Katherine A Hoadley

List of Publications by Citations

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

#	Paper	IF	Citations
139	Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1. *Cancer Cell*, **2010**, 17, 98-110	24.3	4782
138	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
137	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
136	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
135	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. *Cancer Cell*, **2010**, 17, 510-22	24.3	1754
134	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
133	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
132	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
131	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
130	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
129	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
128	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.5	896
127	Virtual microdissection identifies distinct tumor- and stroma-specific subtypes of pancreatic ductal adenocarcinoma. *Nature Genetics*, **2015**, 47, 1168-78	36.3	893
126	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
125	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
124	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
123	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. *Nature Genetics*, **2016**, 48, 607-16	36.3	613

122	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
121	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
120	Impact of Molecular Subtypes in Muscle-invasive Bladder Cancer on Predicting Response and Survival after Neoadjuvant Chemotherapy. *European Urology*, **2017**, 72, 544-554	10.2	411
119	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. *Nature Medicine*, **2018**, 24, 628-637	50.5	410
118	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
117	The chromatin accessibility landscape of primary human cancers. *Science*, **2018**, 362,	33.3	392
116	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
115	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
114	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 517-25	15.9	371
113	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
112	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, 2615-23	2.2	359
111	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, **2017**, 31, 181-193	24.3	350
110	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
109	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
108	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
107	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. *European Urology*, **2020**, 77, 420-433	10.2	309
106	Cell-type-specific responses to chemotherapeutics in breast cancer. *Cancer Research*, **2004**, 64, 4218-26	10.1	307
105	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	20.5	297

104	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
103	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
102	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	24.3	275
101	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
100	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
99	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, 542-9	2.2	242
98	JOINT AND INDIVIDUAL VARIATION EXPLAINED (JIVE) FOR INTEGRATED ANALYSIS OF MULTIPLE DATA TYPES. *Annals of Applied Statistics*, **2013**, 7, 523-542	2.1	239
97	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
96	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
95	EGFR associated expression profiles vary with breast tumor subtype. *BMC Genomics*, **2007**, 8, 258	4.5	208
94	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. *BMC Genomics*, **2014**, 15, 419	4.5	204
93	Molecular subtypes in head and neck cancer exhibit distinct patterns of chromosomal gain and loss of canonical cancer genes. *PLoS ONE*, **2013**, 8, e56823	3.7	204
92	Quantitative MRI radiomics in the prediction of molecular classifications of breast cancer subtypes in the TCGA/TCIA data set. *Npj Breast Cancer*, **2016**, 2,	7.8	200
91	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
90	Lung squamous cell carcinoma mRNA expression subtypes are reproducible, clinically important, and correspond to normal cell types. *Clinical Cancer Research*, **2010**, 16, 4864-75	12.9	194
89	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
88	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	187
87	Prognostic B-cell signatures using mRNA-seq in patients with subtype-specific breast and ovarian cancer. *Clinical Cancer Research*, **2014**, 20, 3818-29	12.9	168

86	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
85	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
84	Genomic basis for RNA alterations in cancer. *Nature*, **2020**, 578, 129-136	50.4	148
83	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. *JAMA Oncology*, **2017**, 3, 1654-1662	13.4	146
82	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
81	miR-181d: a predictive glioblastoma biomarker that downregulates MGMT expression. *Neuro-Oncology*, **2012**, 14, 712-9	1	144
80	RNA expression analysis of formalin-fixed paraffin-embedded tumors. *Laboratory Investigation*, **2007**, 87, 383-91	5.9	136
79	Bladder Cancer Molecular Taxonomy: Summary from a Consensus Meeting. *Bladder Cancer*, **2016**, 2, 37-47	1	134
78	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
77	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. *OncoImmunology*, **2018**, 7, e1490854	7.2	129
76	Oncometabolite D-2-Hydroxyglutarate Inhibits ALKBH DNA Repair Enzymes and Sensitizes IDH Mutant Cells to Alkylating Agents. *Cell Reports*, **2015**, 13, 2353-2361	10.6	115
75	Gene expression patterns associated with p53 status in breast cancer. *BMC Cancer*, **2006**, 6, 276	4.8	107
74	The molecular diversity of Luminal A breast tumors. *Breast Cancer Research and Treatment*, **2013**, 141, 409-20	4.4	90
73	Response and survival of breast cancer intrinsic subtypes following multi-agent neoadjuvant chemotherapy. *BMC Medicine*, **2015**, 13, 303	11.4	87
72	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. *Journal of Clinical Investigation*, **2018**, 128, 1371-1383	15.9	83
71	Impact of tumor microenvironment and epithelial phenotypes on metabolism in breast cancer. *Clinical Cancer Research*, **2013**, 19, 571-85	12.9	73
70	Proteogenomic and metabolomic characterization of human glioblastoma. *Cancer Cell*, **2021**, 39, 509-528.e20	44.5	71
69	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsTData. *Cell Systems*, **2019**, 9, 24-34.e10	10.6	64

