Matthew L Meyerson

List of Publications by Year
in descending order

172	118,111	2963	4870
papers	citations	93 h-index	168 g-index

187	187	187	108381
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pan-ERBB kinase inhibition augments CDK4/6 inhibitor efficacy in oesophageal squamous cell carcinoma. Gut, 2022, 71, 665-675.	6.1	15
2	Long-read sequencing reveals complex patterns of wraparound transcription in polyomaviruses. PLoS Pathogens, 2022, 18, e1010401.	2.1	8
3	Functional Genomic Analysis ofCDK4andCDK6Gene Dependency across Human Cancer Cell Lines. Cancer Research, 2022, 82, 2171-2184.	0.4	12
4	Abstract 3890: Sequencing of 888 pediatric solid tumors informs precision oncology trial design and data sharing initiatives in pediatric cancer. Cancer Research, 2022, 82, 3890-3890.	0.4	0
5	Abstract 2151: Identification and proteogenomic characterization of novel lung adenocarcinoma subtypes with therapeutic relevance. Cancer Research, 2022, 82, 2151-2151.	0.4	0
6	An international report on bacterial communities in esophageal squamous cell carcinoma. International Journal of Cancer, 2022, 151, 1947-1959.	2.3	7
7	Quantification of aneuploidy in targeted sequencing data using ASCETS. Bioinformatics, 2021, 37, 2461-2463.	1.8	21
8	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. Cancer Discovery, 2021, 11, 591-598.	7.7	69
9	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. Clinical Cancer Research, 2021, 27, 1695-1705.	3.2	19
10	Antigen identification for HLA class Iâ€“ and HLA class Iiâ€“restricted T cell receptors using cytokine-capturing antigen-presenting cells. Science Immunology, 2021, 6, .	5.6	22
11	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	2.9	16
12	Genomic Evolution in a Patient With Lung Adenocarcinoma With a Germline EGFR T790M Mutation. JTO Clinical and Research Reports, 2021, 2, 100146.	0.6	0
13	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. Nature Genetics, 2021, 53, 881-894.	9.4	44
14	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. Nature Communications, 2021, 12, 4375.	5.8	39
15	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. Genome Medicine, 2021, 13, 114.	3.6	5
16	Multi-Omics Analysis Identifies MGA as a Negative Regulator of the MYC Pathway in Lung Adenocarcinoma. Molecular Cancer Research, 2020, 18, 574-584.	1.5	33
17	Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2. Genome Medicine, 2020, 12, 108.	3.6	54
18	Bacterial invaders drive CRC progression. Science Signaling, 2020, 13, .	1.6	3

