

Andrew D Cherniack

List of Publications by Year in descending order

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Version: 2024-02-01

160
papers

108,209
citations

4345

89
h-index

9346

148
g-index

175
all docs

175
docs citations

175
times ranked

109358
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
2	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
3	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	13.7	5,055
4	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	13.7	4,572
5	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
6	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
7	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
8	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015, 517, 576-582.	13.7	3,209
9	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
10	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
11	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
12	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
13	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
14	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
15	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
16	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	13.7	2,149
17	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
18	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966

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19	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
20	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
21	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	13.5	1,718
22	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
23	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
24	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	9.4	1,616
25	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
26	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
27	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
28	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
29	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
30	Activation of the PD-1 Pathway Contributes to Immune Escape in EGFR-Driven Lung Tumors. <i>Cancer Discovery</i> , 2013, 3, 1355-1363.	7.7	1,073
31	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
32	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
33	A Tumor Suppressor Complex with GAP Activity for the Rag GTPases That Signal Amino Acid Sufficiency to mTORC1. <i>Science</i> , 2013, 340, 1100-1106.	6.0	863
34	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
35	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
36	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750

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37	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
38	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708
39	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
40	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
41	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
42	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
43	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
44	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
45	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
46	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
47	Interplay of somatic alterations and immune infiltration modulates response to PD-1 blockade in advanced clear cell renal cell carcinoma. <i>Nature Medicine</i> , 2020, 26, 909-918.	15.2	488
48	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016, 6, 914-929.	7.7	485
49	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
50	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
51	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	7.7	422
52	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
53	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
54	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400

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55	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
56	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020, 580, 517-523.	13.7	374
57	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
58	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
59	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
60	Binding of the Ras activator son of sevenless to insulin receptor substrate-1 signaling complexes. <i>Science</i> , 1993, 260, 1950-1952.	6.0	303
61	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
62	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016, 48, 176-182.	9.4	283
63	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
64	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
65	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
66	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
67	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017, 3, 1654.	3.4	208
68	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
69	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
70	Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. <i>Cell</i> , 2021, 184, 6119-6137.e26.	13.5	201
71	Suppression of oxidative metabolism and mitochondrial biogenesis by the transcriptional corepressor RIP140 in mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2005, 116, 125-136.	3.9	198
72	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177

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73	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016, 48, 848-855.	9.4	174
74	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. <i>Nature Communications</i> , 2018, 9, 5450.	5.8	157
75	The genomic landscape of tuberous sclerosis complex. <i>Nature Communications</i> , 2017, 8, 15816.	5.8	154
76	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	7.7	151
77	Diminished Efficacy of Programmed Death-(Ligand)1 Inhibition in STK11- and KEAP1-Mutant Lung Adenocarcinoma Is Affected by KRAS Mutation Status. <i>Journal of Thoracic Oncology</i> , 2022, 17, 399-410.	0.5	151
78	Loss of the retinoblastoma binding protein 2 (RBP2) histone demethylase suppresses tumorigenesis in mice lacking <i>Rb1</i> or <i>Men1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13379-13386.	3.3	143
79	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
80	Molecular Mechanisms of Acquired Resistance to MET Tyrosine Kinase Inhibitors in Patients with MET Exon 14-Mutant NSCLC. <i>Clinical Cancer Research</i> , 2020, 26, 2615-2625.	3.2	129
81	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 5472.	5.8	127
82	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
83	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	2.9	103
84	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. <i>Cancer Discovery</i> , 2018, 8, 108-125.	7.7	99
85	Impact of DNA Damage Response and Repair (DDR) Gene Mutations on Efficacy of PD-(L)1 Immune Checkpoint Inhibition in Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 4135-4142.	3.2	95
86	Disassembly of Son-of-sevenless Proteins from Grb2 during p21 Desensitization by Insulin. <i>Journal of Biological Chemistry</i> , 1995, 270, 1485-1488.	1.6	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. <i>Gastroenterology</i> , 2017, 153, 536-549.e26.	0.6	90
88	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
89	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. <i>Nature Communications</i> , 2018, 9, 2024.	5.8	80
90	Function of neurospora mitochondrial tyrosyl-tRNA synthetase in RNA splicing requires an idiosyncratic domain not found in other synthetases. <i>Cell</i> , 1990, 62, 745-755.	13.5	75

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91	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase IIα-DNA complexes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10642-E10651.	3.3	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.	0.4	70
93	Rapid Intraoperative Molecular Characterization of Glioma. JAMA Oncology, 2015, 1, 662.	3.4	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.	3.2	68
95	Genomic Activation of <i>PPARG</i> Reveals a Candidate Therapeutic Axis in Bladder Cancer. Cancer Research, 2017, 77, 6987-6998.	0.4	65
96	Clinicopathological and genomic correlates of programmed cell death ligand 1 (PD-L1) expression in nonsquamous non-small-cell lung cancer. Annals of Oncology, 2020, 31, 807-814.	0.6	65
97	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. Nature Communications, 2020, 11, 2517.	5.8	60
98	G11 Signaling through ARF6 Regulates F-Actin Mobilization and GLUT4 Glucose Transporter Translocation to the Plasma Membrane. Molecular and Cellular Biology, 2001, 21, 5262-5275.	1.1	59
99	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. Nature Genetics, 2018, 50, 937-943.	9.4	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.	0.8	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.	0.5	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.	0.4	49
103	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	1.6	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.	3.3	46
105	<i>FGFR2</i> Extracellular Domain In-Frame Deletions Are Therapeutically Targetable Genomic Alterations That Function as Oncogenic Drivers in Cholangiocarcinoma. Cancer Discovery, 2021, 11, 2488-2505.	7.7	46
106	Discovery and Features of an Alkylating Signature in Colorectal Cancer. Cancer Discovery, 2021, 11, 2446-2455.	7.7	42
107	Function of the <i>Neurospora crassa</i> 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.	2.0	39
108	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. Nature Communications, 2021, 12, 4375.	5.8	39

