

Joel S Parker

List of Publications by Year in descending order

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208
papers

74,007
citations

5896

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1934

207
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213
all docs

213
docs citations

213
times ranked

75197
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
2	Repeated observation of breast tumor subtypes in independent gene expression data sets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8418-8423.	7.1	4,849
3	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
4	Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes. Journal of Clinical Oncology, 2009, 27, 1160-1167.	1.6	3,730
5	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
6	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
7	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
8	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
9	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
10	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
11	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
12	Ki67 Index, HER2 Status, and Prognosis of Patients With Luminal B Breast Cancer. Journal of the National Cancer Institute, 2009, 101, 736-750.	6.3	1,844
13	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
14	Phenotypic and molecular characterization of the claudin-low intrinsic subtype of breast cancer. Breast Cancer Research, 2010, 12, R68.	5.0	1,748
15	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
16	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
17	The molecular portraits of breast tumors are conserved across microarray platforms. BMC Genomics, 2006, 7, 96.	2.8	1,169
18	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040

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19	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
20	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
21	Intrinsic subtypes of high-grade bladder cancer reflect the hallmarks of breast cancer biology. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3110-3115.	7.1	736
22	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
23	A Comparison of PAM50 Intrinsic Subtyping with Immunohistochemistry and Clinical Prognostic Factors in Tamoxifen-Treated Estrogen Receptor-Positive Breast Cancer. Clinical Cancer Research, 2010, 16, 5222-5232.	7.0	676
24	RNA polymerase is poised for activation across the genome. Nature Genetics, 2007, 39, 1507-1511.	21.4	661
25	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
26	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
27	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
28	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. Journal of Clinical Oncology, 2011, 29, 2342-2349.	1.6	470
29	Prognostic Significance of Progesterone Receptor-Positive Tumor Cells Within Immunohistochemically Defined Luminal A Breast Cancer. Journal of Clinical Oncology, 2013, 31, 203-209.	1.6	464
30	Androgen Receptor Signaling Regulates DNA Repair in Prostate Cancers. Cancer Discovery, 2013, 3, 1245-1253.	9.4	421
31	Adjustment of systematic microarray data biases. Bioinformatics, 2004, 20, 105-114.	4.1	360
32	Topoisomerases facilitate transcription of long genes linked to autism. Nature, 2013, 501, 58-62.	27.8	360
33	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. BMC Medical Genomics, 2015, 8, 54.	1.5	352
34	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
35	Profiling Essential Genes in Human Mammary Cells by Multiplex RNAi Screening. Science, 2008, 319, 617-620.	12.6	294
36	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. Cell, 2019, 179, 1191-1206.e21.	28.9	291

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37	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
38	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw144.	6.3	271
39	Identification of driver genes in hepatocellular carcinoma by exome sequencing. <i>Hepatology</i> , 2013, 58, 1693-1702.	7.3	264
40	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. <i>BMC Genomics</i> , 2014, 15, 419.	2.8	262
41	A 50-Gene Intrinsic Subtype Classifier for Prognosis and Prediction of Benefit from Adjuvant Tamoxifen. <i>Clinical Cancer Research</i> , 2012, 18, 4465-4472.	7.0	258
42	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. <i>Bioinformatics</i> , 2016, 32, 1097-1099.	4.1	255
43	Inhibition of Lapatinib-Induced Kinome Reprogramming in ERBB2-Positive Breast Cancer by Targeting BET Family Bromodomains. <i>Cell Reports</i> , 2015, 11, 390-404.	6.4	254
44	ClearCode34: A Prognostic Risk Predictor for Localized Clear Cell Renal Cell Carcinoma. <i>European Urology</i> , 2014, 66, 77-84.	1.9	234
45	Prognostic B-cell Signatures Using mRNA-Seq in Patients with Subtype-Specific Breast and Ovarian Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 3818-3829.	7.0	230
46	Cells exhibiting strong <i>p16</i> ^{INK4a} 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.	7.1	218
47	An integrated genomics approach identifies drivers of proliferation in luminal-subtype human breast cancer. <i>Nature Genetics</i> , 2014, 46, 1051-1059.	21.4	215
48	Endogenous retroviral signatures predict immunotherapy response in clear cell renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2018, 128, 4804-4820.	8.2	210
49	Male breast cancer: a disease distinct from female breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 173, 37-48.	2.5	205
50	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. <i>Nature Communications</i> , 2017, 8, 15290.	12.8	195
51	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.	7.0	195
52	Genomic analysis identifies unique signatures predictive of brain, lung, and liver relapse. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 523-535.	2.5	189
53	Claudin-low bladder tumors are immune infiltrated and actively immune suppressed. <i>JCI Insight</i> , 2016, 1, e85902.	5.0	179
54	Molecular Features and Survival Outcomes of the Intrinsic Subtypes Within HER2-Positive Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	178