#	Article	IF	Citations
19	Illuminating the noncoding genome in cancer. Nature Cancer, 2020, 1, 864-872.	5.7	37
20	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. Journal of Biological Chemistry, 2020, 295, 3431-3446.	1.6	12
21	Mutational signature in colorectal cancer caused by genotoxic pks+ E. coli. Nature, 2020, 580, 269-273.	13.7	587
22	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. Clinical Cancer Research, 2020, 26, 2556-2564.	3.2	109
23	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. Nature Cancer, 2020, 1, 235-248.	5.7	430
24	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
25	Patterns of chromosome 18 loss of heterozygosity in multifocal ileal neuroendocrine tumors. Genes Chromosomes and Cancer, 2020, 59, 535-539.	1.5	16
26	Comprehensive metagenomic analysis of blastic plasmacytoid dendritic cell neoplasm. Blood Advances, 2020, 4, 1006-1011.	2.5	10
27	Optimization of PDE3A Modulators for SLFN12-Dependent Cancer Cell Killing. ACS Medicinal Chemistry Letters, 2019, 10, 1537-1542.	1.3	17
28	Pooled Genomic Screens Identify Anti-apoptotic Genes as Targetable Mediators of Chemotherapy Resistance in Ovarian Cancer. Molecular Cancer Research, 2019, 17, 2281-2293.	1.5	29
29	Patient-derived lung cancer organoids as in vitro cancer models for therapeutic screening. Nature Communications, 2019, 10, 3991.	5.8	409
30	Commensal Microbiota Promote Lung Cancer Development via Î³Î´ T Cells. Cell, 2019, 176, 998-1013.e16.	13.5	592
31	Circulating Tumor DNA Provides a Sneak Peek into Treatment Responses in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2019, 79, 1038-1040.	0.4	2
32	Genomic and immune profiling of pre-invasive lung adenocarcinoma. Nature Communications, 2019, 10, 5472.	5.8	127
33	Identification and Characterization of Oncogenic SOS1 Mutations in Lung Adenocarcinoma. Molecular Cancer Research, 2019, 17, 1002-1012.	1.5	32
34	Distinct pathways affected by menin versus MLL1/MLL2 in MLL-rearranged acute myeloid leukemia. Experimental Hematology, 2019, 69, 37-42.	0.2	13
35	Autophosphorylation of the carboxylâ€terminal domain is not required for oncogenic transformation by lungâ€cancer derived <scp>EGFR</scp> mutants. International Journal of Cancer, 2018, 143, 679-685.	2.3	8
36	RASâ€“MAPK Reactivation Facilitates Acquired Resistance in FGFR1-Amplified Lung Cancer and Underlies a Rationale for Upfront FGFRâ€“MEK Blockade. Molecular Cancer Therapeutics, 2018, 17, 1526-1539.	1.9	39

#	Article	IF	Citations
37	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
38	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
39	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
40	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
41	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
42	Mechanistic Insights into Transmissible Cancers of Mammals. Cancer Cell, 2018, 33, 543-544.	7.7	4
43	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	15.2	1,224
44	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
45	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
46	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
47	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
48	Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. Leukemia, 2018, 32, 1838-1841.	3.3	42
49	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. Cancer Discovery, 2018, 8, 59-73.	7.7	96
50	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. Cancer Discovery, 2018, 8, 108-125.	7.7	99
51	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. Nature Communications, 2018, 9, 5450.	5.8	157
52	The Amount of Bifidobacterium Genus in Colorectal Carcinoma Tissue in Relation to Tumor Characteristics and Clinical Outcome. American Journal of Pathology, 2018, 188, 2839-2852.	1.9	51
53	Detection of Somatic Structural Variants Enables Quantification and Characterization of Circulating Tumor DNA in Children With Solid Tumors. JCO Precision Oncology, 2018, 2018, 1-13.	1.5	95
54	Mutational processes shape the landscape of TP53 mutations in human cancer. Nature Genetics, 2018, 50, 1381-1387.	9.4	334

#	Article	IF	Citations
55	Fusobacterium nucleatum in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. Cancer Immunology Research, 2018, 6, 1327-1336.	1.6	127
56	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. Nature Genetics, 2018, 50, 937-943.	9.4	55
57	Genotype-targeted local therapy of glioma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8388-E8394.	3.3	40
58	Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330.	13.7	662
59	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
60	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	13.5	258
61	Splicing modulation sensitizes chronic lymphocytic leukemia cells to venetoclax by remodeling mitochondrial apoptotic dependencies. JCI Insight, 2018, 3, .	2.3	39
62	Tumor fraction in cell-free DNA as a biomarker in prostate cancer. JCI Insight, 2018, 3, .	2.3	94
63	Bifidobacterium Genus in Colorectal Carcinoma Tissue in relation to Tumor Characteristics and Patient Survival. FASEB Journal, 2018, 32, 407.3.	0.2	0
64	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. Cell, 2017, 168, 460-472.e14.	13.5	106
65	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. JAMA Oncology, 2017, 3, 801.	3.4	78
66	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
67	MET Exon 14 Mutation Encodes an Actionable Therapeutic Target in Lung Adenocarcinoma. Cancer Research, 2017, 77, 4498-4505.	0.4	57
68	Copy number alterations unmasked as enhancer hijackers. Nature Genetics, 2017, 49, 5-6.	9.4	40
69	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
70	Analysis of Fusobacterium persistence and antibiotic response in colorectal cancer. Science, 2017, 358, 1443-1448.	6.0	983
71	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	5.8	584
72	Institutional implementation of clinical tumor profiling on an unselected cancer population. JCI Insight, 2016, 1, e87062.	2.3	340

