Nikolaus D Schultz

List of Publications by Year
in descending order

241 papers	141,538 citations	944 115 h-index	813 246 g-index
256 all docs	256 docs citations	256 times ranked	110902 citing authors

#	Article	IF	Citations
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	7.7	12,801
2	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.	1.6	11,344
3	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	13.7	10,282
4	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
5	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	9.4	6,265
6	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
7	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
8	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
9	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
10	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	13.7	3,483
11	Integrative Genomic Profiling of Human Prostate Cancer. Cancer Cell, 2010, 18, 11-22.	7.7	3,151
12	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	13.7	2,839
13	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
14	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
15	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	15.2	2,473
16	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
17	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
18	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

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19	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
20	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
21	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
22	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
23	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
24	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
25	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
26	OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	1,266
27	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205
28	Emerging landscape of oncogenic signatures across human cancers. Nature Genetics, 2013, 45, 1127-1133.	9.4	1,190
29	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
30	Evaluating cell lines as tumour models by comparison of genomic profiles. Nature Communications, 2013, 4, 2126.	5.8	1,108
31	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	6.5	980
32	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. Journal of Clinical Investigation, 2016, 126, 1052-1066.	3.9	874
33	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
34	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
35	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
36	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738

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37	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
38	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.	9.4	634
39	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	7.7	633
40	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
41	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
42	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601
43	Mutual exclusivity analysis identifies oncogenic network modules. Genome Research, 2012, 22, 398-406.	2.4	597
44	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	7.7	589
45	Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. Nature Medicine, 2016, 22, 369-378.	15.2	572
46	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
47	A multitude of genes expressed solely in meiotic or postmeiotic spermatogenic cells offers a myriad of contraceptive targets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12201-12206.	3.3	514
48	Response to MET Inhibitors in Patients with Stage IV Lung Adenocarcinomas Harboring *MET* Mutations Causing Exon 14 Skipping. Cancer Discovery, 2015, 5, 842-849.	7.7	514
49	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
50	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
51	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
52	Genome-wide analysis of noncoding regulatory mutations in cancer. Nature Genetics, 2014, 46, 1160-1165.	9.4	469
53	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. JAMA Oncology, 2019, 5, 471.	3.4	426
54	Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.	9.4	411

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55	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
56	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
57	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
58	The mutational landscape of adenoid cystic carcinoma. Nature Genetics, 2013, 45, 791-798.	9.4	394
59	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
60	Pattern discovery and cancer gene identification in integrated cancer genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4245-4250.	3.3	361
61	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. Clinical Cancer Research, 2018, 24, 4154-4161.	3.2	348
62	Somatic mutations of the Parkinson's disease–associated gene PARK2 in glioblastoma and other human malignancies. Nature Genetics, 2010, 42, 77-82.	9.4	336
63	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
64	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
65	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	1.1	318
66	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
67	Ibrutinib Unmasks Critical Role of Bruton Tyrosine Kinase in Primary CNS Lymphoma. Cancer Discovery, 2017, 7, 1018-1029.	7.7	302
68	Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators *BAP1* and *SETD2*: A Report by MSKCC and the KIRC TCGA Research Network. Clinical Cancer Research, 2013, 19, 3259-3267.	3.2	301
69	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
70	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	13.7	295
71	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. Nature Genetics, 2014, 46, 424-426.	9.4	291
72	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

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73	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
74	Prevalence and Co-Occurrence of Actionable Genomic Alterations in High-Grade Bladder Cancer. Journal of Clinical Oncology, 2013, 31, 3133-3140.	0.8	282
75	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	7.7	275
76	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	7.7	275
77	MLL3 Is a Haploinsufficient 7q Tumor Suppressor in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 652-665.	7.7	274
78	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
79	The expanding landscape of â€˜oncohistoneâ€™ mutations in human cancers. Nature, 2019, 567, 473-478.	13.7	271
80	Loss of NF1 in Cutaneous Melanoma Is Associated with RAS Activation and MEK Dependence. Cancer Research, 2014, 74, 2340-2350.	0.4	266
81	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. European Urology, 2017, 72, 952-959.	0.9	263
82	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
83	The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9435-9440.	3.3	246
84	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
85	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
86	An Epidemiologic and Genomic Investigation Into the Obesity Paradox in Renal Cell Carcinoma. Journal of the National Cancer Institute, 2013, 105, 1862-1870.	3.0	231
87	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
88	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	13.5	223
89	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. ELife, 2018, 7, .	2.8	217
90	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	7.7	213

