

Joel S Parker

List of Publications by Citations

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Version: 2024-04-24

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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	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012 , 490, 61-70	50.4	8025
202	Repeated observation of breast tumor subtypes in independent gene expression data sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8418-23	11.5	4262
201	Supervised risk predictor of breast cancer based on intrinsic subtypes. <i>Journal of Clinical Oncology</i> , 2009 , 27, 1160-7	2.2	2866
200	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
199	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
198	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013 , 499, 43-9	50.4	2184
197	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
196	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
195	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
194	Ki67 index, HER2 status, and prognosis of patients with luminal B breast cancer. <i>Journal of the National Cancer Institute</i> , 2009 , 101, 736-50	9.7	1545
193	Phenotypic and molecular characterization of the claudin-low intrinsic subtype of breast cancer. <i>Breast Cancer Research</i> , 2010 , 12, R68	8.3	1428
192	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
191	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
190	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
189	The molecular portraits of breast tumors are conserved across microarray platforms. <i>BMC Genomics</i> , 2006 , 7, 96	4.5	1016
188	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
187	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854

186	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
185	RNA polymerase is poised for activation across the genome. <i>Nature Genetics</i> , 2007 , 39, 1507-11	36.3	582
184	A comparison of PAM50 intrinsic subtyping with immunohistochemistry and clinical prognostic factors in tamoxifen-treated estrogen receptor-positive breast cancer. <i>Clinical Cancer Research</i> , 2010 , 16, 5222-32	12.9	546
183	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
182	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
181	Randomized phase II neoadjuvant comparison between letrozole, anastrozole, and exemestane for postmenopausal women with estrogen receptor-rich stage 2 to 3 breast cancer: clinical and biomarker outcomes and predictive value of the baseline PAM50-based intrinsic subtype--ACOSOG Z1031. <i>Journal of Clinical Oncology</i> , 2011 , 29, 2312-9	2.2	379
180	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	2.1	377
179	Prognostic significance of progesterone receptor-positive tumor cells within immunohistochemically defined luminal A breast cancer. <i>Journal of Clinical Oncology</i> , 2013 , 31, 203-9	2.2	376
178	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
177	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
176	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
175	Adjustment of systematic microarray data biases. <i>Bioinformatics</i> , 2004 , 20, 105-14	7.2	313
174	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
173	Androgen receptor signaling regulates DNA repair in prostate cancers. <i>Cancer Discovery</i> , 2013 , 3, 1245-53	4.4	284
172	Profiling essential genes in human mammary cells by multiplex RNAi screening. <i>Science</i> , 2008 , 319, 617-20	3.3	263
171	Topoisomerases facilitate transcription of long genes linked to autism. <i>Nature</i> , 2013 , 501, 58-62	50.4	261
170	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. <i>BMC Medical Genomics</i> , 2015 , 8, 54	3.7	242
169	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

168	Identification of driver genes in hepatocellular carcinoma by exome sequencing. <i>Hepatology</i> , 2013 , 58, 1693-702	11.2	223
167	A 50-gene intrinsic subtype classifier for prognosis and prediction of benefit from adjuvant tamoxifen. <i>Clinical Cancer Research</i> , 2012 , 18, 4465-72	12.9	215
166	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
165	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
164	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	187
163	ClearCode34: A prognostic risk predictor for localized clear cell renal cell carcinoma. <i>European Urology</i> , 2014 , 66, 77-84	10.2	169
162	Prognostic B-cell signatures using mRNA-seq in patients with subtype-specific breast and ovarian cancer. <i>Clinical Cancer Research</i> , 2014 , 20, 3818-29	12.9	168
161	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
160	Genomic analysis identifies unique signatures predictive of brain, lung, and liver relapse. <i>Breast Cancer Research and Treatment</i> , 2012 , 132, 523-35	4.4	165
159	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
158	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
157	Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. <i>Breast Cancer Research</i> , 2006 , 8, R23	8.3	150
156	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
155	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
154	Characterization of cell lines derived from breast cancers and normal mammary tissues for the study of the intrinsic molecular subtypes. <i>Breast Cancer Research and Treatment</i> , 2013 , 142, 237-55	4.4	132
153	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
152	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
151	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

