

Matthew L Meyerson

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

174 papers	84,556 citations	88 h-index	187 g-index
187 ext. papers	104,814 ext. citations	22 avg, IF	6.92 L-index

#	Paper	IF	Citations
174	EGFR mutations in lung cancer: correlation with clinical response to gefitinib therapy. <i>Science</i> , 2004 , 304, 1497-500	33.3	7937
173	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
172	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	24.3	4782
171	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012 , 483, 603-7	50.4	4648
170	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013 , 499, 214-218	50.4	3616
169	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
168	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. <i>Nature Biotechnology</i> , 2013 , 31, 213-9	44.5	2830
167	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010 , 463, 899-905	50.4	2590
166	Discovery and saturation analysis of cancer genes across 21 tumour types. <i>Nature</i> , 2014 , 505, 495-501	50.4	1990
165	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
164	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
163	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
162	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
161	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	18.3	1614
160	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. <i>Cell</i> , 2012 , 150, 1107-20	50.4	1304
159	Fusobacterium nucleatum potentiates intestinal tumorigenesis and modulates the tumor-immune microenvironment. <i>Cell Host and Microbe</i> , 2013 , 14, 207-15	23.4	1275
158	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012 , 30, 413-21	44.5	1229

157	Prospective derivation of a living organoid biobank of colorectal cancer patients. <i>Cell</i> , 2015 , 161, 933-45	56.2	1215
156	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013 , 45, 1134-40	36.3	1198
155	Genomic analysis identifies association of Fusobacterium with colorectal carcinoma. <i>Genome Research</i> , 2012 , 22, 292-8	9.7	1165
154	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
153	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
152	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
151	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011 , 471, 467-72	50.4	1117
150	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. <i>Nature Genetics</i> , 2012 , 44, 685-9	36.3	1079
149	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
148	Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. <i>Cell</i> , 2013 , 152, 714-26	56.2	1006
147	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011 , 470, 214-20	50.4	984
146	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	56.2	961
145	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1104-10	36.3	919
144	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007 , 450, 893-8	50.4	900
143	Inhibition of telomerase limits the growth of human cancer cells. <i>Nature Medicine</i> , 1999 , 5, 1164-70	50.5	883
142	Punctuated evolution of prostate cancer genomes. <i>Cell</i> , 2013 , 153, 666-77	56.2	862
141	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
140	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, 217-27	24.3	779

139	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018 , 24, 679-690	50.5	659
138	Chromothripsis from DNA damage in micronuclei. <i>Nature</i> , 2015 , 522, 179-84	50.4	635
137	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
136	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015 , 5, 1164-1177	24.4	581
135	Analysis of persistence and antibiotic response in colorectal cancer. <i>Science</i> , 2017 , 358, 1443-1448	33.3	578
134	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014 , 506, 371-5	50.4	541
133	Oncogenic transformation by inhibitor-sensitive and -resistant EGFR mutants. <i>PLoS Medicine</i> , 2005 , 2, e313	11.6	527
132	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
131	Fusobacterium nucleatum in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016 , 65, 1973-1980	49.2	454
130	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014 , 32, 479-84	44.5	434
129	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018 , 560, 325-330	50.4	379
128	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	49.3	377
127	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016 , 6, 914-29	24.4	343
126	Oncotator: cancer variant annotation tool. <i>Human Mutation</i> , 2015 , 36, E2423-9	4.7	332
125	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736	34.3	324
124	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017 , 8, 1324	17.4	314
123	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	17.5	313
122	Commensal Microbiota Promote Lung Cancer Development via T _H Cells. <i>Cell</i> , 2019 , 176, 998-1013.e16	56.2	290

