Katherine A Hoadley

List of Publications by Year in Descending Order

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Version: 2024-04-10

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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.

139	39,352 citations	73	153
papers		h-index	g-index
153 ext. papers	53,036 ext. citations	16.5 avg, IF	5.94 L-index

#	Paper	IF	Citations
139	Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression Breast Cancer Research and Treatment, 2022, 192, 447	4.4	
138	CALGB 40603 (Alliance): Long-Term Outcomes and Genomic Correlates of Response and Survival After Neoadjuvant Chemotherapy With or Without Carboplatin and Bevacizumab in Triple-Negative Breast Cancer <i>Journal of Clinical Oncology</i> , 2022 , JCO2101506	2.2	7
137	BIDIMENSIONAL LINKED MATRIX FACTORIZATION FOR PAN-OMICS PAN-CANCER ANALYSIS Annals of Applied Statistics, 2022 , 16, 193-215	2.1	O
136	Spatial Characterization of Tumor-Infiltrating Lymphocytes and Breast Cancer Progression <i>Cancers</i> , 2022 , 14,	6.6	2
135	Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. <i>Communications Biology</i> , 2021 , 4, 1150	6.7	O
134	UNMASC: tumor-only variant calling with unmatched normal controls. NAR Cancer, 2021, 3, zcab040	5.2	2
133	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021 , 39, 509-5	2 8.ẹ 須0	71
132	Identification of a Novel Inflamed Tumor Microenvironment Signature as a Predictive Biomarker of Bacillus Calmette-Gufin Immunotherapy in Non-Muscle-Invasive Bladder Cancer. <i>Clinical Cancer Research</i> , 2021 , 27, 4599-4609	12.9	4
131	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021 , 2, 100483	1.4	O
130	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkaa072	4.6	3
129	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021 , 39, 38-53.e7	24.3	18
128	An approach for normalization and quality control for NanoString RNA expression data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	15
127	SCISSOR: a framework for identifying structural changes in RNA transcripts. <i>Nature Communications</i> , 2021 , 12, 286	17.4	2
126	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
125	Protein-based immune profiles of basal-like vs. luminal breast cancers. <i>Laboratory Investigation</i> , 2021 , 101, 785-793	5.9	2
124	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021 , 39, 361-379.e16	24.3	50
123	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15

122	Hepatocyte growth factor pathway expression in breast cancer by race and subtype. <i>Breast Cancer Research</i> , 2021 , 23, 80	8.3	1
121	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021 , 184, 5031-5052.e26	56.2	26
120	JOINT AND INDIVIDUAL ANALYSIS OF BREAST CANCER HISTOLOGIC IMAGES AND GENOMIC COVARIATES <i>Annals of Applied Statistics</i> , 2021 , 15, 1697-1722	2.1	2
119	A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival. <i>Cancer Informatics</i> , 2020 , 19, 1176935120907399	2.4	1
118	Virus expression detection reveals RNA-sequencing contamination in TCGA. <i>BMC Genomics</i> , 2020 , 21, 79	4.5	6
117	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020 , 578, 129-136	50.4	148
116	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. <i>PLoS Biology</i> , 2020 , 18, e3000975	9.7	5
115	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020 , 37, 639-654.e6	24.3	56
114	Gain-of-Function Mutations Promote Focal Adhesion Kinase Activation and Dependency in Diffuse Gastric Cancer. <i>Cancer Discovery</i> , 2020 , 10, 288-305	24.4	41
113	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
112	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020 , 77, 420-433	10.2	309
111	Prognostic value of B cells in cutaneous melanoma. <i>Genome Medicine</i> , 2019 , 11, 36	14.4	46
110	The Immune Microenvironment in Hormone Receptor-Positive Breast Cancer Before and After Preoperative Chemotherapy. <i>Clinical Cancer Research</i> , 2019 , 25, 4644-4655	12.9	41
109	Androgen Receptor mRNA Expression in Urothelial Carcinoma of the Bladder: A Retrospective Analysis of Two Independent Cohorts. <i>Translational Oncology</i> , 2019 , 12, 661-668	4.9	8
108	FOXM1 Deubiquitination by USP21 Regulates Cell Cycle Progression and Paclitaxel Sensitivity in Basal-like Breast Cancer. <i>Cell Reports</i> , 2019 , 26, 3076-3086.e6	10.6	39
107	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsTData. <i>Cell Systems</i> , 2019 , 9, 24-34.e10	10.6	64
106	Genetic determinants of the molecular portraits of epithelial cancers. <i>Nature Communications</i> , 2019 , 10, 5666	17.4	8
105	PAM50 Molecular Intrinsic Subtypes in the NursesTHealth Study Cohorts. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 798-806	4	8

