Katherine A Hoadley

List of Publications by Year
in descending order

142 papers	62,861 citations	5876 81 h-index	9073 144 g-index
153 all docs	153 docs citations	153 times ranked	71555 citing authors

#	Article	IF	Citations
1	TP53 Pathway Function, Estrogen Receptor Status, and Breast Cancer Risk Factors in the Carolina Breast Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 124-131.	1.1	2
2	Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression. Breast Cancer Research and Treatment, 2022, 192, 447-455.	1.1	1
3	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. Journal of Clinical Oncology, 2022, 40, 1323-1334.	0.8	62
4	Bidimensional linked matrix factorization for pan-omics pan-cancer analysis. Annals of Applied Statistics, 2022, 16, 193-215.	0.5	9
5	The landscape of immune microenvironments in racially-diverse breast cancer patients. Cancer Epidemiology Biomarkers and Prevention, 2022, , .	1.1	7
6	Spatial Characterization of Tumor-Infiltrating Lymphocytes and Breast Cancer Progression. Cancers, 2022, 14, 2148.	1.7	22
7	Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases. Npj Breast Cancer, 2022, 8, .	2.3	1
8	Prognostic and predictive implications of the intrinsic subtypes and gene expression signatures in early-stage HER2+ breast cancer: A pooled analysis of CALGB 40601, NeoALTTO, and NSABP B-41 trials.. Journal of Clinical Oncology, 2022, 40, 509-509.	0.8	4
9	A hierarchical spike-and-slab model for pan-cancer survival using pan-omic data. BMC Bioinformatics, 2022, 23, .	1.2	0
10	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. JNCI Cancer Spectrum, 2021, 5, pkaa072.	1.4	14
11	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. Cancer Cell, 2021, 39, 38-53.e7.	7.7	65
12	An approach for normalization and quality control for NanoString RNA expression data. Briefings in Bioinformatics, 2021, 22, .	3.2	67
13	SCISSOR: a framework for identifying structural changes in RNA transcripts. Nature Communications, 2021, 12, 286.	5.8	10
14	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	2.9	16
15	Protein-based immune profiles of basal-like vs. luminal breast cancers. Laboratory Investigation, 2021, 101, 785-793.	1.7	9
16	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	7.7	189
17	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	7.7	327
18	Identification of a Novel Inflamed Tumor Microenvironment Signature as a Predictive Biomarker of Bacillus Calmette-Guérin Immunotherapy in Non–Muscle-Invasive Bladder Cancer. Clinical Cancer Research, 2021, 27, 4599-4609.	3.2	26

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19	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. STAR Protocols, 2021, 2, 100483.	0.5	2
20	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
21	Hepatocyte growth factor pathway expression in breast cancer by race and subtype. Breast Cancer Research, 2021, 23, 80.	2.2	2
22	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
23	Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. Communications Biology, 2021, 4, 1150.	2.0	6
24	UNMASC: tumor-only variant calling with unmatched normal controls. NAR Cancer, 2021, 3, zcab040.	1.6	4
25	Joint and individual analysis of breast cancer histologic images and genomic covariates. Annals of Applied Statistics, 2021, 15, 1697-1722.	0.5	4
26	Molecular analysis of TCGA breast cancer histologic types. Cell Genomics, 2021, 1, 100067.	3.0	37
27	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. European Urology, 2020, 77, 420-433.	0.9	741
28	Gain-of-Function *RHOA* Mutations Promote Focal Adhesion Kinase Activation and Dependency in Diffuse Gastric Cancer. Cancer Discovery, 2020, 10, 288-305.	7.7	91
29	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.	0.8	74
30	A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival. Cancer Informatics, 2020, 19, 117693512090739.	0.9	2
31	Reply To Kenneth B. Yatai, Mark J. Dunning, Dennis Wang. Consensus Genomic Subtypes of Muscle-invasive Bladder Cancer: A Step in the Right Direction but Still a Long Way To Go. Eur Urol 2020;77:434â€"5. European Urology, 2020, 77, 436-438.	0.9	1
32	Virus expression detection reveals RNA-sequencing contamination in TCGA. BMC Genomics, 2020, 21, 79.	1.2	21
33	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
34	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	7.7	151
35	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. PLoS Biology, 2020, 18, e3000975.	2.6	7
36	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	2.9	103