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55	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
56	Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. <i>Breast Cancer Research</i> , 2006, 8, R23.	5.0	176
57	An oncogenic Ezh2 mutation induces tumors through global redistribution of histone 3 lysine 27 trimethylation. <i>Nature Medicine</i> , 2016, 22, 632-640.	30.7	176
58	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.	2.2	171
59	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, 237-255.	2.5	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, 241-250.	5.5	160
61	Defining Breast Cancer Intrinsic Subtypes by Quantitative Receptor Expression. <i>Oncologist</i> , 2015, 20, 474-482.	3.7	145
62	Building prognostic models for breast cancer patients using clinical variables and hundreds of gene expression signatures. <i>BMC Medical Genomics</i> , 2011, 4, 3.	1.5	142
63	ABRA: improved coding indel detection via assembly-based realignment. <i>Bioinformatics</i> , 2014, 30, 2813-2815.	4.1	140
64	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.	6.2	134
65	VHL substrate transcription factor ZHX2 as an oncogenic driver in clear cell renal cell carcinoma. <i>Science</i> , 2018, 361, 290-295.	12.6	134
66	Responsiveness of Intrinsic Subtypes to Adjuvant Anthracycline Substitution in the NCIC.CTG MA.5 Randomized Trial. <i>Clinical Cancer Research</i> , 2012, 18, 2402-2412.	7.0	132
67	Treg depletion potentiates checkpoint inhibition in claudin-low breast cancer. <i>Journal of Clinical Investigation</i> , 2017, 127, 3472-3483.	8.2	130
68	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.	9.4	128
69	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 1371-1383.	8.2	126
70	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017, 8, 1231.	12.8	124
71	Concordance among gene expression-based predictors for ER-positive breast cancer treated with adjuvant tamoxifen. <i>Annals of Oncology</i> , 2012, 23, 2866-2873.	1.2	123
72	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, 865-880.	2.5	107

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73	Genetic determinants of cellular addiction to DNA polymerase theta. Nature Communications, 2019, 10, 4286.	12.8	106
74	BRG1/SMARCA4 Inactivation Promotes Non-“Small Cell Lung Cancer Aggressiveness by Altering Chromatin Organization. Cancer Research, 2014, 74, 6486-6498.	0.9	104
75	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
76	Predicting response and survival in chemotherapy-treated triple-negative breast cancer. British Journal of Cancer, 2014, 111, 1532-1541.	6.4	100
77	HER2-Enriched Subtype and ERBB2 Expression in HER2-Positive Breast Cancer Treated with Dual HER2 Blockade. Journal of the National Cancer Institute, 2020, 112, 46-54.	6.3	97
78	Relationship Between Plasma Estradiol Levels and Estrogen-Responsive Gene Expression in Estrogen Receptor-Positive Breast Cancer in Postmenopausal Women. Journal of Clinical Oncology, 2010, 28, 1161-1167.	1.6	94
79	Clinical implementation of the intrinsic subtypes of breast cancer. Lancet Oncology, The, 2010, 11, 718-719.	10.7	92
80	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine, 2016, 13, e1002174.	8.4	86
81	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
82	Identification of Clonal Hematopoiesis Mutations in Solid Tumor Patients Undergoing Unpaired Next-Generation Sequencing Assays. Clinical Cancer Research, 2018, 24, 5918-5924.	7.0	84
83	Enhancing Next-Generation Sequencing-Guided Cancer Care Through Cognitive Computing. Oncologist, 2018, 23, 179-185.	3.7	78
84	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. Nucleic Acids Research, 2014, 42, e107-e107.	14.5	76
85	Germline Analysis from Tumor-“Germline Sequencing Dyads to Identify Clinically Actionable Secondary Findings. Clinical Cancer Research, 2016, 22, 4087-4094.	7.0	75
86	Deep sequencing of gastric carcinoma reveals somatic mutations relevant to personalized medicine. Journal of Translational Medicine, 2011, 9, 119.	4.4	74
87	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. Journal of Clinical Oncology, 2020, 38, 4184-4193.	1.6	74
88	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. Clinical Cancer Research, 2018, 24, 5292-5304.	7.0	73
89	Tumor-homing cytotoxic human induced neural stem cells for cancer therapy. Science Translational Medicine, 2017, 9, .	12.4	71
90	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. Science Translational Medicine, 2021, 13, eabj1578.	12.4	67