104	Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas. <i>Cancer Causes and Control</i> , 2019 , 30, 31-39	2.8	7
103	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. <i>Frontiers in Oncology</i> , 2018 , 8, 584	5.3	9
102	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
101	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
100	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
99	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.	e5162 2	133
98	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
97	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
96	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
95	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
94	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
93	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
92	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
91	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
90	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-2	2 26. @3	56
89	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
88	Intratumor Heterogeneity of the Estrogen Receptor and the Long-term Risk of Fatal Breast Cancer. Journal of the National Cancer Institute, 2018 , 110, 726-733	9.7	27
87	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. <i>Clinical Cancer Research</i> , 2018 , 24, 1845-1852	12.9	47

86	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10	24.3	150
85	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. <i>Nature Medicine</i> , 2018 , 24, 628-637	50.5	410
84	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
83	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018 , 33, 706-720.e9	24.3	275
82	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-68	8 9.æ3	377
81	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8	324.3	228
80	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
79	National Cancer Institute Biospecimen Evidence-Based Practices: Harmonizing Procedures for Nucleic Acid Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. <i>Biopreservation and Biobanking</i> , 2018 , 16, 247-250	2.1	7
78	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
77	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. <i>Cell Reports</i> , 2018 , 24, 1434-1444.e7	10.6	43
76	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
75	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. <i>Oncolmmunology</i> , 2018 , 7, e1490854	7.2	129
74	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406	5 10.6	200
73	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
72	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. <i>Cancer Causes and Control</i> , 2018 , 29, 25-32	2.8	8
71	Racial Differences in PAM50 Subtypes in the Carolina Breast Cancer Study. <i>Journal of the National Cancer Institute</i> , 2018 , 110,	9.7	62
70	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
69	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258

68	TP53 protein levels, RNA-based pathway assessment, and race among invasive breast cancer cases. <i>Npj Breast Cancer</i> , 2018 , 4, 13	7.8	9
67	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
66	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
65	Impact of Molecular Subtypes in Muscle-invasive Bladder Cancer on Predicting Response and Survival after Neoadjuvant Chemotherapy. <i>European Urology</i> , 2017 , 72, 544-554	10.2	411
64	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017 , 3, 1654-1662	13.4	146
63	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
62	Age at diagnosis, obesity, smoking, and molecular subtypes in muscle-invasive bladder cancer. <i>Cancer Causes and Control</i> , 2017 , 28, 539-544	2.8	12
61	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
60	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
59	Nuclear Localized LSR: A Novel Regulator of Breast Cancer Behavior and Tumorigenesis. <i>Molecular Cancer Research</i> , 2017 , 15, 165-178	6.6	17
58	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.	& 2552	961
57	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
56	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-2	. 03.e 1	3 896
55	Use of Molecular Tools to Identify Patients With Indolent Breast Cancers With Ultralow Risk Over 2 Decades. <i>JAMA Oncology</i> , 2017 , 3, 1503-1510	13.4	53
54	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , 2017 , 241, 375-391	9.4	62
53	Quantitative MRI radiomics in the prediction of molecular classifications of breast cancer subtypes in the TCGA/TCIA data set. <i>Npj Breast Cancer</i> , 2016 , 2,	7.8	200
52	Bladder Cancer Molecular Taxonomy: Summary from a Consensus Meeting. <i>Bladder Cancer</i> , 2016 , 2, 37-4	47	134
51	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	187

50	Identification of mRNA isoform switching in breast cancer. BMC Genomics, 2016, 17, 181	4.5	19
49	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
48	Molecular Heterogeneity and Response to Neoadjuvant Human Epidermal Growth Factor Receptor 2 Targeting in CALGB 40601, a Randomized Phase III Trial of Paclitaxel Plus Trastuzumab With or Without Lapatinib. <i>Journal of Clinical Oncology</i> , 2016 , 34, 542-9	2.2	242
47	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. JCI Insight, 2016 , 1, e88755	9.9	37
46	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
45	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. <i>Npj Breast Cancer</i> , 2016 , 2, 16007	7.8	25
44	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-	- 73.6 .3	324
43	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
42	MR Imaging Radiomics Signatures for Predicting the Risk of Breast Cancer Recurrence as Given by Research Versions of MammaPrint, Oncotype DX, and PAM50 Gene Assays. <i>Radiology</i> , 2016 , 281, 382-3	9 ^{20.5}	297
41	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
40	Proteomic profiling of patient-derived glioblastoma xenografts identifies a subset with activated EGFR: implications for drug development. <i>Journal of Neurochemistry</i> , 2015 , 133, 730-8	6	10
39	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
38	Virtual microdissection identifies distinct tumor- and stroma-specific subtypes of pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2015 , 47, 1168-78	36.3	893
37	Oncometabolite D-2-Hydroxyglutarate Inhibits ALKBH DNA Repair Enzymes and Sensitizes IDH Mutant Cells to Alkylating Agents. <i>Cell Reports</i> , 2015 , 13, 2353-2361	10.6	115
36	Update on The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. <i>European Urology Focus</i> , 2015 , 1, 94-95	5.1	4
35	Response and survival of breast cancer intrinsic subtypes following multi-agent neoadjuvant chemotherapy. <i>BMC Medicine</i> , 2015 , 13, 303	11.4	87
34	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
33	Overexpression of miR-146a in basal-like breast cancer cells confers enhanced tumorigenic potential in association with altered p53 status. <i>Carcinogenesis</i> , 2014 , 35, 2567-75	4.6	37