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91	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
92	Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2015, 68, 970-977.	0.9	202
93	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. Nature, 2016, 531, 471-475.	13.7	202
94	<i>PIK3CA</i> Mutations Are Associated With Decreased Benefit to Neoadjuvant Human Epidermal Growth Factor Receptor 2â€"Targeted Therapies in Breast Cancer. Journal of Clinical Oncology, 2015, 33, 1334-1339.	0.8	201
95	Integrative Subtype Discovery in Glioblastoma Using iCluster. PLoS ONE, 2012, 7, e35236.	1.1	196
96	Analysis of microRNA-target interactions across diverse cancer types. Nature Structural and Molecular Biology, 2013, 20, 1325-1332.	3.6	184
97	The metabolic co-regulator PGC1Î± suppresses prostate cancer metastasis. Nature Cell Biology, 2016, 18, 645-656.	4.6	176
98	Distinct Patterns of Dysregulated Expression of Enzymes Involved in Androgen Synthesis and Metabolism in Metastatic Prostate Cancer Tumors. Cancer Research, 2012, 72, 6142-6152.	0.4	175
99	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. Genome Medicine, 2017, 9, 4.	3.6	170
100	Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. Clinical Cancer Research, 2017, 23, 6094-6100.	3.2	161
101	Identification of PHLPP1 as a Tumor Suppressor Reveals the Role of Feedback Activation in PTEN-Mutant Prostate Cancer Progression. Cancer Cell, 2011, 20, 173-186.	7.7	158
102	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. Journal of Clinical Investigation, 2018, 128, 4441-4453.	3.9	155
103	Comprehensive Molecular Characterization of Salivary Duct Carcinoma Reveals Actionable Targets and Similarity to Apocrine Breast Cancer. Clinical Cancer Research, 2016, 22, 4623-4633.	3.2	153
104	Unifying cancer and normal RNA sequencing data from different sources. Scientific Data, 2018, 5, 180061.	2.4	152
105	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
106	Genetic Determinants of Cisplatin Resistance in Patients With Advanced Germ Cell Tumors. Journal of Clinical Oncology, 2016, 34, 4000-4007.	0.8	147
107	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.	3.8	145
108	Cancer cells preferentially lose small chromosomes. International Journal of Cancer, 2013, 132, 2316-2326.	2.3	143

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109	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. Nature Communications, 2016, 7, 13131.	5.8	140
110	A cluster of cooperating tumor-suppressor gene candidates in chromosomal deletions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8212-8217.	3.3	138
111	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. Cancer Cell, 2013, 24, 738-750.	7.7	135
112	Genomic Methods Identify Homologous Recombination Deficiency in Pancreas Adenocarcinoma and Optimize Treatment Selection. Clinical Cancer Research, 2020, 26, 3239-3247.	3.2	135
113	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
114	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.	3.9	134
115	Defining the spermatogonial stem cell. Developmental Biology, 2004, 269, 393-410.	0.9	126
116	Genomic Predictors of Survival in Patients with High-grade Urothelial Carcinoma of the Bladder. European Urology, 2015, 67, 198-201.	0.9	122
117	The molecular diversity of Luminal A breast tumors. Breast Cancer Research and Treatment, 2013, 141, 409-420.	1.1	120
118	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
119	Mismatch Repairâ€"Deficient Rectal Cancer and Resistance to Neoadjuvant Chemotherapy. Clinical Cancer Research, 2020, 26, 3271-3279.	3.2	118
120	<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
121	Synthetic Lethality in ATM-Deficient <i>RAD50</i>-Mutant Tumors Underlies Outlier Response to Cancer Therapy. Cancer Discovery, 2014, 4, 1014-1021.	7.7	114
122	18F-Fluorodeoxy-glucose Positron Emission Tomography Marks MYC-Overexpressing Human Basal-Like Breast Cancers. Cancer Research, 2011, 71, 5164-5174.	0.4	113
123	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
124	Oncogenic Genomic Alterations, Clinical Phenotypes, and Outcomes in Metastatic Castration-Sensitive Prostate Cancer. Clinical Cancer Research, 2020, 26, 3230-3238.	3.2	112
125	Genomic Complexity and AKT Dependence in Serous Ovarian Cancer. Cancer Discovery, 2012, 2, 56-67.	7.7	109
126	Frequent Alterations and Epigenetic Silencing of Differentiation Pathway Genes in Structurally Rearranged Liposarcomas. Cancer Discovery, 2011, 1, 587-597.	7.7	108

