

Andrew D Cherniack

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

149 papers	71,654 citations	80 h-index	175 g-index
175 ext. papers	93,486 ext. citations	22.9 avg, IF	9.25 L-index

#	Paper	IF	Citations
149	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012 , 490, 61-70	50.4	8025
148	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7	50.4	5640
147	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
146	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50	50.4	3310
145	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012 , 489, 519-25	50.4	2820
144	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
143	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
142	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013 , 499, 43-9	50.4	2184
141	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
140	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
139	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
138	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
137	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
136	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
135	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013 , 45, 1134-40	36.3	1198
134	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
133	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125

132	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
131	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
130	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
129	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019 , 569, 503-508	50.4	962
128	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	56.2	961
127	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
126	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-201.e13	56.2	913
125	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	56.2	888
124	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
123	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
122	Activation of the PD-1 pathway contributes to immune escape in EGFR-driven lung tumors. <i>Cancer Discovery</i> , 2013 , 3, 1355-63	24.4	831
121	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
120	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
119	A Tumor suppressor complex with GAP activity for the Rag GTPases that signal amino acid sufficiency to mTORC1. <i>Science</i> , 2013 , 340, 1100-6	33.3	637
118	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
117	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
116	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014 , 506, 371-5	50.4	541
115	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521

114	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
113	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
112	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
111	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
110	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
109	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
108	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
107	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016 , 6, 914-29	24.4	343
106	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
105	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
104	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736.e3	24.3	324
103	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
102	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
101	Binding of the Ras activator son of sevenless to insulin receptor substrate-1 signaling complexes. <i>Science</i> , 1993 , 260, 1950-2	33.3	283
100	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
99	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	24.3	275
98	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
97	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247

96	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
95	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
94	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
93	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016 , 48, 176-82	36.3	210
92	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406	10.6	200
91	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
90	Suppression of oxidative metabolism and mitochondrial biogenesis by the transcriptional corepressor RIP140 in mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2006 , 116, 125-36	15.9	176
89	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020 , 580, 517-523	50.4	172
88	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
87	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	10.6	159
86	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	50.5	155
85	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
84	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	10.6	147
83	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017 , 3, 1654-1662	13.4	146
82	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
81	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016 , 48, 848-55	36.3	135
80	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	42.2	133
79	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121

78	Loss of the retinoblastoma binding protein 2 (RBP2) histone demethylase suppresses tumorigenesis in mice lacking Rb1 or Men1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13379-86	11.5	121
77	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
76	The genomic landscape of tuberous sclerosis complex. <i>Nature Communications</i> , 2017 , 8, 15816	17.4	104
75	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	10.6	85
74	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. <i>Nature Communications</i> , 2018 , 9, 5450	17.4	83
73	Disassembly of Son-of-sevenless Proteins from Grb2 during p21 Desensitization by Insulin. <i>Journal of Biological Chemistry</i> , 1995 , 270, 1485-1488	5.4	75
72	Function of Neurospora mitochondrial tyrosyl-tRNA synthetase in RNA splicing requires an idiosyncratic domain not found in other synthetases. <i>Cell</i> , 1990 , 62, 745-55	56.2	73
71	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. <i>Cancer Discovery</i> , 2018 , 8, 108-125	24.4	67
70	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
69	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. <i>Cell Systems</i> , 2019 , 9, 24-34.e10	10.6	64
68	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	13.3	63
67	Glioblastoma-derived epidermal growth factor receptor carboxyl-terminal deletion mutants are transforming and are sensitive to EGFR-directed therapies. <i>Cancer Research</i> , 2011 , 71, 7587-96	10.1	62
66	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	12.9	60
65	G(alpha)11 signaling through ARF6 regulates F-actin mobilization and GLUT4 glucose transporter translocation to the plasma membrane. <i>Molecular and Cellular Biology</i> , 2001 , 21, 5262-75	4.8	57
64	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.6	56
63	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020 , 37, 639-654.e6	24.3	56
62	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019 , 10, 5472	17.4	56
61	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. <i>Nature Communications</i> , 2018 , 9, 2024	17.4	54