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91	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, 1273-1279.	3.2	64
92	MYC activation cooperates with Vhl and Ink4a/Arf loss to induce clear cell renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15770.	12.8	64
93	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.	9.7	64
94	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, 920-930.	4.1	62
95	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, 276-287.	2.1	59
96	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, 557-566.	2.5	59
97	Assembly-based inference of B-cell receptor repertoires from short read RNA sequencing data with VDJer. <i>Bioinformatics</i> , 2016, 32, 3729-3734.	4.1	59
98	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.	5.0	58
99	Improved indel detection in DNA and RNA via realignment with ABRA2. <i>Bioinformatics</i> , 2019, 35, 2966-2973.	4.1	55
100	A Functional riboSNitch in the 3' Untranslated Region of FKBP5 Alters MicroRNA-320a Binding Efficiency and Mediates Vulnerability to Chronic Post-Traumatic Pain. <i>Journal of Neuroscience</i> , 2018, 38, 8407-8420.	3.6	52
101	Histone deacetylase 11 inhibition promotes breast cancer metastasis from lymph nodes. <i>Nature Communications</i> , 2019, 10, 4192.	12.8	52
102	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> , The, 2020, 21, 1455-1464.	10.7	52
103	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. <i>JCI Insight</i> , 2016, 1, e88755.	5.0	51
104	Chemotherapy and Stem Cell Transplantation Increase p16 INK4a Expression, a Biomarker of T-cell Aging. <i>EBioMedicine</i> , 2016, 11, 227-238.	6.1	49
105	FGFR4 regulates tumor subtype differentiation in luminal breast cancer and metastatic disease. <i>Journal of Clinical Investigation</i> , 2020, 130, 4871-4887.	8.2	49
106	Association between breast cancer subtypes and response to neoadjuvant anastrozole. <i>Steroids</i> , 2011, 76, 736-740.	1.8	48
107	SETD2 Haploinsufficiency for Microtubule Methylation Is an Early Driver of Genomic Instability in Renal Cell Carcinoma. <i>Cancer Research</i> , 2018, 78, 3135-3146.	0.9	48
108	Machine-Learning Prediction of Tumor Antigen Immunogenicity in the Selection of Therapeutic Epitopes. <i>Cancer Immunology Research</i> , 2019, 7, 1591-1604.	3.4	48

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109	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. Breast Cancer Research and Treatment, 2017, 162, 439-450.	2.5	47
110	Development and validation of the new HER2DX assay for predicting pathological response and survival outcome in early-stage HER2-positive breast cancer. EBioMedicine, 2022, 75, 103801.	6.1	47
111	ATR maintains chromosomal integrity during postnatal cerebellar neurogenesis and is required for medulloblastoma formation. Development (Cambridge), 2016, 143, 4038-4052.	2.5	46
112	PIK3CA Mutation in HPV-Associated OPSCC Patients Receiving Deintensified Chemoradiation. Journal of the National Cancer Institute, 2020, 112, 855-858.	6.3	46
113	G Protein Coupled Receptor Kinase 3 Regulates Breast Cancer Migration, Invasion, and Metastasis. PLoS ONE, 2016, 11, e0152856.	2.5	46
114	MicroRNA 9-3p Targets $\beta 1$ Integrin To Sensitize Claudin-Low Breast Cancer Cells to MEK Inhibition. Molecular and Cellular Biology, 2013, 33, 2260-2274.	2.3	44
115	Rapid idiosyncratic mechanisms of clinical resistance to KRAS G12C inhibition. Journal of Clinical Investigation, 2022, 132, .	8.2	43
116	Potential Tumor Suppressor Role for the c-Myb Oncogene in Luminal Breast Cancer. PLoS ONE, 2010, 5, e13073.	2.5	40
117	An Oral Selective Alpha-1A Adrenergic Receptor Agonist Prevents Doxorubicin Cardiotoxicity. JACC Basic To Translational Science, 2017, 2, 39-53.	4.1	40
118	LCCC 1025: a phase II study of everolimus, trastuzumab, and vinorelbine to treat progressive HER2-positive breast cancer brain metastases. Breast Cancer Research and Treatment, 2018, 171, 637-648.	2.5	40
119	Cross-species DNA copy number analyses identifies multiple 1q21-q23 subtype-specific driver genes for breast cancer. Breast Cancer Research and Treatment, 2015, 152, 347-356.	2.5	38
120	Tight Junction Protein Claudin-7 Is Essential for Intestinal Epithelial Stem Cell Self-Renewal and Differentiation. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 641-659.	4.5	38
121	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. PLoS ONE, 2015, 10, e0129280.	2.5	36
122	Separation of breast cancer and organ microenvironment transcriptomes in metastases. Breast Cancer Research, 2019, 21, 36.	5.0	36
123	A multi-omic single-cell landscape of human gynecologic malignancies. Molecular Cell, 2021, 81, 4924-4941.e10.	9.7	36
124	Combined kinase inhibitors of MEK1/2 and either PI3K or PDGFR are efficacious in intracranial triple-negative breast cancer. Neuro-Oncology, 2017, 19, 1481-1493.	1.2	32
125	Epigenomic characterization of latent HIV infection identifies latency regulating transcription factors. PLoS Pathogens, 2021, 17, e1009346.	4.7	32
126	Targeted next generation sequencing identifies clinically actionable mutations in patients with melanoma. Pigment Cell and Melanoma Research, 2014, 27, 653-663.	3.3	31