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37	Prognostic value of B cells in cutaneous melanoma. Genome Medicine, 2019, 11, 36.	3.6	81
38	The Immune Microenvironment in Hormone Receptorâ€"Positive Breast Cancer Before and After Preoperative Chemotherapy. Clinical Cancer Research, 2019, 25, 4644-4655.	3.2	76
39	Androgen Receptor mRNA Expression in Urothelial Carcinoma of the Bladder: A Retrospective Analysis of Two Independent Cohorts. Translational Oncology, 2019, 12, 661-668.	1.7	16
40	FOXM1 Deubiquitination by USP21 Regulates Cell Cycle Progression and Paclitaxel Sensitivity in Basal-like Breast Cancer. Cell Reports, 2019, 26, 3076-3086.e6.	2.9	60
41	Genetic determinants of the molecular portraits of epithelial cancers. Nature Communications, 2019, 10, 5666.	5.8	21
42	PAM50 Molecular Intrinsic Subtypes in the Nurses' Health Study Cohorts. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 798-806.	1.1	26
43	Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas. Cancer Causes and Control, 2019, 30, 31-39.	0.8	14
44	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
45	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
46	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
47	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
48	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
49	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
50	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
51	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
52	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
53	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
54	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683

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55	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
56	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
57	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
58	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.	3.0	55
59	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. Clinical Cancer Research, 2018, 24, 1845-1852.	3.2	84
60	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
61	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. Nature Medicine, 2018, 24, 628-637.	15.2	649
62	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
63	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
64	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
65	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
66	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
67	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. Cancer Causes and Control, 2018, 29, 25-32.	0.8	9
68	Racial Differences in PAM50 Subtypes in the Carolina Breast Cancer Study. Journal of the National Cancer Institute, 2018, 110, 176-182.	3.0	104
69	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	6.0	781
70	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	7.7	422
71	TP53 protein levels, RNA-based pathway assessment, and race among invasive breast cancer cases. Npj Breast Cancer, 2018, 4, 13.	2.3	18
72	National Cancer Institute Biospecimen Evidence-Based Practices: Harmonizing Procedures for Nucleic Acid Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. Biopreservation and Biobanking, 2018, 16, 247-250.	0.5	11

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73	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
74	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. Cell Reports, 2018, 24, 1434-1444.e7.	2.9	73
75	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.	3.2	73
76	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. OncoImmunology, 2018, 7, e1490854.	2.1	200
77	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
78	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	1.3	14
79	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. Journal of Clinical Investigation, 2018, 128, 1371-1383.	3.9	126
80	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	7.7	532
81	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. Breast Cancer Research and Treatment, 2017, 162, 439-450.	1.1	47
82	Impact of Molecular Subtypes in Muscle-invasive Bladder Cancer on Predicting Response and Survival after Neoadjuvant Chemotherapy. European Urology, 2017, 72, 544-554.	0.9	638
83	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. JAMA Oncology, 2017, 3, 1654.	3.4	208
84	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
85	Age at diagnosis, obesity, smoking, and molecular subtypes in muscle-invasive bladder cancer. Cancer Causes and Control, 2017, 28, 539-544.	0.8	14
86	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
87	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
88	Nuclear Localized LSR: A Novel Regulator of Breast Cancer Behavior and Tumorigenesis. Molecular Cancer Research, 2017, 15, 165-178.	1.5	23
89	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
90	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642

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91	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
92	Use of Molecular Tools to Identify Patients With Indolent Breast Cancers With Ultralow Risk Over 2 Decades. JAMA Oncology, 2017, 3, 1503.	3.4	91
93	The molecular basis of breast cancer pathological phenotypes. Journal of Pathology, 2017, 241, 375-391.	2.1	86
94	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine, 2016, 13, e1002174.	3.9	86
95	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. Npj Breast Cancer, 2016, 2, 16007.	2.3	33
96	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
97	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
98	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. Radiology, 2016, 281, 382-391.	3.6	387
99	Quantitative MRI radiomics in the prediction of molecular classifications of breast cancer subtypes in the TCGA/TCIA data set. Npj Breast Cancer, 2016, 2, .	2.3	266
100	Bladder Cancer Molecular Taxonomy: Summary from a Consensus Meeting. Bladder Cancer, 2016, 2, 37-47.	0.2	184
101	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. Journal of the National Cancer Institute, 2016, 108, djw144.	3.0	271
102	Identification of mRNA isoform switching in breast cancer. BMC Genomics, 2016, 17, 181.	1.2	27
103	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
104	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. Journal of Clinical Oncology, 2016, 34, 542-549.	0.8	336
105	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. JCI Insight, 2016, 1, e88755.	2.3	51
106	Oncometabolite D-2-Hydroxyglutarate Inhibits ALKBH DNA Repair Enzymes and Sensitizes IDH Mutant Cells to Alkylating Agents. Cell Reports, 2015, 13, 2353-2361.	2.9	153
107	The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. European Urology Focus, 2015, 1, 94-95.	1.6	7
108	Response and survival of breast cancer intrinsic subtypes following multi-agent neoadjuvant chemotherapy. BMC Medicine, 2015, 13, 303.	2.3	113

