

## List of Publications by Year in descending order

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207  
papers

105,475  
citations

1370

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docs citations

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times ranked

92958  
citing authors

#	ARTICLE	IF	CITATIONS
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
2	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, pl1.	1.6	11,344
3	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
4	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
5	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
6	Integrative Genomic Profiling of Human Prostate Cancer. <i>Cancer Cell</i> , 2010, 18, 11-22.	7.7	3,151
7	Integrative Clinical Genomics of Advanced Prostate Cancer. <i>Cell</i> , 2015, 161, 1215-1228.	13.5	2,660
8	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
9	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , 2017, 23, 703-713.	15.2	2,473
10	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
11	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
12	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
13	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
14	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
15	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
16	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
17	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
18	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485

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19	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
20	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	1.5	1,266
21	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , 2016, 375, 443-453.	13.9	1,205
22	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , 2013, 45, 1127-1133.	9.4	1,190
23	Molecular Determinants of Response to Anti-Programmed Cell Death (PD)-1 and Anti-Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Non-Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. <i>Journal of Clinical Oncology</i> , 2018, 36, 633-641.	0.8	1,109
24	Evaluating cell lines as tumour models by comparison of genomic profiles. <i>Nature Communications</i> , 2013, 4, 2126.	5.8	1,108
25	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	6.5	980
26	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. <i>Journal of Clinical Investigation</i> , 2016, 126, 1052-1066.	3.9	874
27	Genomic correlates of clinical outcome in advanced prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11428-11436.	3.3	839
28	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
29	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
30	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
31	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
32	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. <i>Nature Biotechnology</i> , 2016, 34, 155-163.	9.4	634
33	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , 2018, 34, 427-438.e6.	7.7	633
34	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
35	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
36	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , 2018, 50, 645-651.	9.4	601

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37	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , 2012, 22, 398-406.	2.4	597
38	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2018, 33, 125-136.e3.	7.7	589
39	Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. <i>Nature Medicine</i> , 2016, 22, 369-378.	15.2	572
40	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
41	A multitude of genes expressed solely in meiotic or postmeiotic spermatogenic cells offers a myriad of contraceptive targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12201-12206.	3.3	514
42	Response to MET Inhibitors in Patients with Stage IV Lung Adenocarcinomas Harboring <i>MET</i> Mutations Causing Exon 14 Skipping. <i>Cancer Discovery</i> , 2015, 5, 842-849.	7.7	514
43	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , 2017, 7, 596-609.	7.7	490
44	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
45	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
46	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , 2014, 46, 1160-1165.	9.4	469
47	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. <i>JAMA Oncology</i> , 2019, 5, 471.	3.4	426
48	Genome doubling shapes the evolution and prognosis of advanced cancers. <i>Nature Genetics</i> , 2018, 50, 1189-1195.	9.4	411
49	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
50	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
51	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
52	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , 2013, 45, 791-798.	9.4	394
53	Prospective Genotyping of Hepatocellular Carcinoma: Clinical Implications of Next-Generation Sequencing for Matching Patients to Targeted and Immune Therapies. <i>Clinical Cancer Research</i> , 2019, 25, 2116-2126.	3.2	390
54	Pattern discovery and cancer gene identification in integrated cancer genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4245-4250.	3.3	361