32	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
31	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
30	Molecular features of the basal-like breast cancer subtype based on BRCA1 mutation status. <i>Breast Cancer Research and Treatment</i> , 2014 , 147, 185-91	4.4	33
29	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, 3110-5	11.5	537
28	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. <i>Nucleic Acids Research</i> , 2014 , 42, e107	20.1	59
27	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
26	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013 , 141, 409-20	4.4	90
25	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2013 , 368, 2059-74	59.2	3137
24	Impact of tumor microenvironment and epithelial phenotypes on metabolism in breast cancer. <i>Clinical Cancer Research</i> , 2013 , 19, 571-85	12.9	73
23	JOINT AND INDIVIDUAL VARIATION EXPLAINED (JIVE) FOR INTEGRATED ANALYSIS OF MULTIPLE DATA TYPES. <i>Annals of Applied Statistics</i> , 2013 , 7, 523-542	2.1	239
22	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013 , 123, 517-25	15.9	371
21	Molecular subtypes in head and neck cancer exhibit distinct patterns of chromosomal gain and loss of canonical cancer genes. <i>PLoS ONE</i> , 2013 , 8, e56823	3.7	204
20	miR-181d: a predictive glioblastoma biomarker that downregulates MGMT expression. <i>Neuro-Oncology</i> , 2012 , 14, 712-9	1	144
19	TBCRC 001: randomized phase II study of cetuximab in combination with carboplatin in stage IV triple-negative breast cancer. <i>Journal of Clinical Oncology</i> , 2012 , 30, 2615-23	2.2	359
18	Targeting EGFR induced oxidative stress by PARP1 inhibition in glioblastoma therapy. <i>PLoS ONE</i> , 2010 , 5, e10767	3.7	51
17	Potential tumor suppressor role for the c-Myb oncogene in luminal breast cancer. <i>PLoS ONE</i> , 2010 , 5, e13073	3.7	35
16	Lung squamous cell carcinoma mRNA expression subtypes are reproducible, clinically important, and correspond to normal cell types. <i>Clinical Cancer Research</i> , 2010 , 16, 4864-75	12.9	194
15	Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010 , 17, 98-110	24.3	47 ⁸ 2

LIST OF PUBLICATIONS

14	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. <i>Cancer Cell</i> , 2010 , 17, 510-22	24.3	1754
13	Molecular Signatures of Drug Resistance 2009 , 271-294		
12	Development of an immuno tandem mass spectrometry (iMALDI) assay for EGFR diagnosis. <i>Proteomics - Clinical Applications</i> , 2007 , 1, 1651-9	3.1	51
11	RNA expression analysis of formalin-fixed paraffin-embedded tumors. <i>Laboratory Investigation</i> , 2007 , 87, 383-91	5.9	136
10	EGFR associated expression profiles vary with breast tumor subtype. <i>BMC Genomics</i> , 2007 , 8, 258	4.5	208
9	Gene expression patterns associated with p53 status in breast cancer. <i>BMC Cancer</i> , 2006 , 6, 276	4.8	107
8	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
7	Cell-type-specific responses to chemotherapeutics in breast cancer. Cancer Research, 2004, 64, 4218-26	5 10.1	307
6	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
5	A Consensus Molecular Classification of Muscle-Invasive Bladder Cancer. SSRN Electronic Journal,	1	8
4	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10
3	An approach for normalization and quality control for NanoString RNA expression data		3
2	The consensus molecular classification of muscle-invasive bladder cancer		6
1	Tumor mutational landscape is a record of the pre-malignant state		8