68	The molecular basis of breast cancer pathological phenotypes. *Journal of Pathology*, **2017**, 241, 375-391	9.4	62
67	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. *PLoS Medicine*, **2016**, 13, e1002174	11.6	62
66	Racial Differences in PAM50 Subtypes in the Carolina Breast Cancer Study. *Journal of the National Cancer Institute*, **2018**, 110,	9.7	62
65	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. *Nucleic Acids Research*, **2014**, 42, e107	20.1	59
64	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226	26.3	56
63	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. *Cancer Cell*, **2020**, 37, 639-654.e6	24.3	56
62	Use of Molecular Tools to Identify Patients With Indolent Breast Cancers With Ultralow Risk Over 2 Decades. *JAMA Oncology*, **2017**, 3, 1503-1510	13.4	53
61	Targeting EGFR induced oxidative stress by PARP1 inhibition in glioblastoma therapy. *PLoS ONE*, **2010**, 5, e10767	3.7	51
60	Development of an immuno tandem mass spectrometry (iMALDI) assay for EGFR diagnosis. *Proteomics - Clinical Applications*, **2007**, 1, 1651-9	3.1	51
59	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. *Cancer Cell*, **2021**, 39, 361-379.e16	24.3	50
58	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	12.9	47
57	Prognostic value of B cells in cutaneous melanoma. *Genome Medicine*, **2019**, 11, 36	14.4	46
56	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. *Cell Reports*, **2018**, 24, 1434-1444.e7	10.6	43
55	The Immune Microenvironment in Hormone Receptor-Positive Breast Cancer Before and After Preoperative Chemotherapy. *Clinical Cancer Research*, **2019**, 25, 4644-4655	12.9	41
54	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	12.9	41
53	Gain-of-Function Mutations Promote Focal Adhesion Kinase Activation and Dependency in Diffuse Gastric Cancer. *Cancer Discovery*, **2020**, 10, 288-305	24.4	41
52	FOXM1 Deubiquitination by USP21 Regulates Cell Cycle Progression and Paclitaxel Sensitivity in Basal-like Breast Cancer. *Cell Reports*, **2019**, 26, 3076-3086.e6	10.6	39
51	Overexpression of miR-146a in basal-like breast cancer cells confers enhanced tumorigenic potential in association with altered p53 status. *Carcinogenesis*, **2014**, 35, 2567-75	4.6	37

50	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. *JCI Insight*, **2016**, 1, e88755	9.9	37
49	Potential tumor suppressor role for the c-Myb oncogene in luminal breast cancer. *PLoS ONE*, **2010**, 5, e13073	3.7	35
48	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. *Breast Cancer Research and Treatment*, **2017**, 162, 439-450	4.4	34
47	Molecular features of the basal-like breast cancer subtype based on BRCA1 mutation status. *Breast Cancer Research and Treatment*, **2014**, 147, 185-91	4.4	33
46	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	2.2	28
45	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
44	Proteogenomic characterization of pancreatic ductal adenocarcinoma. *Cell*, **2021**, 184, 5031-5052.e26	56.2	26
43	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. *Npj Breast Cancer*, **2016**, 2, 16007	7.8	25
42	Identification of mRNA isoform switching in breast cancer. *BMC Genomics*, **2016**, 17, 181	4.5	19
41	Prediction of Toxicant-Specific Gene Expression Signatures after Chemotherapeutic Treatment of Breast Cell Lines. *Environmental Health Perspectives*, **2004**, 112, 1607-1613	8.4	18
40	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. *Cancer Cell*, **2021**, 39, 38-53.e7	24.3	18
39	Nuclear Localized LSR: A Novel Regulator of Breast Cancer Behavior and Tumorigenesis. *Molecular Cancer Research*, **2017**, 15, 165-178	6.6	17
38	An approach for normalization and quality control for NanoString RNA expression data. *Briefings in Bioinformatics*, **2021**, 22,	13.4	15
37	A proteogenomic portrait of lung squamous cell carcinoma. *Cell*, **2021**, 184, 4348-4371.e40	56.2	15
36	Age at diagnosis, obesity, smoking, and molecular subtypes in muscle-invasive bladder cancer. *Cancer Causes and Control*, **2017**, 28, 539-544	2.8	12
35	Prediction of toxicant-specific gene expression signatures after chemotherapeutic treatment of breast cell lines. *Environmental Health Perspectives*, **2004**, 112, 1607-13	8.4	12
34	Proteomic profiling of patient-derived glioblastoma xenografts identifies a subset with activated EGFR: implications for drug development. *Journal of Neurochemistry*, **2015**, 133, 730-8	6	10
33	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10

