List of Publications by Year in descending order

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207	105,475	108	208
papers	citations	h-index	g-index
217	217	217	92958
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	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. Annals of Surgery, 2022, 276, e474-e482.	2.1	15
2	Association of genomic profiles and survival in early onset and screeningâ€age colorectal cancer patients with liver metastases resected over 15 years. Journal of Surgical Oncology, 2022, 125, 880-888.	0.8	4
3	Computational methods and translational applications for targeted nextâ€generation sequencing platforms. Genes Chromosomes and Cancer, 2022, 61, 322-331.	1.5	3
4	Distinct Genomic Landscapes in Early-Onset and Late-Onset Endometrial Cancer. JCO Precision Oncology, 2022, 6, e2100401.	1.5	3
5	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
6	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	13.5	223
7	Defining and Targeting Esophagogastric Cancer Genomic Subsets With Patient-Derived Xenografts. JCO Precision Oncology, 2022, 6, e2100242.	1.5	5
8	Genomic and Metabolic Hallmarks of SDH- and FH-deficient Renal Cell Carcinomas. European Urology Focus, 2022, 8, 1278-1288.	1.6	11
9	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .	5.8	63
10	Primary Tumor Location and Outcomes After Cytoreductive Surgery and Intraperitoneal Chemotherapy for Peritoneal Metastases of Colorectal Origin. Annals of Surgical Oncology, 2021, 28, 1109-1117.	0.7	5
11	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. Nature Cancer, 2021, 2, 357-365.	5.7	74
12	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	2.2	52
13	OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.	1.0	51
14	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
15	Next-Generation Sequencing of 487 Esophageal Adenocarcinomas Reveals Independently Prognostic Genomic Driver Alterations and Pathways. Clinical Cancer Research, 2021, 27, 3491-3498.	3.2	8
16	A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. Cell Reports Methods, 2021, 1, 100039.	1.4	8
17	CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746.	0.9	21
18	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Non–Small Cell Lung or Colorectal Cancer. JAMA Network Open, 2021, 4, e2117547.	2.8	20

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19	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.	3.0	66
20	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. Journal of Clinical Oncology, 2021, 39, 2698-2709.	0.8	83
21	Genetic Determinants of Outcome in Intrahepatic Cholangiocarcinoma. Hepatology, 2021, 74, 1429-1444.	3.6	73
22	Therapeutic Implications of Detecting MAPK-Activating Alterations in Cutaneous and Unknown Primary Melanomas. Clinical Cancer Research, 2021, 27, 2226-2235.	3.2	25
23	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
24	Molecular and phenotypic profiling of colorectal cancer patients in West Africa reveals biological insights. Nature Communications, 2021, 12, 6821.	5.8	15
25	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncology, 2020, 6, 84.	3.4	66
26	Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma. JAMA Oncology, 2020, 6, 60.	3.4	112
27	Dickkopf-1 Can Lead to Immune Evasion in Metastatic Castration-Resistant Prostate Cancer. JCO Precision Oncology, 2020, 4, 1167-1179.	1.5	28
28	Accelerating precision medicine in metastatic prostate cancer. Nature Cancer, 2020, 1, 1041-1053.	5.7	45
29	Specific Mutations in APC, but Not Alterations in DNA Damage Response, Associate With Outcomes of Patients With Metastatic Colorectal Cancer. Gastroenterology, 2020, 159, 1975-1978.e4.	0.6	26
30	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2020, 15, 1844-1856.	0.5	83
31	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. Lancet Oncology, The, 2020, 21, 821-831.	5.1	243
32	Oncogenic Genomic Alterations, Clinical Phenotypes, and Outcomes in Metastatic Castration-Sensitive Prostate Cancer. Clinical Cancer Research, 2020, 26, 3230-3238.	3.2	112
33	Ribonucleotide reductase small subunit M2 is a master driver of aggressive prostate cancer. Molecular Oncology, 2020, 14, 1881-1897.	2.1	22
34	Phase and context shape the function of composite oncogenic mutations. Nature, 2020, 582, 100-103.	13.7	31
35	Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. Systems Medicine (New Rochelle, NY), 2020, 3, 22-35.	1.4	7
36	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	9.4	104

