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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	28.9	2,660
2	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	27.8	2,586
3	Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden. Genome Medicine, 2017, 9, 34.	8.2	2,480
4	Clonal neoantigens elicit T cell immunoreactivity and sensitivity to immune checkpoint blockade. Science, 2016, 351, 1463-1469.	12.6	2,445
5	Genomic correlates of response to CTLA-4 blockade in metastatic melanoma. Science, 2015, 350, 207-211.	12.6	2,275
6	Defining a Cancer Dependency Map. Cell, 2017, 170, 564-576.e16.	28.9	1,794
7	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. Nature, 2005, 436, 117-122.	27.8	1,329
8	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. Nature Medicine, 2016, 22, 298-305.	30.7	1,193
9	Lessons from the Cancer Genome. Cell, 2013, 153, 17-37.	28.9	1,133
10	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. Cell, 2018, 175, 984-997.e24.	28.9	892
11	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	9.4	821
12	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865.	6.4	671
13	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	21.4	601
14	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. Cell, 2020, 180, 387-402.e16.	28.9	596
15	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	30.7	508
16	Somatic <i>ERCC2</i> Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. Cancer Discovery, 2014, 4, 1140-1153.	9.4	506
17	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. JAMA Oncology, 2015, 1, 653.	7.1	498
18	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	9.4	485

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19	High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing. Cancer Discovery, 2012, 2, 82-93.	9.4	484
20	A Melanoma Cell State Distinction Influences Sensitivity to MAPK Pathway Inhibitors. Cancer Discovery, 2014, 4, 816-827.	9.4	448
21	Circumventing Cancer Drug Resistance in the Era of Personalized Medicine. Cancer Discovery, 2012, 2, 214-226.	9.4	419
22	Increased Tumor Glycolysis Characterizes Immune Resistance to Adoptive T Cell Therapy. Cell Metabolism, 2018, 27, 977-987.e4.	16.2	398
23	<i>MTAP</i> deletion confers enhanced dependency on the PRMT5 arginine methyltransferase in cancer cells. Science, 2016, 351, 1214-1218.	12.6	396
24	<i>Ex Vivo</i> Profiling of PD-1 Blockade Using Organotypic Tumor Spheroids. Cancer Discovery, 2018, 8, 196-215.	9.4	392
25	RNF43 is frequently mutated in colorectal and endometrial cancers. Nature Genetics, 2014, 46, 1264-1266.	21.4	388
26	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
27	Institutional implementation of clinical tumor profiling on an unselected cancer population. JCI Insight, 2016, 1, e87062.	5.0	340
28	ARID1B is a specific vulnerability in ARID1A-mutant cancers. Nature Medicine, 2014, 20, 251-254.	30.7	336
29	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	16.8	323
30	Lineage dependency and lineage-survival oncogenes in human cancer. Nature Reviews Cancer, 2006, 6, 593-602.	28.4	316
31	Precision Oncology: An Overview. Journal of Clinical Oncology, 2013, 31, 1803-1805.	1.6	304
32	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	21.4	270
33	Acquired BRAF inhibitor resistance: A multicenter meta-analysis of the spectrum and frequencies, clinical behaviour, and phenotypic associations of resistance mechanisms. European Journal of Cancer, 2015, 51, 2792-2799.	2.8	269
34	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	17.5	257
35	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. Cancer Discovery, 2018, 8, 1096-1111.	9.4	256
36	Prostate cancer–associated SPOP mutations confer resistance to BET inhibitors through stabilization of BRD4. Nature Medicine, 2017, 23, 1063-1071.	30.7	240

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37	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. Cancer Cell, 2016, 29, 846-858.	16.8	228
38	Adaptive resistance of melanoma cells to <scp>RAF</scp> inhibition via reversible induction of a slowly dividing deâ€differentiated state. Molecular Systems Biology, 2017, 13, 905.	7.2	202
39	The Genomic Landscape of Intrinsic and Acquired Resistance to Cyclin-Dependent Kinase 4/6 Inhibitors in Patients with Hormone Receptor–Positive Metastatic Breast Cancer. Cancer Discovery, 2020, 10, 1174-1193.	9.4	176
40	gkmSVM: an R package for gapped-kmer SVM. Bioinformatics, 2016, 32, 2205-2207.	4.1	155
41	Future cancer research priorities in the USA: a Lancet Oncology Commission. Lancet Oncology, The, 2017, 18, e653-e706.	10.7	153
42	The impact of tumor profiling approaches and genomic data strategies for cancer precision medicine. Genome Medicine, 2016, 8, 79.	8.2	151
43	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. Cancer Cell, 2015, 27, 397-408.	16.8	150
44	IFNÎ ³ -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. Cell, 2017, 170, 127-141.e15.	28.9	140
45	Metabolomic adaptations and correlates of survival to immune checkpoint blockade. Nature Communications, 2019, 10, 4346.	12.8	139
46	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
47	Pediatric-type nodal follicular lymphoma: a biologically distinct lymphoma with frequent MAPK pathway mutations. Blood, 2016, 128, 1093-1100.	1.4	126
48	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. Nature Biotechnology, 2014, 32, 71-75.	17.5	120
49	Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. Cell Reports, 2016, 17, 1171-1183.	6.4	119
50	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. Cell, 2018, 173, 624-633.e8.	28.9	113
51	Oncologists' and cancer patients' views on whole-exome sequencing and incidental findings: results from the CanSeq study. Genetics in Medicine, 2016, 18, 1011-1019.	2.4	108
52	Systematic Functional Characterization of Resistance to PI3K Inhibition in Breast Cancer. Cancer Discovery, 2016, 6, 1134-1147.	9.4	106
53	Alternative to the soft-agar assay that permits high-throughput drug and genetic screens for cellular transformation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5708-5713.	7.1	105
54	Intermediate basal cells of the prostate: In vitro and in vivo characterization. Prostate, 2003, 55, 206-218.	2.3	97