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55	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. <i>Clinical Cancer Research</i> , 2018, 24, 4154-4161.	3.2	348
56	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
57	Automated Network Analysis Identifies Core Pathways in Glioblastoma. <i>PLoS ONE</i> , 2010, 5, e8918.	1.1	318
58	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. <i>Cancer Cell</i> , 2018, 34, 893-905.e8.	7.7	307
59	Ibrutinib Unmasks Critical Role of Bruton Tyrosine Kinase in Primary CNS Lymphoma. <i>Cancer Discovery</i> , 2017, 7, 1018-1029.	7.7	302
60	Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators <i>BAP1</i> and <i>SETD2</i> : A Report by MSKCC and the KIRC TCGA Research Network. <i>Clinical Cancer Research</i> , 2013, 19, 3259-3267.	3.2	301
61	Copy number alteration burden predicts prostate cancer relapse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11139-11144.	3.3	299
62	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , 2019, 571, 576-579.	13.7	295
63	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. <i>Nature Genetics</i> , 2014, 46, 424-426.	9.4	291
64	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	1.5	286
65	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
66	Prevalence and Co-Occurrence of Actionable Genomic Alterations in High-Grade Bladder Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 3133-3140.	0.8	282
67	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , 2018, 8, 174-183.	7.7	275
68	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , 2018, 8, 49-58.	7.7	275
69	MLL3 Is a Haploinsufficient 7q Tumor Suppressor in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2014, 25, 652-665.	7.7	274
70	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
71	The expanding landscape of <i>oncohistone</i> ™ mutations in human cancers. <i>Nature</i> , 2019, 567, 473-478.	13.7	271
72	Loss of NF1 in Cutaneous Melanoma Is Associated with RAS Activation and MEK Dependence. <i>Cancer Research</i> , 2014, 74, 2340-2350.	0.4	266

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73	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. <i>European Urology</i> , 2017, 72, 952-959.	0.9	263
74	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with EGFR-Mutant Lung Cancers. <i>Clinical Cancer Research</i> , 2019, 25, 1063-1069.	3.2	257
75	The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9435-9440.	3.3	246
76	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014, 24, 1740-1750.	2.4	244
77	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. <i>Lancet Oncology</i> , The, 2020, 21, 821-831.	5.1	243
78	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
79	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. <i>Cell</i> , 2022, 185, 563-575.e11.	13.5	223
80	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. <i>ELife</i> , 2018, 7, .	2.8	217
81	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018, 33, 450-462.e10.	7.7	213
82	Tumor Genetic Analyses of Patients with Metastatic Renal Cell Carcinoma and Extended Benefit from mTOR Inhibitor Therapy. <i>Clinical Cancer Research</i> , 2014, 20, 1955-1964.	3.2	208
83	Genomic Characterization of Upper Tract Urothelial Carcinoma. <i>European Urology</i> , 2015, 68, 970-977.	0.9	202
84	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. <i>Nature</i> , 2016, 531, 471-475.	13.7	202
85	PIK3CA Mutations Are Associated With Decreased Benefit to Neoadjuvant Human Epidermal Growth Factor Receptor Targeted Therapies in Breast Cancer. <i>Journal of Clinical Oncology</i> , 2015, 33, 1334-1339.	0.8	201
86	Integrative Subtype Discovery in Glioblastoma Using iCluster. <i>PLoS ONE</i> , 2012, 7, e35236.	1.1	196
87	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1325-1332.	3.6	184
88	The metabolic co-regulator PGC1 $\alpha$ suppresses prostate cancer metastasis. <i>Nature Cell Biology</i> , 2016, 18, 645-656.	4.6	176
89	Distinct Patterns of Dysregulated Expression of Enzymes Involved in Androgen Synthesis and Metabolism in Metastatic Prostate Cancer Tumors. <i>Cancer Research</i> , 2012, 72, 6142-6152.	0.4	175
90	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , 2017, 9, 4.	3.6	170

