

# Matthew L Meyerson

## List of Publications by Year in descending order

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172  
papers

118,111  
citations

2963

93  
h-index

4870

168  
g-index

187  
all docs

187  
docs citations

187  
times ranked

108381  
citing authors

#	ARTICLE	IF	CITATIONS
1	EGFR Mutations in Lung Cancer: Correlation with Clinical Response to Gefitinib Therapy. <i>Science</i> , 2004, 304, 1497-1500.	6.0	9,038
2	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
3	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012, 483, 603-607.	13.7	6,473
4	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	7.7	6,138
5	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
6	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
7	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. <i>Nature Biotechnology</i> , 2013, 31, 213-219.	9.4	3,934
8	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
9	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010, 463, 899-905.	13.7	3,331
10	Discovery and saturation analysis of cancer genes across 21 tumour types. <i>Nature</i> , 2014, 505, 495-501.	13.7	2,586
11	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
12	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. <i>Genome Biology</i> , 2011, 12, R41.	3.8	2,546
13	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
14	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
15	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
16	<i>Fusobacterium nucleatum</i> Potentiates Intestinal Tumorigenesis and Modulates the Tumor-Immune Microenvironment. <i>Cell Host and Microbe</i> , 2013, 14, 207-215.	5.1	1,913
17	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
18	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742

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19	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	9.4	1,710
20	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945.	13.5	1,710
21	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
22	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
23	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	9.4	1,616
24	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. <i>Cell</i> , 2012, 150, 1107-1120.	13.5	1,591
25	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 292-298.	2.4	1,587
26	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
27	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. <i>Nature Genetics</i> , 2012, 44, 685-689.	9.4	1,300
28	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.	13.7	1,288
29	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018, 24, 679-690.	15.2	1,224
30	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2013, 152, 714-726.	13.5	1,202
31	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1104-1110.	9.4	1,186
32	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	13.7	1,107
33	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	13.5	1,107
34	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	13.7	1,020
35	Inhibition of telomerase limits the growth of human cancer cells. <i>Nature Medicine</i> , 1999, 5, 1164-1170.	15.2	983
36	Analysis of <i>Fusobacterium</i> persistence and antibiotic response in colorectal cancer. <i>Science</i> , 2017, 358, 1443-1448.	6.0	983

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37	Structures of Lung Cancer-Derived EGFR Mutants and Inhibitor Complexes: Mechanism of Activation and Insights into Differential Inhibitor Sensitivity. <i>Cancer Cell</i> , 2007, 11, 217-227.	7.7	933
38	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
39	Chromothripsis from DNA damage in micronuclei. <i>Nature</i> , 2015, 522, 179-184.	13.7	924
40	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.	7.7	821
41	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
42	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	6.1	718
43	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708
44	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
45	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018, 560, 325-330.	13.7	662
46	Oncogenic Transformation by Inhibitor-Sensitive and -Resistant EGFR Mutants. <i>PLoS Medicine</i> , 2005, 2, e313.	3.9	603
47	Commensal Microbiota Promote Lung Cancer Development via $\gamma\delta$ T Cells. <i>Cell</i> , 2019, 176, 998-1013.e16.	13.5	592
48	Mutational signature in colorectal cancer caused by genotoxic <i>pk</i> <sup>+</sup> E. coli. <i>Nature</i> , 2020, 580, 269-273.	13.7	587
49	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.	5.8	584
50	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.	9.4	495
51	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016, 6, 914-929.	7.7	485
52	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
53	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
54	Oncotator: Cancer Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, E2423-E2429.	1.1	448

