Andrew D Cherniack

List of Publications by Year
in descending order

160 papers	108,209 citations	3731 89 h-index	8167 148 g-index
175 all docs	175 docs citations	175 times ranked	101735 citing authors

#	Article	IF	Citations
1	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
2	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
3	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
4	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
5	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
6	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
7	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
8	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
9	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
10	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
11	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
12	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
13	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
14	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
15	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
16	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	27.8	2,149
17	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
18	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966

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19	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
20	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
21	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
22	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
23	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
24	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	21.4	1,616
25	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
26	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
27	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
28	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
29	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	27.8	1,158
30	Activation of the PD-1 Pathway Contributes to Immune Escape in EGFR-Driven Lung Tumors. Cancer Discovery, 2013, 3, 1355-1363.	9.4	1,073
31	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
32	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	21.4	933
33	A Tumor Suppressor Complex with GAP Activity for the Rag GTPases That Signal Amino Acid Sufficiency to mTORC1. Science, 2013, 340, 1100-1106.	12.6	863
34	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
35	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	12.6	781
36	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750

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37	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
38	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	27.8	708
39	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
40	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
41	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
42	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
43	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
44	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
45	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
46	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
47	Interplay of somatic alterations and immune infiltration modulates response to PD-1 blockade in advanced clear cell renal cell carcinoma. Nature Medicine, 2020, 26, 909-918.	30.7	488
48	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	9.4	485
49	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
50	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
51	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
52	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
53	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
54	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.	16.8	400

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55	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
56	Mechanisms and therapeutic implications of hypermutation in gliomas. Nature, 2020, 580, 517-523.	27.8	374
57	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
58	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
59	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
60	Binding of the Ras activator son of sevenless to insulin receptor substrate-1 signaling complexes. Science, 1993, 260, 1950-1952.	12.6	303
61	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
62	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. Nature Genetics, 2016, 48, 176-182.	21.4	283
63	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
64	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
65	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
66	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
67	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. JAMA Oncology, 2017, 3, 1654.	7.1	208
68	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
69	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
70	Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. Cell, 2021, 184, 6119-6137.e26.	28.9	201
71	Suppression of oxidative metabolism and mitochondrial biogenesis by the transcriptional corepressor RIP140 in mouse adipocytes. Journal of Clinical Investigation, 2005, 116, 125-136.	8.2	198
72	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177

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73	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. Nature Genetics, 2016, 48, 848-855.	21.4	174
74	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. Nature Communications, 2018, 9, 5450.	12.8	157
75	The genomic landscape of tuberous sclerosis complex. Nature Communications, 2017, 8, 15816.	12.8	154
76	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
77	Diminished Efficacy of Programmed Death-(Ligand)1 Inhibition in STK11- and KEAP1-Mutant Lung Adenocarcinoma Is Affected by KRAS Mutation Status. Journal of Thoracic Oncology, 2022, 17, 399-410.	1.1	151
78	Loss of the retinoblastoma binding protein 2 (RBP2) histone demethylase suppresses tumorigenesis in mice lacking Rb1 or Men1. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13379-13386.	7.1	143
79	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
80	Molecular Mechanisms of Acquired Resistance to MET Tyrosine Kinase Inhibitors in Patients with MET Exon 14â€“Mutant NSCLC. Clinical Cancer Research, 2020, 26, 2615-2625.	7.0	129
81	Genomic and immune profiling of pre-invasive lung adenocarcinoma. Nature Communications, 2019, 10, 5472.	12.8	127
82	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
83	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
84	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. Cancer Discovery, 2018, 8, 108-125.	9.4	99
85	Impact of DNA Damage Response and Repair (DDR) Gene Mutations on Efficacy of PD-(L)1 Immune Checkpoint Inhibition in Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 4135-4142.	7.0	95
86	Disassembly of Son-of-sevenless Proteins from Grb2 during p21 Desensitization by Insulin. Journal of Biological Chemistry, 1995, 270, 1485-1488.	3.4	90
87	Sporadic Early-Onset Diffuse Gastric Cancers Have High Frequency of Somatic CDH1 Alterations, but Low Frequency of Somatic RHOA Mutations Compared With Late-Onset Cancers. Gastroenterology, 2017, 153, 536-549.e26.	1.3	90
88	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
89	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. Nature Communications, 2018, 9, 2024.	12.8	80
90	Function of neurospora mitochondrial tyrosyl-tRNA synthetase in RNA splicing requires an idiosyncratic domain not found in other synthetases. Cell, 1990, 62, 745-755.	28.9	75