121	Mutational signature in colorectal cancer caused by genotoxic pks E. coli. <i>Nature</i> , 2020 , 580, 269-273	50.4	286
120	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
119	Loss-of-heterozygosity analysis of small-cell lung carcinomas using single-nucleotide polymorphism arrays. <i>Nature Biotechnology</i> , 2000 , 18, 1001-5	44.5	259
118	Institutional implementation of clinical tumor profiling on an unselected cancer population. <i>JCI Insight</i> , 2016 , 1, e87062	9.9	245
117	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VT11A-TCF7L2 fusion. <i>Nature Genetics</i> , 2011 , 43, 964-968	36.3	242
116	Epidermal growth factor receptor activation in glioblastoma through novel missense mutations in the extracellular domain. <i>PLoS Medicine</i> , 2006 , 3, e485	11.6	242
115	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015 , 25, 316-27	9.7	240
114	Genome coverage and sequence fidelity of phi29 polymerase-based multiple strand displacement whole genome amplification. <i>Nucleic Acids Research</i> , 2004 , 32, e71	20.1	236
113	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, 15544-9	11.5	229
112	Whole-exome sequencing reveals frequent genetic alterations in BAP1, NF2, CDKN2A, and CUL1 in malignant pleural mesothelioma. <i>Cancer Research</i> , 2015 , 75, 264-9	10.1	224
111	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. <i>Nature Biotechnology</i> , 2011 , 29, 393-6	44.5	213
110	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016 , 48, 176-82	36.3	210
109	Targeted genomic rearrangements using CRISPR/Cas technology. <i>Nature Communications</i> , 2014 , 5, 3728	17.4	203
108	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406	10.6	200
107	Patient-derived lung cancer organoids as in vitro cancer models for therapeutic screening. <i>Nature Communications</i> , 2019 , 10, 3991	17.4	199
106	EGFR variant heterogeneity in glioblastoma resolved through single-nucleus sequencing. <i>Cancer Discovery</i> , 2014 , 4, 956-71	24.4	199
105	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018 , 50, 1381-1387	36.3	165
104	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. <i>Nature Biotechnology</i> , 2011 , 29, 1109-13	44.5	162

103	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	10.6	159
102	Fusobacterium nucleatum in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016 , 7, e200	4.2	156
101	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018 , 174, 433-447.e19	56.2	155
100	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018 , 28, 581-591	9.7	149
99	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020 , 578, 129-136	50.4	148
98	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. <i>Genome Research</i> , 2014 , 24, 1053-63	9.7	147
97	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
96	Discovering the anti-cancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020 , 1, 235-248	15.4	137
95	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	30.2	133
94	A functional landscape of resistance to ALK inhibition in lung cancer. <i>Cancer Cell</i> , 2015 , 27, 397-408	24.3	123
93	Prognostic Impact of Novel Molecular Subtypes of Small Intestinal Neuroendocrine Tumor. <i>Clinical Cancer Research</i> , 2016 , 22, 250-8	12.9	113
92	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	8.9	113
91	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	3.7	112
90	BreaKmer: detection of structural variation in targeted massively parallel sequencing data using kmers. <i>Nucleic Acids Research</i> , 2015 , 43, e19	20.1	110
89	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <i>Genome Research</i> , 2013 , 23, 228-35	9.7	109
88	Telomerase activation, cellular immortalization and cancer. <i>Annals of Medicine</i> , 2001 , 33, 123-9	1.5	103
87	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , 2016 , 8, 363ra147	17.5	93
86	Near universal detection of alterations in CTNNB1 and Wnt pathway regulators in desmoid-type fibromatosis by whole-exome sequencing and genomic analysis. <i>Genes Chromosomes and Cancer</i> , 2015 , 54, 606-15	5	84

85	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. <i>Nature Communications</i> , 2018 , 9, 5450	17.4	83
84	Cancer genomes evolve by pulverizing single chromosomes. <i>Cell</i> , 2011 , 144, 9-10	56.2	79
83	in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. <i>Cancer Immunology Research</i> , 2018 , 6, 1327-1336	12.5	78
82	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017 , 168, 460-472.e14	56.2	75
81	Allele-dependent variation in the relative cellular potency of distinct EGFR inhibitors. <i>Cancer Biology and Therapy</i> , 2007 , 6, 661-7	4.6	72
80	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. <i>Cancer Discovery</i> , 2018 , 8, 59-73	24.4	67
79	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. <i>Cancer Discovery</i> , 2018 , 8, 108-125	24.4	67
78	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, 7587-96	10.1	62
77	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	6	62
76	Cetuximab response of lung cancer-derived EGF receptor mutants is associated with asymmetric dimerization. <i>Cancer Research</i> , 2013 , 73, 6770-9	10.1	61
75	Calibrating genomic and allelic coverage bias in single-cell sequencing. <i>Nature Communications</i> , 2015 , 6, 6822	17.4	57
74	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 703-711	17.6	56
73	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019 , 10, 5472	17.4	56
72	Rapid Intraoperative Molecular Characterization of Glioma. <i>JAMA Oncology</i> , 2015 , 1, 662-7	13.4	53
71	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. <i>JAMA Oncology</i> , 2017 , 3, 801-809	13.4	51
70	Identification of cancer-cytotoxic modulators of PDE3A by predictive chemogenomics. <i>Nature Chemical Biology</i> , 2016 , 12, 102-8	11.7	51
69	The tumor virus landscape of AIDS-related lymphomas. <i>Blood</i> , 2015 , 125, e14-22	2.2	51
68	Tumor fraction in cell-free DNA as a biomarker in prostate cancer. <i>JCI Insight</i> , 2018 , 3,	9.9	49