150	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
149	Responsiveness of intrinsic subtypes to adjuvant anthracycline substitution in the NCIC.CTG MA.5 randomized trial. <i>Clinical Cancer Research</i> , 2012 , 18, 2402-12	12.9	117
148	Claudin-low bladder tumors are immune infiltrated and actively immune suppressed. <i>JCI Insight</i> , 2016 , 1, e85902	9.9	117
147	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
146	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
145	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
144	ABRA: improved coding indel detection via assembly-based realignment. <i>Bioinformatics</i> , 2014 , 30, 2813-5.2	5.2	107
143	Building prognostic models for breast cancer patients using clinical variables and hundreds of gene expression signatures. <i>BMC Medical Genomics</i> , 2011 , 4, 3	3.7	104
142	Concordance among gene expression-based predictors for ER-positive breast cancer treated with adjuvant tamoxifen. <i>Annals of Oncology</i> , 2012 , 23, 2866-2873	10.3	103
141	Defining breast cancer intrinsic subtypes by quantitative receptor expression. <i>Oncologist</i> , 2015 , 20, 474-87	8.7	102
140	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
139	Relationship between plasma estradiol levels and estrogen-responsive gene expression in estrogen receptor-positive breast cancer in postmenopausal women. <i>Journal of Clinical Oncology</i> , 2010 , 28, 1161-7.2	7.2	88
138	Basal-like Breast cancer DNA copy number losses identify genes involved in genomic instability, response to therapy, and patient survival. <i>Breast Cancer Research and Treatment</i> , 2012 , 133, 865-80	4.4	87
137	Male breast cancer: a disease distinct from female breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019 , 173, 37-48	4.4	85
136	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
135	Treg depletion potentiates checkpoint inhibition in claudin-low breast cancer. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3472-3483	15.9	84
134	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
133	Predicting response and survival in chemotherapy-treated triple-negative breast cancer. <i>British Journal of Cancer</i> , 2014 , 111, 1532-41	8.7	82

132	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
131	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017 , 8, 1231	17.4	79
130	Clinical implementation of the intrinsic subtypes of breast cancer. <i>Lancet Oncology</i> , 2010 , 11, 718-9; author reply 720-1	21.7	79
129	BRG1/SMARCA4 inactivation promotes non-small cell lung cancer aggressiveness by altering chromatin organization. <i>Cancer Research</i> , 2014 , 74, 6486-6498	10.1	76
128	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
127	Deep sequencing of gastric carcinoma reveals somatic mutations relevant to personalized medicine. <i>Journal of Translational Medicine</i> , 2011 , 9, 119	8.5	71
126	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
125	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
124	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. <i>Nucleic Acids Research</i> , 2014 , 42, e107	20.1	59
123	Genetic determinants of cellular addiction to DNA polymerase theta. <i>Nature Communications</i> , 2019 , 10, 4286	17.4	57
122	Agreement in breast cancer classification between microarray and quantitative reverse transcription PCR from fresh-frozen and formalin-fixed, paraffin-embedded tissues. <i>Clinical Chemistry</i> , 2007 , 53, 1273-9	5.5	57
121	Enhancing Next-Generation Sequencing-Guided Cancer Care Through Cognitive Computing. <i>Oncologist</i> , 2018 , 23, 179-185	5.7	54
120	Tumor-homing cytotoxic human induced neural stem cells for cancer therapy. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	53
119	An integration of complementary strategies for gene-expression analysis to reveal novel therapeutic opportunities for breast cancer. <i>Breast Cancer Research</i> , 2009 , 11, R55	8.3	52
118	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
117	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
116	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
115	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

114	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
113	Dysregulation of the epigenome in triple-negative breast cancers: basal-like and claudin-low breast cancers express aberrant DNA hypermethylation. <i>Experimental and Molecular Pathology</i> , 2013 , 95, 276-87	4.4	45
112	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
111	MicroRNA 9-3p targets β integrin to sensitize claudin-low breast cancer cells to MEK inhibition. <i>Molecular and Cellular Biology</i> , 2013 , 33, 2260-74	4.8	41
110	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
109	Association between breast cancer subtypes and response to neoadjuvant anastrozole. <i>Steroids</i> , 2011 , 76, 736-40	2.8	40
108	Assembly-based inference of B-cell receptor repertoires from short read RNA sequencing data with VDJer. <i>Bioinformatics</i> , 2016 , 32, 3729-3734	7.2	39
107	Chemotherapy and Stem Cell Transplantation Increase p16 Expression, a Biomarker of T-cell Aging. <i>EBioMedicine</i> , 2016 , 11, 227-238	8.8	38
106	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
105	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
104	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. <i>JCI Insight</i> , 2016 , 1, e88755	9.9	37
103	Potential tumor suppressor role for the c-Myb oncogene in luminal breast cancer. <i>PLoS ONE</i> , 2010 , 5, e13073	3.7	35
102	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
101	G Protein Coupled Receptor Kinase 3 Regulates Breast Cancer Migration, Invasion, and Metastasis. <i>PLoS ONE</i> , 2016 , 11, e0152856	3.7	34
100	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
99	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
98	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
97	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