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91	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase IIâ€"DNA complexes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10642-E10651.	7.1	75
92	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. Cancer Research, 2011, 71, 7587-7596.	0.9	70
93	Rapid Intraoperative Molecular Characterization of Glioma. JAMA Oncology, 2015, 1, 662.	7.1	68
94	Integrated Genomic and Functional microRNA Analysis Identifies miR-30-5p as a Tumor Suppressor and Potential Therapeutic Nanomedicine in Head and Neck Cancer. Clinical Cancer Research, 2019, 25, 2860-2873.	7.0	68
95	Genomic Activation of PPARG Reveals a Candidate Therapeutic Axis in Bladder Cancer. Cancer Research, 2017, 77, 6987-6998.	0.9	65
96	Clinicopathological and genomic correlates of programmed cell death ligandÂ1 (PD-L1) expression in nonsquamous non-small-cell lung cancer. Annals of Oncology, 2020, 31, 807-814.	1.2	65
97	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. Nature Communications, 2020, 11, 2517.	12.8	60
98	G Î± 11 Signaling through ARF6 Regulates F-Actin Mobilization and GLUT4 Glucose Transporter Translocation to the Plasma Membrane. Molecular and Cellular Biology, 2001, 21, 5262-5275.	2.3	59
99	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. Nature Genetics, 2018, 50, 937-943.	21.4	55
100	Molecular profiling of endometrial carcinoma precursor, primary and metastatic lesions suggests different targets for treatment in obese compared to non-obese patients. Oncotarget, 2015, 6, 1327-1339.	1.8	50
101	SMARCA4 and Other SWItch/Sucrose NonFermentable Family Genomic Alterations in NSCLC: Clinicopathologic Characteristics and Outcomes to Immune Checkpoint Inhibition. Journal of Thoracic Oncology, 2021, 16, 1176-1187.	1.1	49
102	Abstract 3287: An integrated TCGA pan-cancer clinical data resource to drive high quality survival outcome analytics. Cancer Research, 2018, 78, 3287-3287.	0.9	49
103	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	3.4	47
104	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
105	FGFR2Extracellular Domain In-Frame Deletions Are Therapeutically Targetable Genomic Alterations That Function as Oncogenic Drivers in Cholangiocarcinoma. Cancer Discovery, 2021, 11, 2488-2505.	9.4	46
106	Discovery and Features of an Alkylating Signature in Colorectal Cancer. Cancer Discovery, 2021, 11, 2446-2455.	9.4	42
107	Function of the Neurospora crassa mitochondrial tyrosyl-tRNA synthetase in RNA splicing. Role of the idiosyncratic N-terminal extension and different modes of interaction with different group I introns. Journal of Molecular Biology, 2001, 307, 75-92.	4.2	39
108	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. Nature Communications, 2021, 12, 4375.	12.8	39

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109	Activity of PD-1 blockade with nivolumab among patients with recurrent atypical/anaplastic meningioma: phase II trial results. Neuro-Oncology, 2022, 24, 101-113.	1.2	38
110	Divergent Mechanisms for Homologous Desensitization of p21 by Insulin and Growth Factors. Journal of Biological Chemistry, 1995, 270, 23421-23428.	3.4	35
111	Ancestry-specific predisposing germline variants in cancer. Genome Medicine, 2020, 12, 51.	8.2	35
112	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. Npj Breast Cancer, 2016, 2, 16007.	5.2	33
113	Pooled Genomic Screens Identify Anti-apoptotic Genes as Targetable Mediators of Chemotherapy Resistance in Ovarian Cancer. Molecular Cancer Research, 2019, 17, 2281-2293.	3.4	29
114	RPC4046, A Novel Anti-interleukin-13 Antibody, Blocks IL-13 Binding to IL-13 Î±1 and Î±2 Receptors: A Randomized, Double-Blind, Placebo-Controlled, Dose-Escalation First-in-Human Study. Advances in Therapy, 2017, 34, 1364-1381.	2.9	28
115	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. Cell Reports, 2020, 33, 108493.	6.4	28
116	Genomic Characterization of de novo Metastatic Breast Cancer. Clinical Cancer Research, 2021, 27, 1105-1118.	7.0	24
117	Quantification of aneuploidy in targeted sequencing data using ASCETS. Bioinformatics, 2021, 37, 2461-2463.	4.1	21
118	The Protein-tyrosine Kinase Fer Associates with Signaling Complexes Containing Insulin Receptor Substrate-1 and Phosphatidylinositol 3-Kinase. Journal of Biological Chemistry, 2000, 275, 38995-39000.	3.4	19
119	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. Clinical Cancer Research, 2021, 27, 1695-1705.	7.0	19
120	Effects of Verapamil on Histamine and Carbachol-Induced Contraction of Pulmonary Tissues in Vitro. Chest, 1984, 86, 762-766.	0.8	18
121	Role of the Raf/Mitogen-activated Protein Kinase Pathway in p21 Desensitization. Journal of Biological Chemistry, 1996, 271, 16674-16677.	3.4	17
122	PIK3CA Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. Clinical Cancer Research, 2019, 25, 334-345.	7.0	17
123	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
124	Molecular profiling identifies targeted therapy opportunities in pediatric solid cancer. Nature Medicine, 2022, 28, 1581-1589.	30.7	16
125	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. Scientific Reports, 2016, 6, 25521.	3.3	13
126	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. Journal of Biological Chemistry, 2020, 295, 3431-3446.	3.4	12