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91	Identification of PHLPP1 as a Tumor Suppressor Reveals the Role of Feedback Activation in PTEN-Mutant Prostate Cancer Progression. <i>Cancer Cell</i> , 2011, 20, 173-186.	7.7	158
92	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 4441-4453.	3.9	155
93	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018, 5, 180061.	2.4	152
94	Genomic Alterations Observed in Colitis-Associated Cancers Are Distinct From Those Found in Sporadic Colorectal Cancers and Vary by Type of Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2016, 151, 278-287.e6.	0.6	147
95	Genetic Determinants of Cisplatin Resistance in Patients With Advanced Germ Cell Tumors. <i>Journal of Clinical Oncology</i> , 2016, 34, 4000-4007.	0.8	147
96	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , 2015, 16, 45.	3.8	145
97	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. <i>Nature Communications</i> , 2016, 7, 13131.	5.8	140
98	A cluster of cooperating tumor-suppressor gene candidates in chromosomal deletions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8212-8217.	3.3	138
99	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. <i>Cancer Cell</i> , 2013, 24, 738-750.	7.7	135
100	Genomic Methods Identify Homologous Recombination Deficiency in Pancreas Adenocarcinoma and Optimize Treatment Selection. <i>Clinical Cancer Research</i> , 2020, 26, 3239-3247.	3.2	135
101	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
102	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , 2019, 129, 4276-4289.	3.9	134
103	Defining the spermatogonial stem cell. <i>Developmental Biology</i> , 2004, 269, 393-410.	0.9	126
104	Genomic Predictors of Survival in Patients with High-grade Urothelial Carcinoma of the Bladder. <i>European Urology</i> , 2015, 67, 198-201.	0.9	122
105	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
106	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
107	<i>EGFR</i> and <i>MET</i> Amplifications Determine Response to HER2 Inhibition in <i>ERBB2</i> -Amplified Esophagogastric Cancer. <i>Cancer Discovery</i> , 2019, 9, 199-209.	7.7	115
108	Synthetic Lethality in ATM-Deficient <i>RAD50</i> -Mutant Tumors Underlies Outlier Response to Cancer Therapy. <i>Cancer Discovery</i> , 2014, 4, 1014-1021.	7.7	114

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109	18F-Fluorodeoxy-glucose Positron Emission Tomography Marks MYC-Overexpressing Human Basal-Like Breast Cancers. <i>Cancer Research</i> , 2011, 71, 5164-5174.	0.4	113
110	Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma. <i>JAMA Oncology</i> , 2020, 6, 60.	3.4	112
111	Oncogenic Genomic Alterations, Clinical Phenotypes, and Outcomes in Metastatic Castration-Sensitive Prostate Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 3230-3238.	3.2	112
112	Genomic Complexity and AKT Dependence in Serous Ovarian Cancer. <i>Cancer Discovery</i> , 2012, 2, 56-67.	7.7	109
113	Frequent Alterations and Epigenetic Silencing of Differentiation Pathway Genes in Structurally Rearranged Liposarcomas. <i>Cancer Discovery</i> , 2011, 1, 587-597.	7.7	108
114	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1893-1898.	2.5	106
115	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	1.1	104
116	Genomic Differences Between "Primary" and "Secondary" Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. <i>European Urology</i> , 2019, 75, 231-239.	0.9	104
117	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	9.4	104
118	KMT2C mediates the estrogen dependence of breast cancer through regulation of ER $\alpha$ enhancer function. <i>Oncogene</i> , 2018, 37, 4692-4710.	2.6	102
119	Mitochondrial respiratory gene expression is suppressed in many cancers. <i>ELife</i> , 2017, 6, .	2.8	102
120	Somatic <i>POLE</i> mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. <i>Neuro-Oncology</i> , 2015, 17, 1356-1364.	0.6	94
121	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015, 1, 197-209.	2.9	94
122	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. <i>Cancer Cell</i> , 2017, 32, 155-168.e6.	7.7	93
123	Platinum-Based Chemotherapy in Metastatic Prostate Cancer With DNA Repair Gene Alterations. <i>JCO Precision Oncology</i> , 2020, 4, 355-366.	1.5	93
124	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. <i>PLoS ONE</i> , 2013, 8, e80306.	1.1	90
125	Chemotherapy Resistance in Diffuse-Type Gastric Adenocarcinoma Is Mediated by RhoA Activation in Cancer Stem-Like Cells. <i>Clinical Cancer Research</i> , 2016, 22, 971-983.	3.2	89
126	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. <i>PLoS ONE</i> , 2011, 6, e24709.	1.1	88