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109	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
110	Proteomic profiling of patientâ€derived glioblastoma xenografts identifies a subset with activated <scp>EGFR</scp>: implications for drug development. Journal of Neurochemistry, 2015, 133, 730-738.	2.1	11
111	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
112	Virtual microdissection identifies distinct tumor- and stroma-specific subtypes of pancreatic ductal adenocarcinoma. Nature Genetics, 2015, 47, 1168-1178.	9.4	1,491
113	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
114	Prognostic B-cell Signatures Using mRNA-Seq in Patients with Subtype-Specific Breast and Ovarian Cancer. Clinical Cancer Research, 2014, 20, 3818-3829.	3.2	230
115	Overexpression of miR-146a in basal-like breast cancer cells confers enhanced tumorigenic potential in association with altered p53 status. Carcinogenesis, 2014, 35, 2567-2575.	1.3	43
116	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
117	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. BMC Genomics, 2014, 15, 419.	1.2	262
118	Molecular features of the basal-like breast cancer subtype based on BRCA1 mutation status. Breast Cancer Research and Treatment, 2014, 147, 185-191.	1.1	37
119	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.	3.3	736
120	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. Nucleic Acids Research, 2014, 42, e107-e107.	6.5	76
121	The molecular diversity of Luminal A breast tumors. Breast Cancer Research and Treatment, 2013, 141, 409-420.	1.1	120
122	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
123	Impact of Tumor Microenvironment and Epithelial Phenotypes on Metabolism in Breast Cancer. Clinical Cancer Research, 2013, 19, 571-585.	3.2	84
124	Joint and individual variation explained (JIVE) for integrated analysis of multiple data types. Annals of Applied Statistics, 2013, 7, 523-542.	0.5	367
125	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. Journal of Clinical Investigation, 2013, 123, 517-25.	3.9	462
126	Molecular Subtypes in Head and Neck Cancer Exhibit Distinct Patterns of Chromosomal Gain and Loss of Canonical Cancer Genes. PLoS ONE, 2013, 8, e56823.	1.1	263

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127	miR-181d: a predictive glioblastoma biomarker that downregulates MGMT expression. Neuro-Oncology, 2012, 14, 712-719.	0.6	167
128	TBCRC 001: Randomized Phase II Study of Cetuximab in Combination With Carboplatin in Stage IV Triple-Negative Breast Cancer. Journal of Clinical Oncology, 2012, 30, 2615-2623.	0.8	413
129	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
130	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	7.7	2,078
131	Targeting EGFR Induced Oxidative Stress by PARP1 Inhibition in Glioblastoma Therapy. PLoS ONE, 2010, 5, e10767.	1.1	59
132	Potential Tumor Suppressor Role for the c-Myb Oncogene in Luminal Breast Cancer. PLoS ONE, 2010, 5, e13073.	1.1	40
133	Lung Squamous Cell Carcinoma mRNA Expression Subtypes Are Reproducible, Clinically Important, and Correspond to Normal Cell Types. Clinical Cancer Research, 2010, 16, 4864-4875.	3.2	259
134	Molecular Signatures of Drug Resistance. , 2009, , 271-294.		0
135	Development of an immuno tandem mass spectrometry (iMALDI) assay for EGFR diagnosis. Proteomics - Clinical Applications, 2007, 1, 1651-1659.	0.8	56
136	RNA expression analysis of formalin-fixed paraffin-embedded tumors. Laboratory Investigation, 2007, 87, 383-391.	1.7	151
137	EGFR associated expression profiles vary with breast tumor subtype. BMC Genomics, 2007, 8, 258.	1.2	234
138	Gene expression patterns associated with p53 status in breast cancer. BMC Cancer, 2006, 6, 276.	1.1	128
139	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. Environmental Health Perspectives, 2004, 112, 1607-1613.	2.8	17
140	Cell-Type-Specific Responses to Chemotherapeutics in Breast Cancer. Cancer Research, 2004, 64, 4218-4226.	0.4	321
141	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. Environmental Health Perspectives, 2004, 112, 1607-1613.	2.8	21
142	A Consensus Molecular Classification of Muscle-Invasive Bladder Cancer. SSRN Electronic Journal, 0, , .	0.4	9