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127	A predominant enhancer co-amplified with the SOX2 oncogene is necessary and sufficient for its expression in squamous cancer. Nature Communications, 2021, 12, 7139.	12.8	12
128	Functional comparison of recombinant acidic mammalian chitinase with enzyme from murine bronchoalveolar lavage. Protein Expression and Purification, 2011, 75, 55-62.	1.3	11
129	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors. , 2015, , .		10
130	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
131	Endometrial Carcinoma Recurrence Score (ECARS) validates to identify aggressive disease and associates with markers of epithelialâ€"mesenchymal transition and PI3K alterations. Gynecologic Oncology, 2014, 134, 599-606.	1.4	8
132	Effect of STK11 mutations on efficacy of PD-1 inhibition in non-small cell lung cancer (NSCLC) and dependence on KRAS mutation status.. Journal of Clinical Oncology, 2020, 38, e15113-e15113.	1.6	7
133	Near haploidization is a genomic hallmark which defines a molecular subgroup of giant cell glioblastoma. Neuro-Oncology Advances, 2020, 2, vdaa155.	0.7	4
134	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas.. Journal of Clinical Oncology, 2017, 35, 4500-4500.	1.6	4
135	Genomic landscape of de novo stage IV breast cancer.. Journal of Clinical Oncology, 2019, 37, 1022-1022.	1.6	3
136	DNMT3A mutation to identify a subset of non-small cell lung cancers with increased sensitivity to PD-(L)1 blockade.. Journal of Clinical Oncology, 2021, 39, 9113-9113.	1.6	2
137	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. STAR Protocols, 2021, 2, 100483.	1.2	2
138	Analytical protocol to identify local ancestry-associated molecular features in cancer. STAR Protocols, 2021, 2, 100766.	1.2	2
139	Abstract 2976: Comprehensive Pan-Genomic characterization of adrenocortical carcinoma. , 2015, , .		2
140	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project. , 2015, , .		2
141	Genetic clues can be used to predict whether early-stage cancer will form an invasive tumour. Nature, 2019, 566, 336-337.	27.8	1
142	Precision medicine approach in kidney cancer: A pan renal cell carcinoma (RCC) study across three cancer genome atlas (TCGA) datasets for clinically relevant target identification.. Journal of Clinical Oncology, 2015, 33, 4564-4564.	1.6	1
143	Comprehensive characterization of 412 muscle invasive urothelial carcinomas: Final analysis of The Cancer Genome Atlas (TCGA) project.. Journal of Clinical Oncology, 2016, 34, 405-405.	1.6	1
144	Changes in tumor mutational burden in serially biopsied non-small cell lung cancer.. Journal of Clinical Oncology, 2019, 37, e14286-e14286.	1.6	1

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145	Distinct MET alterations to induce a common phenotype and to define a MET-driven subset of papillary RCC: Results from the Cancer Genome Atlas (TCGA) Kidney Renal Papillary (KIRP) Working Group.. Journal of Clinical Oncology, 2015, 33, 4521-4521.	1.6	1
146	Abstract 3413: A pan-cancer atlas of genomic, epigenomic and transcriptomic alterations in the TGF-Î² pathway. , 2018, , .		1
147	Abstract 3003: Loss of heterozygosity of essential genes represents a novel class of cancer vulnerabilities. , 2018, , .		1
148	Genomic correlates of acquired resistance to PD-(L)1 blockade in patients with advanced non-small cell lung cancer (NSCLC).. Journal of Clinical Oncology, 2022, 40, 9021-9021.	1.6	1
149	Clinicopathologic, genomic, and tumor microenvironment correlates of aneuploidy and immunotherapy outcomes in NSCLC.. Journal of Clinical Oncology, 2021, 39, 9119-9119.	1.6	0
150	Changes in PD-L1 tumor proportion score are associated with CD274 gene (encoding PD-L1) copy number variation in non-small cell lung cancer.. Journal of Clinical Oncology, 2021, 39, 9029-9029.	1.6	0
151	Somatic genomic alterations in urothelial cancer: Results of the Cancer Genome Atlas (TCGA) bladder cancer (BC) analysis.. Journal of Clinical Oncology, 2014, 32, 285-285.	1.6	0
152	Abstract 987: Comprehensive characterization of urothelial bladder cancer: a TCGA Project update. , 2014, , .		0
153	Abstract 4692: Relationships between somatic genomic alterations, tumor stage and progression-free survival in cervical cancer. , 2014, , .		0
154	Abstract PR08:NF1,MET, andRIT1mutations are RAS-pathway driver events in lung adenocarcinoma. , 2014, , .		0
155	Abstract 128: Comprehensive molecular characterization of 412 muscle-invasive urothelial bladder carcinomas: final analysis of The Cancer Genome Atlas (TCGA) project. , 2016, , .		0
156	Abstract 2028: PDE3A modulation for cancer therapy. , 2017, , .		0
157	Abstract 3002: Genome engineering approaches to generate models of chromosome arm-level cancer aneuploidy. , 2018, , .		0
158	Abstract 907: Bioinformatic method to define epigenetically regulated enhancer elements associated with cancer. , 2019, , .		0
159	Characterizing the landscape of genomic variants in high-risk pediatric osteosarcoma.. Journal of Clinical Oncology, 2020, 38, 11530-11530.	1.6	0
160	Correction: Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12.. Journal of Biological Chemistry, 2020, 295, 16464-16467.	3.4	0