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List of Publications by Citations

96 papers	25,190 citations	63 h-index	128 g-index
128 ext. papers	35,531 ext. citations	20 avg, IF	7.18 L-index

#	Paper	IF	Citations
96	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature*, **2012**, 486, 346-52	50.4	3479
95	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
94	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. *Nature*, **2012**, 486, 395-9	50.4	1417
93	ARID1A mutations in endometriosis-associated ovarian carcinomas. *New England Journal of Medicine*, **2010**, 363, 1532-43	59.2	1208
92	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
91	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
90	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
89	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
88	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
87	PyClone: statistical inference of clonal population structure in cancer. *Nature Methods*, **2014**, 11, 396-8	21.6	584
86	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
85	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. *Nature*, **2015**, 518, 422-6	50.4	451
84	deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. *PLoS Computational Biology*, **2011**, 7, e1001138	5	409
83	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
82	Patient-derived xenografts undergo mouse-specific tumor evolution. *Nature Genetics*, **2017**, 49, 1567-1575	36.3	384
81	Genetic and transcriptional evolution alters cancer cell line drug response. *Nature*, **2018**, 560, 325-330	50.4	379
80	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377

79	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
78	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. *Cancer Discovery*, **2016**, 6, 914-29	24.4	343
77	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
76	Recurrent somatic DICER1 mutations in nonepithelial ovarian cancers. *New England Journal of Medicine*, **2012**, 366, 234-42	59.2	332
75	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
74	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
73	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. *Nature Communications*, **2017**, 8, 1324	17.4	314
72	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
71	Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. *Journal of Pathology*, **2013**, 231, 21-34	9.4	292
70	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018** , 33, 690-705.e9	24.3	277
69	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
68	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
67	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
66	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. *Genome Research*, **2014**, 24, 1881-93	9.7	218
65	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. *Nature Genetics*, **2016**, 48, 758-67	36.3	209
64	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
63	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. *Genome Research*, **2012**, 22, 1995-2007	9.7	181
62	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. *Bioinformatics*, **2010**, 26, 730-6	7.2	174

61	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
60	Genomic Heterogeneity as a Barrier to Precision Medicine in Gastroesophageal Adenocarcinoma. *Cancer Discovery*, **2018**, 8, 37-48	24.4	162
59	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
58	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. *Genome Biology*, **2012**, 13, R124	18.3	156
57	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. *Cell*, **2018**, 174, 433-447.e19	56.2	155
56	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
55	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
54	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
53	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
52	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. *Nature Genetics*, **2017**, 49, 856-865	36.3	141
51	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. *Bioinformatics*, **2012**, 28, 907-13	7.2	136
50	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
49	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
48	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. *Journal of Clinical Oncology*, **2018**, 36, 543-553	2.2	113
47	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
46	Whole-exome sequencing of cell-free DNA and circulating tumor cells in multiple myeloma. *Nature Communications*, **2018**, 9, 1691	17.4	103
45	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. *Science Translational Medicine*, **2016**, 8, 363ra147	17.5	93
44	Multifocal endometriotic lesions associated with cancer are clonal and carry a high mutation burden. *Journal of Pathology*, **2015**, 236, 201-9	9.4	92

43	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
42	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. *Nature Communications*, **2015**, 6, 8554	17.4	71
41	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. *Cell Reports*, **2017**, 19, 218-224	10.6	67
40	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. *Cancer Discovery*, **2018**, 8, 108-125	24.4	67
39	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
38	Tumor growth inhibition by olaparib in BRCA2 germline-mutated patient-derived ovarian cancer tissue xenografts. *Clinical Cancer Research*, **2011**, 17, 783-91	12.9	64
37	Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring. *Nature Medicine*, **2020**, 26, 1114-1124	50.5	63
36	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. *Nature Genetics*, **2020**, 52, 790-799	36.3	62
35	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
34	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
33	Genomic and immune profiling of pre-invasive lung adenocarcinoma. *Nature Communications*, **2019**, 10, 5472	17.4	56
32	Combined TP53 and RB1 Loss Promotes Prostate Cancer Resistance to a Spectrum of Therapeutics and Confers Vulnerability to Replication Stress. *Cell Reports*, **2020**, 31, 107669	10.6	55
31	Tumor fraction in cell-free DNA as a biomarker in prostate cancer. *JCI Insight*, **2018**, 3,	9.9	49
30	Detection of circulating tumour DNA is associated with inferior outcomes in Ewing sarcoma and osteosarcoma: a report from the Children's Oncology Group. *British Journal of Cancer*, **2018**, 119, 615-621	8.7	47
29	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. *Nature Communications*, **2016**, 7, 12160	17.4	36
28	Detection of Somatic Structural Variants Enables Quantification and Characterization of Circulating Tumor DNA in Children With Solid Tumors. *JCO Precision Oncology*, **2018**, 2018,	3.6	36
27	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. *Clinical Cancer Research*, **2020**, 26, 2556-2564	12.9	32
26	Using next-generation sequencing for the diagnosis of rare disorders: a family with retinitis pigmentosa and skeletal abnormalities. *Journal of Pathology*, **2011**, 225, 12-8	9.4	26