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37	Systemic Chemotherapy for Metastatic Colitis-Associated Cancer Has a Worse Outcome Than Sporadic Colorectal Cancer: Matched Case Cohort Analysis. Clinical Colorectal Cancer, 2020, 19, e151-e156.	1.0	11
38	Regorafenib in Combination with Firstâ€Line Chemotherapy for Metastatic Esophagogastric Cancer. Oncologist, 2020, 25, e68-e74.	1.9	10
39	Characteristics and Outcome of <i>AKT1</i> E17K-Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. Cancer Discovery, 2020, 10, 526-535.	7.7	36
40	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. Clinical Cancer Research, 2020, 26, 1077-1085.	3.2	62
41	Pan-cancer Analysis of CDK12 Alterations Identifies a Subset of Prostate Cancers with Distinct Genomic and Clinical Characteristics. European Urology, 2020, 78, 671-679.	0.9	72
42	Platinum-Based Chemotherapy in Metastatic Prostate Cancer With DNA Repair Gene Alterations. JCO Precision Oncology, 2020, 4, 355-366.	1.5	93
43	Genomic Methods Identify Homologous Recombination Deficiency in Pancreas Adenocarcinoma and Optimize Treatment Selection. Clinical Cancer Research, 2020, 26, 3239-3247.	3.2	135
44	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with <i>EGFR</i> -Mutant Lung Cancers. Clinical Cancer Research, 2019, 25, 1063-1069.	3.2	257
45	Phase II study of trastuzumab with modified docetaxel, cisplatin, and 5 fluorouracil in metastatic HER2-positive gastric cancer. Gastric Cancer, 2019, 22, 355-362.	2.7	11
46	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.	5.8	48
47	Clinical and Molecular Predictors of Response to Immune Checkpoint Inhibitors in Patients with Advanced Esophagogastric Cancer. Clinical Cancer Research, 2019, 25, 6160-6169.	3.2	73
48	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	13.7	295
49	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. Molecular and Cellular Proteomics, 2019, 18, 1893-1898.	2.5	106
50	Genomic stratification beyond Ras/Bâ€Raf in colorectal liver metastasis patients treated with hepatic arterial infusion. Cancer Medicine, 2019, 8, 6538-6548.	1.3	8
51	Analysis of Tumor Genomic Pathway Alterations Using Broad-Panel Next-Generation Sequencing in Surgically Resected Lung Adenocarcinoma. Clinical Cancer Research, 2019, 25, 7475-7484.	3.2	30
52	Genomic correlates of clinical outcome in advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11428-11436.	3.3	839
53	The expanding landscape of â€~oncohistone' mutations in human cancers. Nature, 2019, 567, 473-478.	13.7	271
54	Efficacy of Combined VEGFR1-3, PDGF $\hat{\mathbf{l}}^2$, and FGFR1-3 Blockade Using Nintedanib for Esophagogastric Cancer. Clinical Cancer Research, 2019, 25, 3811-3817.	3.2	10

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55	Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. JCO Precision Oncology, 2019, 3, 1-13.	1.5	6
56	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Non–Small-Cell Lung Cancer. JCO Precision Oncology, 2019, 3, 1-12.	1.5	58
57	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. JAMA Oncology, 2019, 5, 471.	3.4	426
58	<i>EGFR</i> and <i>MET</i> Amplifications Determine Response to HER2 Inhibition in <i>ERBB2</i> -Amplified Esophagogastric Cancer. Cancer Discovery, 2019, 9, 199-209.	7.7	115
59	Genetic and Epigenetic Determinants of Aggressiveness in Cribriform Carcinoma of the Prostate. Molecular Cancer Research, 2019, 17, 446-456.	1.5	44
60	Prospective Genotyping of Hepatocellular Carcinoma: Clinical Implications of Next-Generation Sequencing for Matching Patients to Targeted and Immune Therapies. Clinical Cancer Research, 2019, 25, 2116-2126.	3.2	390
61	FOLFCIS Treatment and Genomic Correlates of Response in Advanced Anal Squamous Cell Cancer. Clinical Colorectal Cancer, 2019, 18, e39-e52.	1.0	21
62	Genomic Differences Between "Primary―and "Secondary―Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. European Urology, 2019, 75, 231-239.	0.9	104
63	Data Portals and Analysis. , 2019, , 169-196.		1
64	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.	3.9	134
65	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. ELife, 2019, 8, .	2.8	31
66	Unifying cancer and normal RNA sequencing data from different sources. Scientific Data, 2018, 5, 180061.	2.4	152
67	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
68	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
69	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
70	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
71	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
72	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417