60	Rapid Intraoperative Molecular Characterization of Glioma. <i>JAMA Oncology</i> , 2015 , 1, 662-7	13.4	53
59	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase II-DNA complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E10642-E10651	11.5	47
58	Molecular profiling of endometrial carcinoma precursor, primary and metastatic lesions suggests different targets for treatment in obese compared to non-obese patients. <i>Oncotarget</i> , 2015 , 6, 1327-39	3.3	42
57	Integrated Genomic and Functional microRNA Analysis Identifies miR-30-5p as a Tumor Suppressor and Potential Therapeutic Nanomedicine in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 2860-2873	12.9	41
56	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	12.9	41
55	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. <i>Journal of Molecular Biology</i> , 2001 , 307, 75-92	6.5	38
54	Genetic modifiers of EGFR dependence in non-small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 18661-6	11.5	37
53	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018 , 50, 937-943	36.3	35
52	Clinicopathological and genomic correlates of programmed cell death ligand1 (PD-L1) expression in nonsquamous non-small-cell lung cancer. <i>Annals of Oncology</i> , 2020 , 31, 807-814	10.3	34
51	Genomic Activation of Reveals a Candidate Therapeutic Axis in Bladder Cancer. <i>Cancer Research</i> , 2017 , 77, 6987-6998	10.1	34
50	Divergent mechanisms for homologous desensitization of p21ras by insulin and growth factors. <i>Journal of Biological Chemistry</i> , 1995 , 270, 23421-8	5.4	33
49	Abstract 3287: An integrated TCGA pan-cancer clinical data resource to drive high quality survival outcome analytics 2018 ,		27
48	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	7.8	25
47	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. <i>Nature Communications</i> , 2020 , 11, 2517	17.4	21
46	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. <i>Cancer Immunology Research</i> , 2020 , 8, 1075-1084	12.5	21
45	RPC4046, A Novel Anti-interleukin-13 Antibody, Blocks IL-13 Binding to IL-13 α and β Receptors: A Randomized, Double-Blind, Placebo-Controlled, Dose-Escalation First-in-Human Study. <i>Advances in Therapy</i> , 2017 , 34, 1364-1381	4.1	19
44	Role of the Raf/mitogen-activated protein kinase pathway in p21ras desensitization. <i>Journal of Biological Chemistry</i> , 1996 , 271, 16674-7	5.4	17
43	The protein-tyrosine kinase <i>fer</i> associates with signaling complexes containing insulin receptor substrate-1 and phosphatidylinositol 3-kinase. <i>Journal of Biological Chemistry</i> , 2000 , 275, 38995-9000	5.4	16

42	Effects of verapamil on histamine-and carbachol-induced contraction of pulmonary tissues in vitro. <i>Chest</i> , 1984 , 86, 762-6	5.3	16
41	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	6.6	15
40	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> , 2021 ,	8.9	14
39	Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. <i>Cell</i> , 2021 , 184, 6119-6137.e26	56.2	13
38	Ancestry-specific predisposing germline variants in cancer. <i>Genome Medicine</i> , 2020 , 12, 51	14.4	12
37	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	4.9	11
36	Extracellular Domain In-Frame Deletions Are Therapeutically Targetable Genomic Alterations That Function as Oncogenic Drivers in Cholangiocarcinoma. <i>Cancer Discovery</i> , 2021 , 11, 2488-2505	24.4	11
35	Genomic Characterization of Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2021 , 27, 1105-1118	12.9	11
34	Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. <i>Clinical Cancer Research</i> , 2019 , 25, 334-345	12.9	9
33	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. <i>Clinical Cancer Research</i> , 2021 , 27, 1695-1705	12.9	9
32	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	4.9	8
31	Functional comparison of recombinant acidic mammalian chitinase with enzyme from murine bronchoalveolar lavage. <i>Protein Expression and Purification</i> , 2011 , 75, 55-62	2	8
30	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors 2015 ,		7
29	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	10.6	7
28	Activity of PD-1 blockade with Nivolumab among patients with recurrent atypical/anaplastic meningioma: Phase II trial results. <i>Neuro-Oncology</i> , 2021 ,	1	7
27	Discovery and Features of an Alkylating Signature in Colorectal Cancer. <i>Cancer Discovery</i> , 2021 , 11, 2446-2455	24.5	7
26	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
25	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. <i>Nature Communications</i> , 2021 , 12, 4375	17.4	7

24	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	5.4	6
23	SMARCA4 and Other SWItch/Sucrose NonFermentable Family Genomic Alterations in NSCLC: Clinicopathologic Characteristics and Outcomes to Immune Checkpoint Inhibition. <i>Journal of Thoracic Oncology</i> , 2021 , 16, 1176-1187	8.9	6
22	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas 2018 ,		5
21	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	2.2	5
20	The tumor microenvironment drives transcriptional phenotypes and their plasticity in metastatic pancreatic cancer		5
19	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas.. <i>Journal of Clinical Oncology</i> , 2017 , 35, 4500-4500	2.2	4
18	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021 , 37, 2461-2463	2.2	4
17	Genomic landscape of de novo stage IV breast cancer.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 1022-1022	2.2	3
16	The Tangent copy-number inference pipeline for cancer genome analyses		3
15	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	17.4	3
14	Near haploidization is a genomic hallmark which defines a molecular subgroup of giant cell glioblastoma. <i>Neuro-Oncology Advances</i> , 2020 , 2, vdaa155	0.9	2
13	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project 2015 ,		2
12	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	2.2	1
11	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	2.2	1
10	Changes in tumor mutational burden in serially biopsied non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e14286-e14286	2.2	1
9	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities		1
8	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.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 4521-4521	2.2	1
7	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	2.2	1

6	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021 , 2, 100483	1.4	○
5	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021 , 2, 100766	1.4	○
4	Characterizing the landscape of genomic variants in high-risk pediatric osteosarcoma.. <i>Journal of Clinical Oncology</i> , 2020 , 38, 11530-11530	2.2	
3	Somatic genomic alterations in urothelial cancer: Results of the Cancer Genome Atlas (TCGA) bladder cancer (BC) analysis.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 285-285	2.2	
2	Clinicopathologic, genomic, and tumor microenvironment correlates of aneuploidy and immunotherapy outcomes in NSCLC.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 9119-9119	2.2	
1	Changes in PD-L1 tumor proportion score are associated with CD274 gene (encoding PD-L1) copy number variation in non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 9029-9029	2.2	