32	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. *Frontiers in Oncology*, **2018**, 8, 584	5.3	9
31	TP53 protein levels, RNA-based pathway assessment, and race among invasive breast cancer cases. *Npj Breast Cancer*, **2018**, 4, 13	7.8	9
30	Androgen Receptor mRNA Expression in Urothelial Carcinoma of the Bladder: A Retrospective Analysis of Two Independent Cohorts. *Translational Oncology*, **2019**, 12, 661-668	4.9	8
29	A Consensus Molecular Classification of Muscle-Invasive Bladder Cancer. *SSRN Electronic Journal*,	1	8
28	Tumor mutational landscape is a record of the pre-malignant state		8
27	Genetic determinants of the molecular portraits of epithelial cancers. *Nature Communications*, **2019** , 10, 5666	17.4	8
26	PAM50 Molecular Intrinsic Subtypes in the NursesTHealth Study Cohorts. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 798-806	4	8
25	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. *Cancer Causes and Control*, **2018**, 29, 25-32	2.8	8
24	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	2.1	7
23	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**, JCO2101506	2.2	7
22	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	2.8	7
21	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. *Cell Reports*, **2021**, 34, 108707	10.6	7
20	Virus expression detection reveals RNA-sequencing contamination in TCGA. *BMC Genomics*, **2020**, 21, 79	4.5	6
19	The consensus molecular classification of muscle-invasive bladder cancer		6
18	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. *PLoS Biology*, **2020**, 18, e3000975	9.7	5
17	Update on The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. *European Urology Focus*, **2015**, 1, 94-95	5.1	4
16	Identification of a Novel Inflamed Tumor Microenvironment Signature as a Predictive Biomarker of Bacillus Calmette-Guﬁn Immunotherapy in Non-Muscle-Invasive Bladder Cancer. *Clinical Cancer Research*, **2021**, 27, 4599-4609	12.9	4
15	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

List of Publications

14	An approach for normalization and quality control for NanoString RNA expression data		3
13	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. *JNCI Cancer Spectrum*, **2021**, 5, pkaa072	4.6	3
12	UNMASC: tumor-only variant calling with unmatched normal controls. *NAR Cancer*, **2021**, 3, zcab040	5.2	2
11	SCISSOR: a framework for identifying structural changes in RNA transcripts. *Nature Communications* , **2021**, 12, 286	17.4	2
10	Protein-based immune profiles of basal-like vs. luminal breast cancers. *Laboratory Investigation*, **2021**, 101, 785-793	5.9	2
9	JOINT AND INDIVIDUAL ANALYSIS OF BREAST CANCER HISTOLOGIC IMAGES AND GENOMIC COVARIATES.. *Annals of Applied Statistics*, **2021**, 15, 1697-1722	2.1	2
8	Spatial Characterization of Tumor-Infiltrating Lymphocytes and Breast Cancer Progression.. *Cancers* , **2022**, 14,	6.6	2
7	A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival. *Cancer Informatics*, **2020**, 19, 1176935120907399	2.4	1
6	Hepatocyte growth factor pathway expression in breast cancer by race and subtype. *Breast Cancer Research*, **2021**, 23, 80	8.3	1
5	Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. *Communications Biology*, **2021**, 4, 1150	6.7	0
4	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. *STAR Protocols*, **2021**, 2, 100483	1.4	0
3	BIDIMENSIONAL LINKED MATRIX FACTORIZATION FOR PAN-OMICS PAN-CANCER ANALYSIS.. *Annals of Applied Statistics*, **2022**, 16, 193-215	2.1	0
2	Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression.. *Breast Cancer Research and Treatment*, **2022**, 192, 447	4.4	
1	Molecular Signatures of Drug Resistance **2009**, 271-294		