8, 54	3.7	242
72	MicroRNA circulating in the early aftermath of motor vehicle collision predict persistent pain development and suggest a role for microRNA in sex-specific pain differences. <i>Molecular Pain</i> , 2015 , 11, 66	3.4	23
71	Towards unraveling the human tooth transcriptome: the dentome. <i>PLoS ONE</i> , 2015 , 10, e0124801	3.7	18
70	Combined Targeted DNA Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using UNCseq and NGScopy, and RNA Sequencing Using UNCqer for the Detection of Genetic Aberrations in NSCLC. <i>PLoS ONE</i> , 2015 , 10, e0129280	3.7	31
69	Efficacy of Carboplatin Alone and in Combination with ABT888 in Intracranial Murine Models of BRCA-Mutated and BRCA-Wild-Type Triple-Negative Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 920-30	6.1	50
68	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26088-102	5.4	22
67	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
66	Abstract S3-06: Mutational analysis of CALGB 40601 (Alliance), a neoadjuvant phase III trial of weekly paclitaxel (T) and trastuzumab (H) with or without lapatinib (L) for HER2-positive breast cancer 2015 ,		3
65	A novel biomarker to predict sensitivity to enzalutamide (ENZA) in TNBC.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 1083-1083	2.2	21
64	Mutation of androgen receptor N-terminal phosphorylation site Tyr-267 leads to inhibition of nuclear translocation and DNA binding. <i>PLoS ONE</i> , 2015 , 10, e0126270	3.7	10
63	Recurrence-free Survival Among Patients With ER+/PR+/HER2- Breast Cancers is Predicted by Expression of the Estrogen Response Signature. <i>FASEB Journal</i> , 2015 , 29, 926.2	0.9	1
62	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
61	ClearCode34: A prognostic risk predictor for localized clear cell renal cell carcinoma. <i>European Urology</i> , 2014 , 66, 77-84	10.2	169

60	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. <i>Genome Research</i> , 2014 , 24, 241-50	9.7	124
59	ABRA: improved coding indel detection via assembly-based realignment. <i>Bioinformatics</i> , 2014 , 30, 2813-5.2	5.2	107
58	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15544-9	11.5	229
57	Reply to Alexander S. Parker, Brad C. Leibovich, Jeanette E. Eckel-Passow, John C. Cheville@ letter to the editor re: Samira A. Brooks, A. Rose Brannon, Joel S. Parker, et al. ClearCode34: a prognostic risk predictor for localized clear cell renal cell carcinoma. <i>Eur Urol</i> 2014;66:77-84. <i>European Urology</i> , 2014 , 66, e92	10.2	
56	Predicting response and survival in chemotherapy-treated triple-negative breast cancer. <i>British Journal of Cancer</i> , 2014 , 111, 1532-41	8.7	82
55	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. <i>BMC Genomics</i> , 2014 , 15, 419	4.5	204
54	TBCRC 018: phase II study of iniparib in combination with irinotecan to treat progressive triple negative breast cancer brain metastases. <i>Breast Cancer Research and Treatment</i> , 2014 , 146, 557-66	4.4	48
53	An integrated genomics approach identifies drivers of proliferation in luminal-subtype human breast cancer. <i>Nature Genetics</i> , 2014 , 46, 1051-9	36.3	158
52	Intrinsic subtypes of high-grade bladder cancer reflect the hallmarks of breast cancer biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 3110-5	11.5	537
51	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. <i>Nucleic Acids Research</i> , 2014 , 42, e107	20.1	59
50	Molecular features and survival outcomes of the intrinsic subtypes within HER2-positive breast cancer. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	132
49	Prenatal arsenic exposure and the epigenome: altered microRNAs associated with innate and adaptive immune signaling in newborn cord blood. <i>Environmental and Molecular Mutagenesis</i> , 2014 , 55, 196-208	3.2	141
48	Targeted next generation sequencing identifies clinically actionable mutations in patients with melanoma. <i>Pigment Cell and Melanoma Research</i> , 2014 , 27, 653-63	4.5	28
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