67	Complete hematologic response of early T-cell progenitor acute lymphoblastic leukemia to the secretase inhibitor BMS-906024: genetic and epigenetic findings in an outlier case. <i>Journal of Physical Education and Sports Management</i> , 2015 , 1, a000539	2.8	40
66	Dynamic epigenetic regulation by menin during pancreatic islet tumor formation. <i>Molecular Cancer Research</i> , 2015 , 13, 689-98	6.6	39
65	Exon 14 Mutation Encodes an Actionable Therapeutic Target in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017 , 77, 4498-4505	10.1	38
64	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, 18661-6	11.5	37
63	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,	3.6	36
62	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018 , 50, 937-943	36.3	35
61	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. <i>International Journal of Cancer</i> , 2015 , 137, 776-83	7.5	33
60	SOS1 mutations are rare in human malignancies: implications for Noonan Syndrome patients. <i>Genes Chromosomes and Cancer</i> , 2008 , 47, 253-9	5	33
59	Frequent HIN-1 Promoter Methylation and Lack of Expression in Multiple Human Tumor Types. <i>Molecular Cancer Research</i> , 2004 , 2, 489-494	6.6	33
58	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 2556-2564	12.9	32
57	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	5.8	31
56	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	11.5	29
55	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, 4676-84	10.1	29
54	Characterization of DDR2 Inhibitors for the Treatment of DDR2 Mutated Nonsmall Cell Lung Cancer. <i>ACS Chemical Biology</i> , 2015 , 10, 2687-96	4.9	28
53	NSCLC Driven by DDR2 Mutation Is Sensitive to Dasatinib and JQ1 Combination Therapy. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 2382-2389	6.1	28
52	RAS-MAPK Reactivation Facilitates Acquired Resistance in -Amplified Lung Cancer and Underlies a Rationale for Upfront FGFR-MEK Blockade. <i>Molecular Cancer Therapeutics</i> , 2018 , 17, 1526-1539	6.1	27
51	Therapeutic Targeting of Oncogenic K-Ras by a Covalent Catalytic Site Inhibitor. <i>Angewandte Chemie</i> , 2014 , 126, 203-208	3.6	26
50	Copy number alterations unmasked as enhancer hijackers. <i>Nature Genetics</i> , 2016 , 49, 5-6	36.3	25

49	Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. <i>Leukemia</i> , 2018 , 32, 1838-1841	10.7	24
48	Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2. <i>Genome Medicine</i> , 2020 , 12, 108	14.4	22
47	Splicing modulation sensitizes chronic lymphocytic leukemia cells to venetoclax by remodeling mitochondrial apoptotic dependencies. <i>JCI Insight</i> , 2018 , 3,	9.9	21
46	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. <i>Cancer Discovery</i> , 2021 , 11, 591-598	24.4	20
45	Malawi polyomavirus is a prevalent human virus that interacts with known tumor suppressors. <i>Journal of Virology</i> , 2015 , 89, 857-62	6.6	18
44	Identification and Characterization of Oncogenic Mutations in Lung Adenocarcinoma. <i>Molecular Cancer Research</i> , 2019 , 17, 1002-1012	6.6	18
43	Recurrent allelic deletions of chromosome arms 15q and 16q in human small cell lung carcinomas. <i>Genes Chromosomes and Cancer</i> , 2000 , 27, 323-31	5	17
42	Metagenomic Characterization of Microbial Communities Within the Deeper Layers of the Ileum in Crohn's Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016 , 2, 563-566.e5	7.9	16
41	Identification of an "Exceptional Responder" Cell Line to MEK1 Inhibition: Clinical Implications for MEK-Targeted Therapy. <i>Molecular Cancer Research</i> , 2016 , 14, 207-15	6.6	16
40	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	6.6	15
39	Illuminating the noncoding genome in cancer.. <i>Nature Cancer</i> , 2020 , 1, 864-872	15.4	14
38	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	6.6	13
37	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10
36	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. <i>Clinical Cancer Research</i> , 2021 , 27, 1695-1705	12.9	9
35	Pugh et al. reply. <i>Nature</i> , 2015 , 520, E12-4	50.4	8
34	Kmt2a cooperates with menin to suppress tumorigenesis in mouse pancreatic islets. <i>Cancer Biology and Therapy</i> , 2016 , 17, 1274-1281	4.6	8
33	Patterns of chromosome 18 loss of heterozygosity in multifocal ileal neuroendocrine tumors. <i>Genes Chromosomes and Cancer</i> , 2020 , 59, 535-539	5	8
32	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	7.5	7