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7 3	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
74	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
7 5	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
76	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
77	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
78	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
79	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
80	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
81	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
82	G2S: a web-service for annotating genomic variants on 3D protein structures. Bioinformatics, 2018, 34, 1949-1950.	1.8	10
83	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	7.7	275
84	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	7.7	589
85	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
86	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.	7.7	400
87	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
88	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
89	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
90	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601

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91	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	7.7	213
92	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. Clinical Cancer Research, 2018, 24, 1965-1973.	3.2	85
93	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	7.7	275
94	American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange: From Inception to First Data Release and Beyondâ€"Lessons Learned and Member Institutions' Perspectives. JCO Clinical Cancer Informatics, 2018, 2, 1-14.	1.0	33
95	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. Journal of Clinical Oncology, 2018, 36, 633-641.	0.8	1,109
96	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. Journal of Clinical Investigation, 2018, 128, 4441-4453.	3.9	155
97	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. Cancer Cell, 2018, 34, 893-905.e8.	7.7	307
98	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î ² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
99	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	7.7	633
100	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. Clinical Cancer Research, 2018, 24, 4154-4161.	3.2	348
101	KMT2C mediates the estrogen dependence of breast cancer through regulation of ERα enhancer function. Oncogene, 2018, 37, 4692-4710.	2.6	102
102	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
103	Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.	9.4	411
104	<i>KMT2C</i> Mutations in Diffuse-Type Gastric Adenocarcinoma Promote Epithelial-to-Mesenchymal Transition. Clinical Cancer Research, 2018, 24, 6556-6569.	3.2	70
105	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. ELife, 2018, 7, .	2.8	217
106	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. Genome Medicine, 2017, 9, 4.	3.6	170
107	ARF Confers a Context-Dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. Cancer Research, 2017, 77, 1035-1046.	0.4	15
108	Recurrent patterns of DNA copy number alterations in tumors reflect metabolic selection pressures. Molecular Systems Biology, 2017, 13, 914.	3.2	73

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109	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	15.2	2,473
110	Multicenter phase II study of temozolomide and myeloablative chemotherapy with autologous stem cell transplant for newly diagnosed anaplastic oligodendroglioma. Neuro-Oncology, 2017, 19, 1380-1390.	0.6	35
111	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
112	Ibrutinib Unmasks Critical Role of Bruton Tyrosine Kinase in Primary CNS Lymphoma. Cancer Discovery, 2017, 7, 1018-1029.	7.7	302
113	ERF mutations reveal a balance of ETS factors controlling prostate oncogenesis. Nature, 2017, 546, 671-675.	13.7	70
114	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.	1.8	50
115	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.	7.7	490
116	Morphological characterization of colorectal cancers in The Cancer Genome Atlas reveals distinct morphology–molecular associations: clinical and biological implications. Modern Pathology, 2017, 30, 599-609.	2.9	74
117	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
118	The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing $\mbox{\sc i}\mbox{\sc FAK-/i}\mbox{\sc i}\mbox{\sc Science Signaling, 2017, 10, .}$	1.6	52
119	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. Cancer Cell, 2017, 32, 155-168.e6.	7.7	93
120	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
121	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. European Urology, 2017, 72, 952-959.	0.9	263
122	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	286
123	OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	1,266
124	Mitochondrial respiratory gene expression is suppressed in many cancers. ELife, 2017, 6, .	2.8	102
125	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. PLoS Computational Biology, 2016, 12, e1004765.	1.5	32
126	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205