#	Article	IF	Citations
73	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. PLoS Genetics, 2016, 12, e1006242.	1.5	93
74	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
75	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
76	Fusobacterium nucleatum in Colorectal Carcinoma Tissue According to Tumor Location. Clinical and Translational Gastroenterology, 2016, 7, e200.	1.3	225
77	Kmt2a cooperates with menin to suppress tumorigenesis in mouse pancreatic islets. Cancer Biology and Therapy, 2016, 17, 1274-1281.	1.5	11
78	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. Science Translational Medicine, 2016, 8, 363ra147.	5.8	126
79	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	7.7	485
80	Metagenomic Characterization of Microbial Communities In Situ Within the Deeper Layers of the Ileum in Crohnâ€™s Disease. Cellular and Molecular Gastroenterology and Hepatology, 2016, 2, 563-566.e5.	2.3	23
81	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. Nature Genetics, 2016, 48, 176-182.	9.4	283
82	Identification of cancer-cytotoxic modulators of PDE3A by predictive chemogenomics. Nature Chemical Biology, 2016, 12, 102-108.	3.9	72
83	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
84	Identification of an â€œExceptional Responderâ€•Cell Line to MEK1 Inhibition: Clinical Implications for MEK-Targeted Therapy. Molecular Cancer Research, 2016, 14, 207-215.	1.5	23
85	Fusobacterium nucleatumin colorectal carcinoma tissue and patient prognosis. Gut, 2016, 65, 1973-1980.	6.1	718
86	Prognostic Impact of Novel Molecular Subtypes of Small Intestinal Neuroendocrine Tumor. Clinical Cancer Research, 2016, 22, 250-258.	3.2	149
87	Comprehensive Genetic Interrogation of Circulating Multiple Myeloma Cells at Single Cell Resolution. Blood, 2016, 128, 800-800.	0.6	0
88	The tumor virus landscape of AIDS-related lymphomas. Blood, 2015, 125, e14-e22.	0.6	67
89	Near universal detection of alterations in <scp>CTNNB1</scp> and <scp>Wnt</scp> pathway regulators in desmoidâ€type fibromatosis by wholeâ€exome sequencing and genomic analysis. Genes Chromosomes and Cancer, 2015, 54, 606-615.	1.5	138
90	Oncotator: Cancer Variant Annotation Tool. Human Mutation, 2015, 36, E2423-E2429.	1.1	448

#	Article	IF	Citations
91	Chromothripsis from DNA damage inÂmicronuclei. Nature, 2015, 522, 179-184.	13.7	924
92	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. International Journal of Cancer, 2015, 137, 776-783.	2.3	39
93	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. Genome Research, 2015, 25, 316-327.	2.4	343
94	Dynamic Epigenetic Regulation by Menin During Pancreatic Islet Tumor Formation. Molecular Cancer Research, 2015, 13, 689-698.	1.5	49
95	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
96	Updated Frequency of EGFR and KRAS Mutations in NonSmall-Cell Lung Cancer in Latin America: The Latin-American Consortium for the Investigation of Lung Cancer (CLICaP). Journal of Thoracic Oncology, 2015, 10, 838-843.	0.5	156
97	Calibrating genomic and allelic coverage bias in single-cell sequencing. Nature Communications, 2015, 6, 6822.	5.8	74
98	Pugh et al. reply. Nature, 2015, 520, E12-E14.	13.7	8
99	BreaKmer: detection of structural variation in targeted massively parallel sequencing data using kmers. Nucleic Acids Research, 2015, 43, e19-e19.	6.5	161
100	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710
101	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. Cancer Cell, 2015, 27, 397-408.	7.7	150
102	Characterization of DDR2 Inhibitors for the Treatment of DDR2 Mutated Nonsmall Cell Lung Cancer. ACS Chemical Biology, 2015, 10, 2687-2696.	1.6	43
103	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	7.7	821
104	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
105	Complete hematologic response of early T-cell progenitor acute lymphoblastic leukemia to the Î³-secretase inhibitor BMS-906024: genetic and epigenetic findings in an outlier case. Journal of Physical Education and Sports Management, 2015, 1, a000539.	0.5	47
106	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
107	NSCLC Driven by DDR2 Mutation Is Sensitive to Dasatinib and JQ1 Combination Therapy. Molecular Cancer Therapeutics, 2015, 14, 2382-2389.	1.9	29
108	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. Nature Structural and Molecular Biology, 2015, 22, 703-711.	3.6	72