31	Optimization of PDE3A Modulators for SLFN12-Dependent Cancer Cell Killing. <i>ACS Medicinal Chemistry Letters</i> , 2019 , 10, 1537-1542	4.3	7
30	Distinct pathways affected by menin versus MLL1/MLL2 in MLL-rearranged acute myeloid leukemia. <i>Experimental Hematology</i> , 2019 , 69, 37-42	3.1	7
29	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
28	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. <i>Nature Communications</i> , 2021 , 12, 4375	17.4	7
27	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	5.4	6
26	Non-oncology drugs are a source of previously unappreciated anti-cancer activity		6
25	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. <i>Nature Genetics</i> , 2021 , 53, 881-894	36.3	6
24	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
23	Human genetic variation and disease. <i>Lancet, The</i> , 2003 , 362, 259-60	40	4
22	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021 , 37, 2461-2463	7.1	4
21	The Tangent copy-number inference pipeline for cancer genome analyses		3
20	Comprehensive metagenomic analysis of blastic plasmacytoid dendritic cell neoplasm. <i>Blood Advances</i> , 2020 , 4, 1006-1011	7.8	3
19	Circulating Tumor DNA Provides a Sneak Peek into Treatment Responses in Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2019 , 79, 1038-1040	10.1	2
18	Mechanistic Insights into Transmissible Cancers of Mammals. <i>Cancer Cell</i> , 2018 , 33, 543-544	24.3	2
17	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,	28	2
16	Pan-ERBB kinase inhibition augments CDK4/6 inhibitor efficacy in oesophageal squamous cell carcinoma. <i>Gut</i> , 2021 ,	19.2	2
15	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021 , 13, 114	14.4	2
14	SF3B1 Mutation Alters The Selection Of 3SRNA Splice Sites In Chronic Lymphocytic Leukemia. <i>Blood</i> , 2013 , 122, 117-117	2.2	1

13	Oncogenic ARAF as a new driver in lung adenocarcinoma.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 11034-11034	10.34	1
12	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.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 4521-4521	2.2	1
11	Next-Generation Sequencing for the Identification of Transplantation-Associated Pathogens. <i>Blood</i> , 2012 , 120, LBA-4-LBA-4	2.2	1
10	Bacterial invaders drive CRC progression. <i>Science Signaling</i> , 2020 , 13,	8.8	1
9	Long-read sequencing reveals complex patterns of wraparound transcription in polyomaviruses.. <i>PLoS Pathogens</i> , 2022 , 18, e1010401	7.6	1
8	Molecular Biology, Genomics, Proteomics, and Mouse Models of Human Cancer 2017 , 1-31		
7	High-Throughput Sequence Analysis of the Tyrosine Kinome in Acute Myeloid Leukemia.. <i>Blood</i> , 2007 , 110, 886-886	2.2	
6	Bifidobacterium Genus in Colorectal Carcinoma Tissue in relation to Tumor Characteristics and Patient Survival. <i>FASEB Journal</i> , 2018 , 32, 407.3	0.9	
5	Comprehensive Genetic Interrogation of Circulating Multiple Myeloma Cells at Single Cell Resolution. <i>Blood</i> , 2016 , 128, 800-800	2.2	
4	Large-Scale CLL Genome Analysis Reveals Novel Cancer Genes, Including SF3B1. <i>Blood</i> , 2011 , 118, 463-463	6.3	
3	The Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2012 , 120, 5-5	2.2	
2	High Throughput Sequencing-Based Pathogen Discovery In Multiple Myeloma. <i>Blood</i> , 2013 , 122, 5322-5322	3.22	
1	Genomic Evolution in a Patient With Lung Adenocarcinoma With a Germline T790M Mutation. <i>JTO Clinical and Research Reports</i> , 2021 , 2, 100146	1.4	