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127	The metabolic co-regulator PGC1α suppresses prostate cancer metastasis. Nature Cell Biology, 2016, 18, 645-656.	4.6	176
128	Genomic Alterations Observed in Colitis-Associated Cancers Are Distinct From Those Found in Sporadic Colorectal Cancers and Vary by Type of Inflammatory Bowel Disease. Gastroenterology, 2016, 151, 278-287.e6.	0.6	147
129	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
130	Genetic Determinants of Cisplatin Resistance in Patients With Advanced Germ Cell Tumors. Journal of Clinical Oncology, 2016, 34, 4000-4007.	0.8	147
131	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. Nature Communications, 2016, 7, 13131.	5.8	140
132	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. Nucleic Acids Research, 2016, 44, D986-D991.	6. 5	21
133	rcellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. Bioinformatics, 2016, 32, 1272-1274.	1.8	39
134	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. Nature, 2016, 531, 471-475.	13.7	202
135	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Clinics in Laboratory Medicine, 2016, 36, 153-181.	0.7	6
136	Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. Nature Medicine, 2016, 22, 369-378.	15.2	572
137	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.	9.4	634
138	Chemotherapy Resistance in Diffuse-Type Gastric Adenocarcinoma Is Mediated by RhoA Activation in Cancer Stem-Like Cells. Clinical Cancer Research, 2016, 22, 971-983.	3.2	89
139	Multiplexed immunofluorescence delineates proteomic cancer cell states associated with metabolism. JCI Insight, $2016,1,.$	2.3	41
140	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. Journal of Clinical Investigation, 2016, 126, 1052-1066.	3.9	874
141	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
142	Genomic Predictors of Survival in Patients with High-grade Urothelial Carcinoma of the Bladder. European Urology, 2015, 67, 198-201.	0.9	122
143	<i>PIK3CA</i> Mutations Are Associated With Decreased Benefit to Neoadjuvant Human Epidermal Growth Factor Receptor 2–Targeted Therapies in Breast Cancer. Journal of Clinical Oncology, 2015, 33, 1334-1339.	0.8	201
144	Response to MET Inhibitors in Patients with Stage IV Lung Adenocarcinomas Harboring <i>MET</i> Mutations Causing Exon 14 Skipping. Cancer Discovery, 2015, 5, 842-849.	7.7	514

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145	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
146	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Surgical Pathology Clinics, 2015, 8, 269-288.	0.7	5
147	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.	3.8	145
148	Identifying Actionable Targets through Integrative Analyses of GEM Model and Human Prostate Cancer Genomic Profiling. Molecular Cancer Therapeutics, 2015, 14, 278-288.	1.9	29
149	Somatic <i>POLE</i> mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. Neuro-Oncology, 2015, 17, 1356-1364.	0.6	94
150	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. Neuro-Oncology, 2015, 17, 1344-1355.	0.6	40
151	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
152	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. Cell Systems, 2015, 1, 197-209.	2.9	94
153	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
154	Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2015, 68, 970-977.	0.9	202
155	Expression of the Carboxy-Terminal Portion of MUC16/CA125 Induces Transformation and Tumor Invasion. PLoS ONE, 2015, 10, e0126633.	1.1	41
156	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
157	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. Bioinformatics, 2014, 30, 2051-2059.	1.8	30
158	Copy number alteration burden predicts prostate cancer relapse. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11139-11144.	3.3	299
159	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
160	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. Nature Genetics, 2014, 46, 424-426.	9.4	291
161	Synthetic Lethality in ATM-Deficient <i>RAD50</i> Cancer Therapy. Cancer Discovery, 2014, 4, 1014-1021.	7.7	114
162	Loss of NF1 in Cutaneous Melanoma Is Associated with RAS Activation and MEK Dependence. Cancer Research, 2014, 74, 2340-2350.	0.4	266

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163	Tumor Genetic Analyses of Patients with Metastatic Renal Cell Carcinoma and Extended Benefit from mTOR Inhibitor Therapy. Clinical Cancer Research, 2014, 20, 1955-1964.	3.2	208
164	MLL3 Is a Haploinsufficient 7q Tumor Suppressor in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 652-665.	7.7	274
165	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750.	2.4	244
166	Loss of the tyrosine phosphatase PTPRD leads to aberrant STAT3 activation and promotes gliomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8149-8154.	3.3	80
167	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	1.2	24
168	Genome-wide analysis of noncoding regulatory mutations in cancer. Nature Genetics, 2014, 46, 1160-1165.	9.4	469
169	Collection, integration and analysis of cancer genomic profiles: from data to insight. Current Opinion in Genetics and Development, 2014, 24, 92-98.	1.5	22
170	Analytic and Clinical Validation of a Prostate Cancer–Enhanced Messenger RNA Detection Assay in Whole Blood as a Prognostic Biomarker for Survival. European Urology, 2014, 65, 1191-1197.	0.9	66
171	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. Oncotarget, 2014, 5, 8083-8092.	0.8	55
172	Evaluating cell lines as tumour models by comparison of genomic profiles. Nature Communications, 2013, 4, 2126.	5 . 8	1,108
173	Analysis of microRNA-target interactions across diverse cancer types. Nature Structural and Molecular Biology, 2013, 20, 1325-1332.	3.6	184
174	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
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