96	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
95	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
94	Histone deacetylase 11 inhibition promotes breast cancer metastasis from lymph nodes. <i>Nature Communications</i> , 2019 , 10, 4192	17.4	27
93	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
92	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
91	Differential methylation relative to breast cancer subtype and matched normal tissue reveals distinct patterns. <i>Breast Cancer Research and Treatment</i> , 2013 , 142, 365-80	4.4	26
90	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
89	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
88	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
87	Spatially distinct neutrophil responses within the inflammatory lesions of pneumonic plague. <i>MBio</i> , 2015 , 6, e01530-15	7.8	22
86	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
85	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
84	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019 , 21, 36	8.3	21
83	A novel biomarker to predict sensitivity to enzalutamide (ENZA) in TNBC.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 1083-1083	2.2	21
82	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
81	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
80	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</i> , 2020 , 21, 1455-1464	21.7	20
79	Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016 , 17, 181	4.5	19

78	Towards unraveling the human tooth transcriptome: the dentome. <i>PLoS ONE</i> , 2015 , 10, e0124801	3.7	18
77	Modulators of prostate cancer cell proliferation and viability identified by short-hairpin RNA library screening. <i>PLoS ONE</i> , 2012 , 7, e34414	3.7	18
76	BlackOPs: increasing confidence in variant detection through mappability filtering. <i>Nucleic Acids Research</i> , 2013 , 41, e178	20.1	18
75	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. <i>Environmental Health Perspectives</i> , 2004 , 112, 1607-1613	8.4	18
74	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021 , 372,	33.3	18
73	Improved indel detection in DNA and RNA via realignment with ABRA2. <i>Bioinformatics</i> , 2019 , 35, 2966-2973	18	
72	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
71	Disease burden and conditioning regimens in ASCT1221, a randomized phase II trial in children with juvenile myelomonocytic leukemia: A Children@Oncology Group study. <i>Pediatric Blood and Cancer</i> , 2018 , 65, e27034	3	17
70	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
69	Tumor Heterogeneity: Focus on the Leaves, the Trees, or the Forest?. <i>Cancer Cell</i> , 2015 , 28, 149-50	24.3	16
68	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
67	Insulin-like growth factor-1 receptor inhibitor, AMG-479, in cetuximab-refractory head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2011 , 33, 1804-8	4.2	16
66	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
65	Gene expression profile of pulpitis. <i>Genes and Immunity</i> , 2016 , 17, 239-43	4.4	16
64	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
63	ReQON: a Bioconductor package for recalibrating quality scores from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2012 , 13, 221	3.6	15
62	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
61	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

60	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
59	Epstein-Barr Virus-Positive Cancers Show Altered B-Cell Clonality. <i>MSystems</i> , 2018 , 3,	7.6	14
58	Micro-scale genomic DNA copy number aberrations as another means of mutagenesis in breast cancer. <i>PLoS ONE</i> , 2012 , 7, e51719	3.7	12
57	Prediction of toxicant-specific gene expression signatures after chemotherapeutic treatment of breast cell lines. <i>Environmental Health Perspectives</i> , 2004 , 112, 1607-13	8.4	12
56	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. <i>Melanoma Research</i> , 2018 , 28, 380-389	3.3	12
55	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
54	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 1349-1361	4.3	11
53	A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. <i>Cell Reports</i> , 2020 , 30, 1385-1399.e7	10.6	11
52	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
51	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
50	Identification of Germline Variants in Tumor Genomic Sequencing Analysis. <i>Journal of Molecular Diagnostics</i> , 2018 , 20, 123-125	5.1	11
49	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
48	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
47	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
46	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. <i>Science Translational Medicine</i> , 2021 , 13, eabj1578	17.5	10
45	Immunophenotyping and Transcriptomic Outcomes in PDX-Derived TNBC Tissue. <i>Molecular Cancer Research</i> , 2017 , 15, 429-438	6.6	9
44	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. <i>Frontiers in Oncology</i> , 2018 , 8, 584	5.3	9
43	Gene expression-phenotype associations in adults with eosinophilic esophagitis. <i>Digestive and Liver Disease</i> , 2018 , 50, 804-811	3.3	9

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1	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, e82	10.2	