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127	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. <i>Clinical Cancer Research</i> , 2018, 24, 1965-1973.	3.2	85
128	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1844-1856.	0.5	83
129	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. <i>Journal of Clinical Oncology</i> , 2021, 39, 2698-2709.	0.8	83
130	Loss of the tyrosine phosphatase PTPRD leads to aberrant STAT3 activation and promotes gliomagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8149-8154.	3.3	80
131	Morphological characterization of colorectal cancers in The Cancer Genome Atlas reveals distinct morphologyâ€“molecular associations: clinical and biological implications. <i>Modern Pathology</i> , 2017, 30, 599-609.	2.9	74
132	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. <i>Nature Cancer</i> , 2021, 2, 357-365.	5.7	74
133	Recurrent patterns of DNA copy number alterations in tumors reflect metabolic selection pressures. <i>Molecular Systems Biology</i> , 2017, 13, 914.	3.2	73
134	Clinical and Molecular Predictors of Response to Immune Checkpoint Inhibitors in Patients with Advanced Esophagogastric Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 6160-6169.	3.2	73
135	Genetic Determinants of Outcome in Intrahepatic Cholangiocarcinoma. <i>Hepatology</i> , 2021, 74, 1429-1444.	3.6	73
136	Pan-cancer Analysis of CDK12 Alterations Identifies a Subset of Prostate Cancers with Distinct Genomic and Clinical Characteristics. <i>European Urology</i> , 2020, 78, 671-679.	0.9	72
137	ERF mutations reveal a balance of ETS factors controlling prostate oncogenesis. <i>Nature</i> , 2017, 546, 671-675.	13.7	70
138	<i>KMT2C</i> Mutations in Diffuse-Type Gastric Adenocarcinoma Promote Epithelial-to-Mesenchymal Transition. <i>Clinical Cancer Research</i> , 2018, 24, 6556-6569.	3.2	70
139	<i>MLH1</i> â€“silenced and nonâ€“silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. <i>Journal of Pathology</i> , 2013, 229, 99-110.	2.1	67
140	Analytic and Clinical Validation of a Prostate Cancerâ€“Enhanced Messenger RNA Detection Assay in Whole Blood as a Prognostic Biomarker for Survival. <i>European Urology</i> , 2014, 65, 1191-1197.	0.9	66
141	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. <i>JAMA Oncology</i> , 2020, 6, 84.	3.4	66
142	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1683-1692.	3.0	66
143	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. <i>Nature Communications</i> , 2022, 13, .	5.8	63
144	Coaltered <i>Ras/B-raf</i> and <i>TP53</i> Is Associated with Extremes of Survivorship and Distinct Patterns of Metastasis in Patients with Metastatic Colorectal Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1077-1085.	3.2	62

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145	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Nonâ€“Small-Cell Lung Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	1.5	58
146	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. <i>Oncotarget</i> , 2014, 5, 8083-8092.	0.8	55
147	The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing <i>FAK</i>. <i>Science Signaling</i> , 2017, 10, .	1.6	52
148	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. <i>JAMA Surgery</i> , 2021, 156, e205601.	2.2	52
149	OncoTree: A Cancer Classification System for Precision Oncology. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 221-230.	1.0	51
150	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. <i>Bioinformatics</i> , 2017, 33, 2238-2240.	1.8	50
151	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019, 10, 3682.	5.8	48
152	Accelerating precision medicine in metastatic prostate cancer. <i>Nature Cancer</i> , 2020, 1, 1041-1053.	5.7	45
153	Genetic and Epigenetic Determinants of Aggressiveness in Cribriform Carcinoma of the Prostate. <i>Molecular Cancer Research</i> , 2019, 17, 446-456.	1.5	44
154	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	9.4	44
155	Multiplexed immunofluorescence delineates proteomic cancer cell states associated with metabolism. <i>JCI Insight</i> , 2016, 1, .	2.3	41
156	Expression of the Carboxy-Terminal Portion of MUC16/CA125 Induces Transformation and Tumor Invasion. <i>PLoS ONE</i> , 2015, 10, e0126633.	1.1	41
157	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. <i>Neuro-Oncology</i> , 2015, 17, 1344-1355.	0.6	40
158	rCellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. <i>Bioinformatics</i> , 2016, 32, 1272-1274.	1.8	39
159	MEF Promotes Stemness in the Pathogenesis of Gliomas. <i>Cell Stem Cell</i> , 2012, 11, 836-844.	5.2	37
160	Characteristics and Outcome of <i>AKT1</i>E17K-Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. <i>Cancer Discovery</i> , 2020, 10, 526-535.	7.7	36
161	Multicenter phase II study of temozolomide and myeloablative chemotherapy with autologous stem cell transplant for newly diagnosed anaplastic oligodendroglioma. <i>Neuro-Oncology</i> , 2017, 19, 1380-1390.	0.6	35
162	53BP1 Is a Haploinsufficient Tumor Suppressor and Protects Cells from Radiation Response in Glioma. <i>Cancer Research</i> , 2012, 72, 5250-5260.	0.4	34