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55	Structural, Biochemical, and Clinical Characterization of Epidermal Growth Factor Receptor (EGFR) Exon 20 Insertion Mutations in Lung Cancer. <i>Science Translational Medicine</i> , 2013, 5, 216ra177.	5.8	438
56	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020, 1, 235-248.	5.7	430
57	Patient-derived lung cancer organoids as in vitro cancer models for therapeutic screening. <i>Nature Communications</i> , 2019, 10, 3991.	5.8	409
58	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015, 25, 316-327.	2.4	343
59	Institutional implementation of clinical tumor profiling on an unselected cancer population. <i>JCI Insight</i> , 2016, 1, e87062.	2.3	340
60	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387.	9.4	334
61	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
62	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	3.3	317
63	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. <i>PLoS Medicine</i> , 2006, 3, e485.	3.9	298
64	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. <i>Nature Biotechnology</i> , 2011, 29, 393-396.	9.4	289
65	Whole-Exome Sequencing Reveals Frequent Genetic Alterations in <i>BAP1</i> , <i>NF2</i> , <i>CDKN2A</i> , and <i>CUL1</i> in Malignant Pleural Mesothelioma. <i>Cancer Research</i> , 2015, 75, 264-269.	0.4	289
66	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591.	2.4	288
67	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
68	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016, 48, 176-182.	9.4	283
69	Loss-of-heterozygosity analysis of small-cell lung carcinomas using single-nucleotide polymorphism arrays. <i>Nature Biotechnology</i> , 2000, 18, 1001-1005.	9.4	282
70	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
71	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. <i>Nature Genetics</i> , 2011, 43, 964-968.	9.4	270
72	Genome coverage and sequence fidelity of $\Phi$ 29 polymerase-based multiple strand displacement whole genome amplification. <i>Nucleic Acids Research</i> , 2004, 32, e71-e71.	6.5	266

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73	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018, 174, 433-447.e19.	13.5	258
74	Targeted genomic rearrangements using CRISPR/Cas technology. <i>Nature Communications</i> , 2014, 5, 3728.	5.8	252
75	<i>EGFR</i> Variant Heterogeneity in Glioblastoma Resolved through Single-Nucleus Sequencing. <i>Cancer Discovery</i> , 2014, 4, 956-971.	7.7	251
76	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
77	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
78	<i>Fusobacterium nucleatum</i> in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e200.	1.3	225
79	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. <i>Nature Biotechnology</i> , 2011, 29, 1109-1113.	9.4	204
80	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. <i>Genome Research</i> , 2014, 24, 1053-1063.	2.4	191
81	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. <i>PLoS ONE</i> , 2014, 9, e87361.	1.1	168
82	BreKmer: detection of structural variation in targeted massively parallel sequencing data using kmers. <i>Nucleic Acids Research</i> , 2015, 43, e19-e19.	6.5	161
83	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. <i>Nature Communications</i> , 2018, 9, 5450.	5.8	157
84	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). <i>Journal of Thoracic Oncology</i> , 2015, 10, 838-843.	0.5	156
85	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. <i>Cancer Cell</i> , 2015, 27, 397-408.	7.7	150
86	Prognostic Impact of Novel Molecular Subtypes of Small Intestinal Neuroendocrine Tumor. <i>Clinical Cancer Research</i> , 2016, 22, 250-258.	3.2	149
87	Near universal detection of alterations in <i>CTNNB1</i> and Wnt pathway regulators in desmoid-type fibromatosis by whole-exome sequencing and genomic analysis. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 606-615.	1.5	138
88	<i>Fusobacterium nucleatum</i> in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. <i>Cancer Immunology Research</i> , 2018, 6, 1327-1336.	1.6	127
89	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 5472.	5.8	127
90	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , 2016, 8, 363ra147.	5.8	126

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91	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <i>Genome Research</i> , 2013, 23, 228-235.	2.4	124
92	Telomerase activation, cellular immortalization and cancer. <i>Annals of Medicine</i> , 2001, 33, 123-129.	1.5	121
93	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 2556-2564.	3.2	109
94	Cancer Genomes Evolve by Pulverizing Single Chromosomes. <i>Cell</i> , 2011, 144, 9-10.	13.5	107
95	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017, 168, 460-472.e14.	13.5	106
96	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. <i>Cancer Discovery</i> , 2018, 8, 108-125.	7.7	99
97	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. <i>Cancer Discovery</i> , 2018, 8, 59-73.	7.7	96
98	Detection of Somatic Structural Variants Enables Quantification and Characterization of Circulating Tumor DNA in Children With Solid Tumors. <i>JCO Precision Oncology</i> , 2018, 2018, 1-13.	1.5	95
99	Tumor fraction in cell-free DNA as a biomarker in prostate cancer. <i>JCI Insight</i> , 2018, 3, .	2.3	94
100	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. <i>PLoS Genetics</i> , 2016, 12, e1006242.	1.5	93
101	Cetuximab Response of Lung Cancerâ€“Derived EGF Receptor Mutants Is Associated with Asymmetric Dimerization. <i>Cancer Research</i> , 2013, 73, 6770-6779.	0.4	87
102	Allele-dependent variation in the relative cellular potency of distinct EGFR inhibitors. <i>Cancer Biology and Therapy</i> , 2007, 6, 661-667.	1.5	83
103	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. <i>JAMA Oncology</i> , 2017, 3, 801.	3.4	78
104	Calibrating genomic and allelic coverage bias in single-cell sequencing. <i>Nature Communications</i> , 2015, 6, 6822.	5.8	74
105	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 703-711.	3.6	72
106	Identification of cancer-cytotoxic modulators of PDE3A by predictive chemogenomics. <i>Nature Chemical Biology</i> , 2016, 12, 102-108.	3.9	72
107	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. <i>Cancer Research</i> , 2011, 71, 7587-7596.	0.4	70
108	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. <i>Cancer Discovery</i> , 2021, 11, 591-598.	7.7	69