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127	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
128	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.	1.1	104
129	Genomic Differences Between â€œPrimaryâ€•and â€œSecondaryâ€•Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. European Urology, 2019, 75, 231-239.	0.9	104
130	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	9.4	104
131	KMT2C mediates the estrogen dependence of breast cancer through regulation of ERÎ± enhancer function. Oncogene, 2018, 37, 4692-4710.	2.6	102
132	Mitochondrial respiratory gene expression is suppressed in many cancers. ELife, 2017, 6, .	2.8	102
133	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 527-541.e8.	7.7	99
134	Somatic *POLE* mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. Neuro-Oncology, 2015, 17, 1356-1364.	0.6	94
135	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. Cell Systems, 2015, 1, 197-209.	2.9	94
136	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. Cancer Cell, 2017, 32, 155-168.e6.	7.7	93
137	Platinum-Based Chemotherapy in Metastatic Prostate Cancer With DNA Repair Gene Alterations. JCO Precision Oncology, 2020, 4, 355-366.	1.5	93
138	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. PLoS ONE, 2013, 8, e80306.	1.1	90
139	Identification of low abundance microbiome in clinical samples using whole genome sequencing. Genome Biology, 2015, 16, 265.	3.8	90
140	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
141	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. PLoS ONE, 2011, 6, e24709.	1.1	88
142	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
143	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2020, 15, 1844-1856.	0.5	83
144	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. Journal of Clinical Oncology, 2021, 39, 2698-2709.	0.8	83

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145	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
146	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF-Î² pathway and reveal microRNA regulation of TGFBR2. Silence: A Journal of RNA Regulation, 2011, 2, 3.	8.0	78
147	Morphological characterization of colorectal cancers in The Cancer Genome Atlas reveals distinct morphologyâ€"molecular associations: clinical and biological implications. Modern Pathology, 2017, 30, 599-609.	2.9	74
148	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
149	Recurrent patterns of DNA copy number alterations in tumors reflect metabolic selection pressures. Molecular Systems Biology, 2017, 13, 914.	3.2	73
150	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
151	Genetic Determinants of Outcome in Intrahepatic Cholangiocarcinoma. Hepatology, 2021, 74, 1429-1444.	3.6	73
152	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
153	ERF mutations reveal a balance of ETS factors controlling prostate oncogenesis. Nature, 2017, 546, 671-675.	13.7	70
154	<i>KMT2C</i> Mutations in Diffuse-Type Gastric Adenocarcinoma Promote Epithelial-to-Mesenchymal Transition. Clinical Cancer Research, 2018, 24, 6556-6569.	3.2	70
155	<i>MLH1</i>â€"silenced and nonâ€"silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	2.1	67
156	Analytic and Clinical Validation of a Prostate Cancerâ€"Enhanced Messenger RNA Detection Assay in Whole Blood as a Prognostic Biomarker for Survival. European Urology, 2014, 65, 1191-1197.	0.9	66
157	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncology, 2020, 6, 84.	3.4	66
158	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.	3.0	66
159	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .	5.8	63
160	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
161	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Nonâ€"Small-Cell Lung Cancer. JCO Precision Oncology, 2019, 3, 1-12.	1.5	58
162	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. Oncotarget, 2014, 5, 8083-8092.	0.8	55

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163	BRCA1 Immunohistochemistry in a Molecularly Characterized Cohort of Ovarian High-Grade Serous Carcinomas. American Journal of Surgical Pathology, 2013, 37, 138-146.	2.1	54
164	The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing *FAK*. Science Signaling, 2017, 10, .	1.6	52
165	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	2.2	52
166	OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.	1.0	51
167	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.	1.8	50
168	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.	5.8	48
169	Accelerating precision medicine in metastatic prostate cancer. Nature Cancer, 2020, 1, 1041-1053.	5.7	45
170	Genetic and Epigenetic Determinants of Aggressiveness in Cribriform Carcinoma of the Prostate. Molecular Cancer Research, 2019, 17, 446-456.	1.5	44
171	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
172	Multiplexed immunofluorescence delineates proteomic cancer cell states associated with metabolism. JCI Insight, 2016, 1, .	2.3	41
173	Expression of the Carboxy-Terminal Portion of MUC16/CA125 Induces Transformation and Tumor Invasion. PLoS ONE, 2015, 10, e0126633.	1.1	41
174	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. Neuro-Oncology, 2015, 17, 1344-1355.	0.6	40
175	rcellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. Bioinformatics, 2016, 32, 1272-1274.	1.8	39
176	MEF Promotes Stemness in the Pathogenesis of Gliomas. Cell Stem Cell, 2012, 11, 836-844.	5.2	37
177	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
178	Characteristics and Outcome of *AKT1* E17K-Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. Cancer Discovery, 2020, 10, 526-535.	7.7	36
179	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
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