#	ARTICLE	IF	CITATIONS
163	American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange: From Inception to First Data Release and Beyondâ€™”Lessons Learned and Member Institutionsâ€™™ Perspectives. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-14.	1.0	33
164	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. <i>PLoS Computational Biology</i> , 2016, 12, e1004765.	1.5	32
165	Phase and context shape the function of composite oncogenic mutations. <i>Nature</i> , 2020, 582, 100-103.	13.7	31
166	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. <i>ELife</i> , 2019, 8, .	2.8	31
167	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. <i>Bioinformatics</i> , 2014, 30, 2051-2059.	1.8	30
168	Analysis of Tumor Genomic Pathway Alterations Using Broad-Panel Next-Generation Sequencing in Surgically Resected Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 7475-7484.	3.2	30
169	Using MEMo to Discover Mutual Exclusivity Modules in Cancer. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 8.17.	25.8	29
170	Identifying Actionable Targets through Integrative Analyses of GEM Model and Human Prostate Cancer Genomic Profiling. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 278-288.	1.9	29
171	Dickkopf-1 Can Lead to Immune Evasion in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Precision Oncology</i> , 2020, 4, 1167-1179.	1.5	28
172	Specific Mutations in APC, but Not Alterations in DNA Damage Response, Associate With Outcomes of Patients With Metastatic Colorectal Cancer. <i>Gastroenterology</i> , 2020, 159, 1975-1978.e4.	0.6	26
173	Therapeutic Implications of Detecting MAPK-Activating Alterations in Cutaneous and Unknown Primary Melanomas. <i>Clinical Cancer Research</i> , 2021, 27, 2226-2235.	3.2	25
174	Integrating biological pathways and genomic profiles with ChiBE 2. <i>BMC Genomics</i> , 2014, 15, 642.	1.2	24
175	Collection, integration and analysis of cancer genomic profiles: from data to insight. <i>Current Opinion in Genetics and Development</i> , 2014, 24, 92-98.	1.5	22
176	Ribonucleotide reductase small subunit M2 is a master driver of aggressive prostate cancer. <i>Molecular Oncology</i> , 2020, 14, 1881-1897.	2.1	22
177	Expression patterns of mitotic and meiotic cell cycle regulators in testicular cancer and development. <i>International Journal of Cancer</i> , 2005, 116, 207-217.	2.3	21
178	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	6.5	21
179	FOLFCIS Treatment and Genomic Correlates of Response in Advanced Anal Squamous Cell Cancer. <i>Clinical Colorectal Cancer</i> , 2019, 18, e39-e52.	1.0	21
180	CD38 in Advanced Prostate Cancers. <i>European Urology</i> , 2021, 79, 736-746.	0.9	21