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127	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, s12990-015-0069.	2.1	30
128	Spatially Distinct Neutrophil Responses within the Inflammatory Lesions of Pneumonic Plague. <i>MBio</i> , 2015, 6, e01530-15.	4.1	30
129	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 26088-26102.	3.4	29
130	Prospective assessment of serum periostin as a biomarker for diagnosis and monitoring of eosinophilic oesophagitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2016, 44, 189-197.	3.7	29
131	A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. <i>Cell Reports</i> , 2020, 30, 1385-1399.e7.	6.4	29
132	Modulators of Prostate Cancer Cell Proliferation and Viability Identified by Short-Hairpin RNA Library Screening. <i>PLoS ONE</i> , 2012, 7, e34414.	2.5	28
133	Differential methylation relative to breast cancer subtype and matched normal tissue reveals distinct patterns. <i>Breast Cancer Research and Treatment</i> , 2013, 142, 365-380.	2.5	28
134	Gene expression profile of pulpitis. <i>Genes and Immunity</i> , 2016, 17, 239-243.	4.1	28
135	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.	2.5	28
136	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.	7.0	28
137	Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016, 17, 181.	2.8	27
138	SynthEx: a synthetic-normal-based DNA sequencing tool for copy number alteration detection and tumor heterogeneity profiling. <i>Genome Biology</i> , 2017, 18, 66.	8.8	26
139	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.	4.8	26
140	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.	1.5	26
141	PAM50 Molecular Intrinsic Subtypes in the Nurses' Health Study Cohorts. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 798-806.	2.5	26
142	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.	5.0	24
143	A novel biomarker to predict sensitivity to enzalutamide (ENZA) in TNBC.. <i>Journal of Clinical Oncology</i> , 2015, 33, 1083-1083.	1.6	24
144	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1349-1361.	0.7	23

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145	A pan-cancer analysis of the frequency of DNA alterations across cell cycle activity levels. <i>Oncogene</i> , 2020, 39, 5430-5440.	5.9	23
146	Towards Unraveling the Human Tooth Transcriptome: The Dentome. <i>PLoS ONE</i> , 2015, 10, e0124801.	2.5	22
147	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.	14.5	22
148	Alternate Metabolic Programs Define Regional Variation of Relevant Biological Features in Renal Cell Carcinoma Progression. <i>Clinical Cancer Research</i> , 2016, 22, 2950-2959.	7.0	21
149	Genetic determinants of the molecular portraits of epithelial cancers. <i>Nature Communications</i> , 2019, 10, 5666.	12.8	21
150	Virus expression detection reveals RNA-sequencing contamination in TCGA. <i>BMC Genomics</i> , 2020, 21, 79.	2.8	21
151	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. <i>Environmental Health Perspectives</i> , 2004, 112, 1607-1613.	6.0	21
152	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.	6.5	20
153	An Immunocompetent Mouse Model of HPV16(+) Head and Neck Squamous Cell Carcinoma. <i>Cell Reports</i> , 2019, 29, 1660-1674.e7.	6.4	20
154	ReQON: a Bioconductor package for recalibrating quality scores from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2012, 13, 221.	2.6	19
155	BlackOPS: increasing confidence in variant detection through mappability filtering. <i>Nucleic Acids Research</i> , 2013, 41, e178-e178.	14.5	19
156	Tumor Heterogeneity: Focus on the Leaves, the Trees, or the Forest?. <i>Cancer Cell</i> , 2015, 28, 149-150.	16.8	19
157	CPT1A and fatty acid β -oxidation are essential for tumor cell growth and survival in hormone receptor-positive breast cancer. <i>NAR Cancer</i> , 2021, 3, zcab035.	3.1	19
158	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, .	6.0	19
159	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.	1.9	18
160	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. <i>Environmental Health Perspectives</i> , 2004, 112, 1607-1613.	6.0	17
161	Comprehensive Molecular Characterization of Urachal Adenocarcinoma Reveals Commonalities With Colorectal Cancer, Including a Hypermutable Phenotype. <i>JCO Precision Oncology</i> , 2017, 1, 1-12.	3.0	17
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