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109	Rapid Intraoperative Molecular Characterization of Glioma. <i>JAMA Oncology</i> , 2015, 1, 662.	3.4	68
110	The tumor virus landscape of AIDS-related lymphomas. <i>Blood</i> , 2015, 125, e14-e22.	0.6	67
111	<i>MET</i> Exon 14 Mutation Encodes an Actionable Therapeutic Target in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017, 77, 4498-4505.	0.4	57
112	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018, 50, 937-943.	9.4	55
113	Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2. <i>Genome Medicine</i> , 2020, 12, 108.	3.6	54
114	The Amount of Bifidobacterium Genus in Colorectal Carcinoma Tissue in Relation to Tumor Characteristics and Clinical Outcome. <i>American Journal of Pathology</i> , 2018, 188, 2839-2852.	1.9	51
115	Dynamic Epigenetic Regulation by Menin During Pancreatic Islet Tumor Formation. <i>Molecular Cancer Research</i> , 2015, 13, 689-698.	1.5	49
116	Complete hematologic response of early T-cell progenitor acute lymphoblastic leukemia to the $\beta$ -secretase inhibitor BMS-906024: genetic and epigenetic findings in an outlier case. <i>Journal of Physical Education and Sports Management</i> , 2015, 1, a000539.	0.5	47
117	Genetic modifiers of EGFR dependence in non-small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18661-18666.	3.3	46
118	Frequent HIN-1 Promoter Methylation and Lack of Expression in Multiple Human Tumor Types. <i>Molecular Cancer Research</i> , 2004, 2, 489-494.	1.5	46
119	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. <i>Nature Genetics</i> , 2021, 53, 881-894.	9.4	44
120	Characterization of DDR2 Inhibitors for the Treatment of <i>DDR2</i> Mutated Nonsmall Cell Lung Cancer. <i>ACS Chemical Biology</i> , 2015, 10, 2687-2696.	1.6	43
121	Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. <i>Leukemia</i> , 2018, 32, 1838-1841.	3.3	42
122	<i>SOS1</i> mutations are rare in human malignancies: Implications for Noonan syndrome patients. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 253-259.	1.5	40
123	Copy number alterations unmasked as enhancer hijackers. <i>Nature Genetics</i> , 2017, 49, 5-6.	9.4	40
124	Genotype-targeted local therapy of glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8388-E8394.	3.3	40
125	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. <i>International Journal of Cancer</i> , 2015, 137, 776-783.	2.3	39
126	RAS $\rightarrow$ MAPK Reactivation Facilitates Acquired Resistance in <i>FGFR1</i> -Amplified Lung Cancer and Underlies a Rationale for Upfront FGFR $\rightarrow$ MEK Blockade. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1526-1539.	1.9	39