#	ARTICLE	IF	CITATIONS
181	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Nonâ€“Small Cell Lung or Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2117547.	2.8	20
182	ARF Confers a Context-Dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. <i>Cancer Research</i> , 2017, 77, 1035-1046.	0.4	15
183	Distinct Genomic Profiles are Associated With Conversion to Resection and Survival in Patients With Initially Unresectable Colorectal Liver Metastases Treated With Systemic and Hepatic Artery Chemotherapy. <i>Annals of Surgery</i> , 2022, 276, e474-e482.	2.1	15
184	Molecular and phenotypic profiling of colorectal cancer patients in West Africa reveals biological insights. <i>Nature Communications</i> , 2021, 12, 6821.	5.8	15
185	Phase II study of trastuzumab with modified docetaxel, cisplatin, and 5 fluorouracil in metastatic HER2-positive gastric cancer. <i>Gastric Cancer</i> , 2019, 22, 355-362.	2.7	11
186	Systemic Chemotherapy for Metastatic Colitis-Associated Cancer Has a Worse Outcome Than Sporadic Colorectal Cancer: Matched Case Cohort Analysis. <i>Clinical Colorectal Cancer</i> , 2020, 19, e151-e156.	1.0	11
187	Genomic and Metabolic Hallmarks of SDH- and FH-deficient Renal Cell Carcinomas. <i>European Urology Focus</i> , 2022, 8, 1278-1288.	1.6	11
188	G2S: a web-service for annotating genomic variants on 3D protein structures. <i>Bioinformatics</i> , 2018, 34, 1949-1950.	1.8	10
189	Efficacy of Combined VEGFR1-3, PDGFÎ±/Î², and FGFR1-3 Blockade Using Nintedanib for Esophagogastric Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 3811-3817.	3.2	10
190	Regorafenib in Combination with Firstâ€“Line Chemotherapy for Metastatic Esophagogastric Cancer. <i>Oncologist</i> , 2020, 25, e68-e74.	1.9	10
191	Genomic stratification beyond Ras/Bâ€“Raf in colorectal liver metastasis patients treated with hepatic arterial infusion. <i>Cancer Medicine</i> , 2019, 8, 6538-6548.	1.3	8
192	Next-Generation Sequencing of 487 Esophageal Adenocarcinomas Reveals Independently Prognostic Genomic Driver Alterations and Pathways. <i>Clinical Cancer Research</i> , 2021, 27, 3491-3498.	3.2	8
193	A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. <i>Cell Reports Methods</i> , 2021, 1, 100039.	1.4	8
194	Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. <i>Systems Medicine (New Rochelle, N Y)</i> , 2020, 3, 22-35.	1.4	7
195	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. <i>Clinics in Laboratory Medicine</i> , 2016, 36, 153-181.	0.7	6
196	Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. <i>JCO Precision Oncology</i> , 2019, 3, 1-13.	1.5	6
197	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. <i>Surgical Pathology Clinics</i> , 2015, 8, 269-288.	0.7	5
198	Primary Tumor Location and Outcomes After Cytoreductive Surgery and Intraperitoneal Chemotherapy for Peritoneal Metastases of Colorectal Origin. <i>Annals of Surgical Oncology</i> , 2021, 28, 1109-1117.	0.7	5

#	ARTICLE	IF	CITATIONS
199	Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 44-55.	0.7	5
200	Defining and Targeting Esophagogastric Cancer Genomic Subsets With Patient-Derived Xenografts. JCO Precision Oncology, 2022, 6, e2100242.	1.5	5
201	Association of genomic profiles and survival in early onset and screening age colorectal cancer patients with liver metastases resected over 15 years. Journal of Surgical Oncology, 2022, 125, 880-888.	0.8	4
202	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer. JCO Clinical Cancer Informatics, 2022, 6, e2100144.	1.0	4
203	Computational methods and translational applications for targeted next-generation sequencing platforms. Genes Chromosomes and Cancer, 2022, 61, 322-331.	1.5	3
204	Distinct Genomic Landscapes in Early-Onset and Late-Onset Endometrial Cancer. JCO Precision Oncology, 2022, 6, e2100401.	1.5	3
205	Exploring the clinical significance of serous tubal intraepithelial carcinoma associated with advanced high-grade serous ovarian cancer: A Memorial Sloan Kettering Team Ovary Study. Gynecologic Oncology, 2021, 160, 696-703.	0.6	2
206	Data Portals and Analysis. , 2019, , 169-196.		1
207	Spermatogonial Stem Cells in the Rat and Mouse. , 2004, , 179-185.		1