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55	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. Cancer Discovery, 2017, 7, 973-983.	9.4	94
56	Inherited DNA-Repair Defects in Colorectal Cancer. American Journal of Human Genetics, 2018, 102, 401-414.	6.2	89
57	Binding of TMPRSS2-ERG to BAF Chromatin Remodeling Complexes Mediates Prostate Oncogenesis. Molecular Cell, 2018, 71, 554-566.e7.	9.7	77
58	MAPK Pathway Suppression Unmasks Latent DNA Repair Defects and Confers a Chemical Synthetic Vulnerability in <i>BRAF-, NRAS</i> -, and <i>NF1</i> -Mutant Melanomas. Cancer Discovery, 2019, 9, 526-545.	9.4	73
59	Genotyping Cancer-Associated Genes in Chordoma Identifies Mutations in Oncogenes and Areas of Chromosomal Loss Involving CDKN2A, PTEN, and SMARCB1. PLoS ONE, 2014, 9, e101283.	2.5	72
60	Prospective Enterprise-Level Molecular Genotyping of a Cohort of Cancer Patients. Journal of Molecular Diagnostics, 2014, 16, 660-672.	2.8	70
61	Rapid Intraoperative Molecular Characterization of Glioma. JAMA Oncology, 2015, 1, 662.	7.1	68
62	Long-term drug administration in the adult zebrafish using oral gavage for cancer preclinical studies. DMM Disease Models and Mechanisms, 2016, 9, 811-20.	2.4	61
63	Long-term Benefit of PD-L1 Blockade in Lung Cancer Associated with <i>JAK3</i> Activation. Cancer Immunology Research, 2015, 3, 855-863.	3.4	60
64	Combined Pan-RAF and MEK Inhibition Overcomes Multiple Resistance Mechanisms to Selective RAF Inhibitors. Molecular Cancer Therapeutics, 2015, 14, 2700-2711.	4.1	59
65	Truncating PREX2 mutations activate its GEF activity and alter gene expression regulation in NRAS-mutant melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1296-305.	7.1	59
66	A brain-penetrant RAF dimer antagonist for the noncanonical BRAF oncoprotein of pediatric low-grade astrocytomas. Neuro-Oncology, 2017, 19, now261.	1.2	55
67	Genetic modifiers of EGFR dependence in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18661-18666.	7.1	46
68	PLZF, a Tumor Suppressor Genetically Lost in Metastatic Castration-Resistant Prostate Cancer, Is a Mediator of Resistance to Androgen Deprivation Therapy. Cancer Research, 2015, 75, 1944-1948.	0.9	46
69	Assigning clinical meaning to somatic and germ-line whole-exome sequencing data in a prospective cancer precision medicine study. Genetics in Medicine, 2017, 19, 787-795.	2.4	46
70	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2015, 1, 238.	7.1	44
71	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. Cell Systems, 2017, 5, 105-118.e9.	6.2	40
72	Whole-Exome Sequencing in Two Extreme Phenotypes of Response to VEGF-Targeted Therapies in Patients With Metastatic Clear Cell Renal Cell Carcinoma. Journal of the National Comprehensive Cancer Network: INCCN. 2016. 14, 820-824.	4.9	36

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73	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	2.5	34
74	From Integrated Genomics to Tumor Lineage Dependency. Cancer Research, 2006, 66, 2506-2508.	0.9	27
75	Mechanisms of resistance (MoR) to DNA damaging therapy (tx) in BRCA1/2-deficient (d) metastatic breast cancer (MBC) Journal of Clinical Oncology, 2016, 34, 542-542.	1.6	27
76	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. Cancer Cell, 2022, 40, 524-544.e5.	16.8	23
77	Whole-Genome Sequencing and Cancer Therapy: Is Too Much Ever Enough?: Figure 1 Cancer Discovery, 2012, 2, 766-768.	9.4	19
78	Genetic Effect of Chemotherapy Exposure in Children of Testicular Cancer Survivors. Clinical Cancer Research, 2016, 22, 2183-2189.	7.0	15
79	The fuzzy world of precision medicine: deliberations of a precision medicine tumor board. Personalized Medicine, 2017, 14, 37-50.	1.5	15
80	Mechanisms of Resistance to Mitogen-Activated Protein Kinase Pathway Inhibition in BRAF-Mutant Melanoma. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2012, , 680-684.	3.8	7
81	Increased Local Disorder of DNA Methylation Forms the Basis of High Intra-Leukemic Epigenetic Heterogeneity and Enhances CLL Evolution. Blood, 2013, 122, 596-596.	1.4	4
82	On or Off Target: Mutations, Models, and Predictions. Science Translational Medicine, 2010, 2, 35ps28.	12.4	3
83	Inclusion of the ASH1 gene that governs the neuroendocrine differentiation of lung epithelium as an additional prototypic 'lineage-survival oncogene'. Nature Reviews Cancer, 2007, 7, 68-68.	28.4	Ο