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109	Activity of PD-1 blockade with nivolumab among patients with recurrent atypical/anaplastic meningioma: phase II trial results. <i>Neuro-Oncology</i> , 2022, 24, 101-113.	0.6	38
110	Divergent Mechanisms for Homologous Desensitization of p21 by Insulin and Growth Factors. <i>Journal of Biological Chemistry</i> , 1995, 270, 23421-23428.	1.6	35
111	Ancestry-specific predisposing germline variants in cancer. <i>Genome Medicine</i> , 2020, 12, 51.	3.6	35
112	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. <i>Npj Breast Cancer</i> , 2016, 2, 16007.	2.3	33
113	Pooled Genomic Screens Identify Anti-apoptotic Genes as Targetable Mediators of Chemotherapy Resistance in Ovarian Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 2281-2293.	1.5	29
114	RPC4046, A Novel Anti-interleukin-13 Antibody, Blocks IL-13 Binding to IL-13 $\hat{1}$ and $\hat{2}$ Receptors: A Randomized, Double-Blind, Placebo-Controlled, Dose-Escalation First-in-Human Study. <i>Advances in Therapy</i> , 2017, 34, 1364-1381.	1.3	28
115	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. <i>Cell Reports</i> , 2020, 33, 108493.	2.9	28
116	Genomic Characterization of <i>de novo</i> Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 1105-1118.	3.2	24
117	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021, 37, 2461-2463.	1.8	21
118	The Protein-tyrosine Kinase Fer Associates with Signaling Complexes Containing Insulin Receptor Substrate-1 and Phosphatidylinositol 3-Kinase. <i>Journal of Biological Chemistry</i> , 2000, 275, 38995-39000.	1.6	19
119	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. <i>Clinical Cancer Research</i> , 2021, 27, 1695-1705.	3.2	19
120	Effects of Verapamil on Histamine and Carbachol-Induced Contraction of Pulmonary Tissues in Vitro. <i>Chest</i> , 1984, 86, 762-766.	0.4	18
121	Role of the Raf/Mitogen-activated Protein Kinase Pathway in p21 Desensitization. <i>Journal of Biological Chemistry</i> , 1996, 271, 16674-16677.	1.6	17
122	<i>PIK3CA</i> Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 334-345.	3.2	17
123	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	2.9	16
124	Molecular profiling identifies targeted therapy opportunities in pediatric solid cancer. <i>Nature Medicine</i> , 2022, 28, 1581-1589.	15.2	16
125	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. <i>Scientific Reports</i> , 2016, 6, 25521.	1.6	13
126	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. <i>Journal of Biological Chemistry</i> , 2020, 295, 3431-3446.	1.6	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. <i>Nature Communications</i> , 2021, 12, 7139.	5.8	12
128	Functional comparison of recombinant acidic mammalian chitinase with enzyme from murine bronchoalveolar lavage. <i>Protein Expression and Purification</i> , 2011, 75, 55-62.	0.6	11
129	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors. , ,		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 epithelial-mesenchymal transition and PI3K alterations. <i>Gynecologic Oncology</i> , 2014, 134, 599-606.	0.6	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.. <i>Journal of Clinical Oncology</i> , 2020, 38, e15113-e15113.	0.8	7
133	Near haploidization is a genomic hallmark which defines a molecular subgroup of giant cell glioblastoma. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa155.	0.4	4
134	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas.. <i>Journal of Clinical Oncology</i> , 2017, 35, 4500-4500.	0.8	4
135	Genomic landscape of de novo stage IV breast cancer.. <i>Journal of Clinical Oncology</i> , 2019, 37, 1022-1022.	0.8	3
136	DNMT3A mutation to identify a subset of non-small cell lung cancers with increased sensitivity to PD-(L)1 blockade.. <i>Journal of Clinical Oncology</i> , 2021, 39, 9113-9113.	0.8	2
137	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021, 2, 100483.	0.5	2
138	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021, 2, 100766.	0.5	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. <i>Nature</i> , 2019, 566, 336-337.	13.7	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.. <i>Journal of Clinical Oncology</i> , 2015, 33, 4564-4564.	0.8	1
143	Comprehensive characterization of 412 muscle invasive urothelial carcinomas: Final analysis of The Cancer Genome Atlas (TCGA) project.. <i>Journal of Clinical Oncology</i> , 2016, 34, 405-405.	0.8	1
144	Changes in tumor mutational burden in serially biopsied non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2019, 37, e14286-e14286.	0.8	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.	0.8	1
146	Abstract 3413: A pan-cancer atlas of genomic, epigenomic and transcriptomic alterations in the TGF- β 2 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.	0.8	1
149	Clinicopathologic, genomic, and tumor microenvironment correlates of aneuploidy and immunotherapy outcomes in NSCLC.. Journal of Clinical Oncology, 2021, 39, 9119-9119.	0.8	0
150	Changes in PD-L1 tumor proportion score are associated with <i>CD274</i> gene (encoding PD-L1) copy number variation in non-small cell lung cancer.. Journal of Clinical Oncology, 2021, 39, 9029-9029.	0.8	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.	0.8	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.	0.8	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.	1.6	0