#	Article	IF	Citations
109	Rapid Intraoperative Molecular Characterization of Glioma. JAMA Oncology, 2015, 1, 662.	3.4	68
110	Whole-Exome Sequencing Reveals Frequent Genetic Alterations in BAP1, NF2, CDKN2A, and CUL1 in Malignant Pleural Mesothelioma. Cancer Research, 2015, 75, 264-269.	0.4	289
111	Malawi Polyomavirus Is a Prevalent Human Virus That Interacts with Known Tumor Suppressors. Journal of Virology, 2015, 89, 857-862.	1.5	21
112	Distinct MET alterations to induce a common phenotype and to define a MET-driven subset of papillary RCC: Results from the Cancer Genome Atlas (TCGA) Kidney Renal Papillary (KIRP) Working Group.. Journal of Clinical Oncology, 2015, 33, 4521-4521.	0.8	1
113	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. PLoS ONE, 2014, 9, e87361.	1.1	168
114	Genetic modifiers of EGFR dependence in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18661-18666.	3.3	46
115	EGFR Variant Heterogeneity in Glioblastoma Resolved through Single-Nucleus Sequencing. Cancer Discovery, 2014, 4, 956-971.	7.7	251
116	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
117	Kinase Domain Activation of FGFR2 Yields High-Grade Lung Adenocarcinoma Sensitive to a Pan-FGFR Inhibitor in a Mouse Model of NSCLC. Cancer Research, 2014, 74, 4676-4684.	0.4	31
118	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	9.4	495
119	Targeted genomic rearrangements using CRISPR/Cas technology. Nature Communications, 2014, 5, 3728.	5.8	252
120	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. Genome Research, 2014, 24, 1053-1063.	2.4	191
121	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
122	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	13.7	2,586
123	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	3.3	317
124	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
125	Oncogenic ARAF as a new driver in lung adenocarcinoma.. Journal of Clinical Oncology, 2014, 32, 11034-11034.	0.8	1
126	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060

#	Article	IF	Citations
127	Fusobacterium nucleatum Potentiates Intestinal Tumorigenesis and Modulates the Tumor-Immune Microenvironment. Cell Host and Microbe, 2013, 14, 207-215.	5.1	1,913
128	Structural, Biochemical, and Clinical Characterization of Epidermal Growth Factor Receptor (EGFR) Exon 20 Insertion Mutations in Lung Cancer. Science Translational Medicine, 2013, 5, 216ra177.	5.8	438
129	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
130	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	9.4	1,616
131	Cetuximab Response of Lung Cancerâ€“Derived EGF Receptor Mutants Is Associated with Asymmetric Dimerization. Cancer Research, 2013, 73, 6770-6779.	0.4	87
132	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	13.5	1,202
133	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nature Biotechnology, 2013, 31, 213-219.	9.4	3,934
134	Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677.	13.5	1,107
135	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
136	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. Genome Research, 2013, 23, 228-235.	2.4	124
137	SF3B1 Mutation Alters The Selection Of 3' RNA Splice Sites In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 117-117.	0.6	2
138	High Throughput Sequencing-Based Pathogen Discovery In Multiple Myeloma. Blood, 2013, 122, 5322-5322.	0.6	0
139	Genomic analysis identifies association of Fusobacterium with colorectal carcinoma. Genome Research, 2012, 22, 292-298.	2.4	1,587
140	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
141	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. Nature Genetics, 2012, 44, 1104-1110.	9.4	1,186
142	Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology, 2012, 30, 413-421.	9.4	1,710
143	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
144	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 2012, 483, 603-607.	13.7	6,473