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127	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. <i>Nature Communications</i> , 2021, 12, 4375.	5.8	39
128	Splicing modulation sensitizes chronic lymphocytic leukemia cells to venetoclax by remodeling mitochondrial apoptotic dependencies. <i>JCI Insight</i> , 2018, 3, .	2.3	39
129	Illuminating the noncoding genome in cancer. <i>Nature Cancer</i> , 2020, 1, 864-872.	5.7	37
130	Multi-Omics Analysis Identifies MGA as a Negative Regulator of the MYC Pathway in Lung Adenocarcinoma. <i>Molecular Cancer Research</i> , 2020, 18, 574-584.	1.5	33
131	Identification and Characterization of Oncogenic <i>SOS1</i> Mutations in Lung Adenocarcinoma. <i>Molecular Cancer Research</i> , 2019, 17, 1002-1012.	1.5	32
132	Kinase Domain Activation of FGFR2 Yields High-Grade Lung Adenocarcinoma Sensitive to a Pan-FGFR Inhibitor in a Mouse Model of NSCLC. <i>Cancer Research</i> , 2014, 74, 4676-4684.	0.4	31
133	NSCLC Driven by <i>DDR2</i> Mutation Is Sensitive to Dasatinib and JQ1 Combination Therapy. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 2382-2389.	1.9	29
134	Pooled Genomic Screens Identify Anti-apoptotic Genes as Targetable Mediators of Chemotherapy Resistance in Ovarian Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 2281-2293.	1.5	29
135	Metagenomic Characterization of Microbial Communities In Situ Within the Deeper Layers of the Ileum in Crohn's Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016, 2, 563-566.e5.	2.3	23
136	Identification of an "Exceptional Responder" Cell Line to MEK1 Inhibition: Clinical Implications for MEK-Targeted Therapy. <i>Molecular Cancer Research</i> , 2016, 14, 207-215.	1.5	23
137	Antigen identification for HLA class I and HLA class II-restricted T cell receptors using cytokine-capturing antigen-presenting cells. <i>Science Immunology</i> , 2021, 6, .	5.6	22
138	Recurrent allelic deletions of chromosome arms 15q and 16q in human small cell lung carcinomas. , 2000, 27, 323-331.		21
139	Malawi Polyomavirus Is a Prevalent Human Virus That Interacts with Known Tumor Suppressors. <i>Journal of Virology</i> , 2015, 89, 857-862.	1.5	21
140	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021, 37, 2461-2463.	1.8	21
141	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. <i>Clinical Cancer Research</i> , 2021, 27, 1695-1705.	3.2	19
142	Optimization of PDE3A Modulators for SLFN12-Dependent Cancer Cell Killing. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1537-1542.	1.3	17
143	Patterns of chromosome 18 loss of heterozygosity in multifocal ileal neuroendocrine tumors. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 535-539.	1.5	16
144	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	2.9	16

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145	Pan-ERBB kinase inhibition augments CDK4/6 inhibitor efficacy in oesophageal squamous cell carcinoma. <i>Gut</i> , 2022, 71, 665-675.	6.1	15
146	Distinct pathways affected by menin versus MLL1/MLL2 in MLL-rearranged acute myeloid leukemia. <i>Experimental Hematology</i> , 2019, 69, 37-42.	0.2	13
147	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. <i>Journal of Biological Chemistry</i> , 2020, 295, 3431-3446.	1.6	12
148	Functional Genomic Analysis of <i>CDK4</i> and <i>CDK6</i> Gene Dependency across Human Cancer Cell Lines. <i>Cancer Research</i> , 2022, 82, 2171-2184.	0.4	12
149	Kmt2a cooperates with menin to suppress tumorigenesis in mouse pancreatic islets. <i>Cancer Biology and Therapy</i> , 2016, 17, 1274-1281.	1.5	11
150	Comprehensive metagenomic analysis of blastic plasmacytoid dendritic cell neoplasm. <i>Blood Advances</i> , 2020, 4, 1006-1011.	2.5	10
151	Pugh et al. reply. <i>Nature</i> , 2015, 520, E12-E14.	13.7	8
152	Autophosphorylation of the carboxyl-terminal domain is not required for oncogenic transformation by lung cancer derived EGFR mutants. <i>International Journal of Cancer</i> , 2018, 143, 679-685.	2.3	8
153	Long-read sequencing reveals complex patterns of wraparound transcription in polyomaviruses. <i>PLoS Pathogens</i> , 2022, 18, e1010401.	2.1	8
154	An international report on bacterial communities in esophageal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2022, 151, 1947-1959.	2.3	7
155	Human genetic variation and disease. <i>Lancet</i> , The, 2003, 362, 259-260.	6.3	5
156	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021, 13, 114.	3.6	5
157	Mechanistic Insights into Transmissible Cancers of Mammals. <i>Cancer Cell</i> , 2018, 33, 543-544.	7.7	4
158	Bacterial invaders drive CRC progression. <i>Science Signaling</i> , 2020, 13, .	1.6	3
159	High-Throughput Sequence Analysis of the Tyrosine Kinome in Acute Myeloid Leukemia.. <i>Blood</i> , 2007, 110, 886-886.	0.6	3
160	Circulating Tumor DNA Provides a Sneak Peek into Treatment Responses in Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1038-1040.	0.4	2
161	SF3B1 Mutation Alters The Selection Of 3' RNA Splice Sites In Chronic Lymphocytic Leukemia. <i>Blood</i> , 2013, 122, 117-117.	0.6	2
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