25	-Mutated Prostate Cancer: Clinical Outcomes With Standard Therapies and Immune Checkpoint Blockade. *JCO Precision Oncology*, **2020**, 4, 382-392	3.6	26
24	Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. *Leukemia*, **2018**, 32, 1838-1841	10.7	24
23	Detection of Circulating Tumor DNA in Patients With Leiomyosarcoma With Progressive Disease. *JCO Precision Oncology*, **2019**, 2019,	3.6	22
22	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. *Cancer Discovery*, **2021**, 11, 591-598	24.4	20
21	ReMixT: clone-specific genomic structure estimation in cancer. *Genome Biology*, **2017**, 18, 140	18.3	18
20	An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. *Blood*, **2015**, 125, 959-66	2.2	18
19	Genomic distinctions between metastatic lower and upper tract urothelial carcinoma revealed through rapid autopsy. *JCI Insight*, **2019**, 5,	9.9	14
18	The Metastatic Breast Cancer (MBC) project: Accelerating translational research through direct patient engagement.. *Journal of Clinical Oncology*, **2017**, 35, 1076-1076	2.2	8
17	Whole-Exome Sequencing and Targeted Deep Sequencing of cfDNA Enables a Comprehensive Mutational Profiling of Multiple Myeloma. *Blood*, **2016**, 128, 197-197	2.2	7
16	Distinguishing somatic and germline copy number events in cancer patient DNA hybridized to whole-genome SNP genotyping arrays. *Methods in Molecular Biology*, **2013**, 973, 355-72	1.4	5
15	Mutation discovery in regions of segmental cancer genome amplifications with CoNAn-SNV: a mixture model for next generation sequencing of tumors. *PLoS ONE*, **2012**, 7, e41551	3.7	4
14	Liquid biopsy detection of genomic alterations in pediatric brain tumors from cell-free DNA in peripheral blood, CSF, and urine.. *Neuro-Oncology*, **2022**,	1	4
13	Multiplexed functional genomic analysis of 5Tuntranslated region mutations across the spectrum of prostate cancer. *Nature Communications*, **2021**, 12, 4217	17.4	4
12	Abstract 3247: Genome-wide cell-free DNA mutation integration for sensitive cancer detection **2018**,		3
11	Patient-derived xenografts undergo murine-specific tumor evolution		3
10	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. *Genome Medicine*, **2021**, 13, 114	14.4	2
9	Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma.. *Cell Reports Medicine*, **2022**, 3, 100500	18	2
8	GENE-07. LIQUID BIOPSY DETECTION OF GENOMIC ALTERATIONS IN PEDIATRIC BRAIN TUMORS FROM CELL-FREE DNA IN PERIPHERAL BLOOD, CSF, AND URINE. *Neuro-Oncology*, **2019**, 21, ii82-ii82	1	1

List of Publications

7	Tumor fraction in circulating free DNA as a biomarker of disease dynamics in metastatic prostate cancer.. *Journal of Clinical Oncology*, **2018**, 36, 195-195	2.2	1
6	Genomic attributes of homology-directed DNA repair deficiency in metastatic prostate cancer. *JCI Insight*, **2021**, 6,	9.9	1
5	DNA-based copy number analysis confirms genomic evolution of PDX models.. *Npj Precision Oncology*, **2022**, 6, 30	9.8	1
4	Modeling clonal structure over narrow time frames via circulating tumor DNA in metastatic breast cancer. *Genome Medicine*, **2021**, 13, 89	14.4	0
3	Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. *Npj Precision Oncology*, **2021**, 5, 83	9.8	0
2	Genome-wide copy number analysis of cell-free DNA from patients with chemotherapy-resistant metastatic triple-negative breast cancer.. *Journal of Clinical Oncology*, **2017**, 35, 1092-1092	2.2	
1	Large-Scale High Resolution Integration of Copy Number and Gene Expression in DLBCL Reveals Focal and Frequent Deletions in Chromatin Modifying Genes with Outcome Correlation. *Blood*, **2012**, 120, 295-295	2.2	