#	Article	IF	Citations
145	Next-Generation Sequencing for the Identification of Transplantation-Associated Pathogens. Blood, 2012, 120, LBA-4-LBA-4.	0.6	1
146	The Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 5-5.	0.6	1
147	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. Nature Biotechnology, 2011, 29, 393-396.	9.4	289
148	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. Genome Biology, 2011, 12, R41.	3.8	2,546
149	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	9.4	270
150	Cancer Genomes Evolve by Pulverizing Single Chromosomes. Cell, 2011, 144, 9-10.	13.5	107
151	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. Nature Biotechnology, 2011, 29, 1109-1113.	9.4	204
152	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. Cancer Research, 2011, 71, 7587-7596.	0.4	70
153	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
154	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	13.7	1,288
155	Large-Scale CLL Genome Analysis Reveals Novel Cancer Genes, Including SF3B1. Blood, 2011, 118, 463-463.	0.6	0
156	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
157	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	13.7	3,331
158	SOS1 mutations are rare in human malignancies: Implications for Noonan syndrome patients. Genes Chromosomes and Cancer, 2008, 47, 253-259.	1.5	40
159	Allele-dependent variation in the relative cellular potency of distinct EGFR inhibitors. Cancer Biology and Therapy, 2007, 6, 661-667.	1.5	83
160	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
161	Structures of Lung Cancer-Derived EGFR Mutants and Inhibitor Complexes: Mechanism of Activation and Insights into Differential Inhibitor Sensitivity. Cancer Cell, 2007, 11, 217-227.	7.7	933
162	High-Throughput Sequence Analysis of the Tyrosine Kinome in Acute Myeloid Leukemia.. Blood, 2007, 110, 886-886.	0.6	3

#	Article	IF	Citations
163	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. PLoS Medicine, 2006, 3, e485.	3.9	298
164	Oncogenic Transformation by Inhibitor-Sensitive and -Resistant EGFR Mutants. PLoS Medicine, 2005, 2, e313.	3.9	603
165	Genome coverage and sequence fidelity of Â29 polymerase-based multiple strand displacement whole genome amplification. Nucleic Acids Research, 2004, 32, e71-e71.	6.5	266
166	EGFR Mutations in Lung Cancer: Correlation with Clinical Response to Gefitinib Therapy. Science, 2004, 304, 1497-1500.	6.0	9,038
167	Frequent HIN-1 Promoter Methylation and Lack of Expression in Multiple Human Tumor Types. Molecular Cancer Research, 2004, 2, 489-494.	1.5	46
168	Human genetic variation and disease. Lancet, The, 2003, 362, 259-260.	6.3	5
169	Telomerase activation, cellular immortalization and cancer. Annals of Medicine, 2001, 33, 123-129.	1.5	121
170	Recurrent allelic deletions of chromosome arms 15q and 16q in human small cell lung carcinomas. , 2000, 27, 323-331.		21
171	Loss-of-heterozygosity analysis of small-cell lung carcinomas using single-nucleotide polymorphism arrays. Nature Biotechnology, 2000, 18, 1001-1005.	9.4	282
172	Inhibition of telomerase limits the growth of human cancer cells. Nature Medicine, 1999, 5, 1164-1170.	15.2	983