

# P Andrew Futreal

## List of Publications by Year in descending order

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Version: 2024-02-01

220  
papers

63,386  
citations

14124

69  
h-index

3037

194  
g-index

249  
all docs

249  
docs citations

249  
times ranked

76932  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations of the BRAF gene in human cancer. <i>Nature</i> , 2002, 417, 949-954.	13.7	9,374
2	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
3	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. <i>New England Journal of Medicine</i> , 2012, 366, 883-892.	13.9	6,769
4	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	6.0	3,126
5	The cancer genome. <i>Nature</i> , 2009, 458, 719-724.	13.7	2,904
6	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004, 4, 177-183.	12.8	2,868
7	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. <i>Cell</i> , 2011, 144, 27-40.	13.5	2,020
8	COSMIC: mining complete cancer genomes in the Catalogue of Somatic Mutations in Cancer. <i>Nucleic Acids Research</i> , 2011, 39, D945-D950.	6.5	2,015
9	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
10	Mutational Processes Molding the Genomes of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 979-993.	13.5	1,673
11	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012, 486, 400-404.	13.7	1,535
12	The Life History of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 994-1007.	13.5	1,249
13	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. <i>Nature</i> , 2010, 467, 1109-1113.	13.7	1,200
14	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. <i>Nature Genetics</i> , 2014, 46, 225-233.	9.4	1,103
15	Loss of IFN- $\gamma$ Pathway Genes in Tumor Cells as a Mechanism of Resistance to Anti-CTLA-4 Therapy. <i>Cell</i> , 2016, 167, 397-404.e9.	13.5	1,009
16	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010, 463, 184-190.	13.7	972
17	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. <i>Science</i> , 2014, 346, 256-259.	6.0	834
18	Analysis of Immune Signatures in Longitudinal Tumor Samples Yields Insight into Biomarkers of Response and Mechanisms of Resistance to Immune Checkpoint Blockade. <i>Cancer Discovery</i> , 2016, 6, 827-837.	7.7	785

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19	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	5.8	741
20	Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i> -Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. <i>Cancer Discovery</i> , 2015, 5, 860-877.	7.7	696
21	Integrated molecular analysis of tumor biopsies on sequential CTLA-4 and PD-1 blockade reveals markers of response and resistance. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	689
22	Intratumor Heterogeneity: Seeing the Wood for the Trees. <i>Science Translational Medicine</i> , 2012, 4, 127ps10.	5.8	443
23	Emerging patterns of somatic mutations in cancer. <i>Nature Reviews Genetics</i> , 2013, 14, 703-718.	7.7	442
24	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018, 173, 611-623.e17.	13.5	398
25	Chromosomal Instability Confers Intrinsic Multidrug Resistance. <i>Cancer Research</i> , 2011, 71, 1858-1870.	0.4	391
26	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	6.0	369
27	Neoadjuvant nivolumab or nivolumab plus ipilimumab in operable non-small cell lung cancer: the phase 2 randomized NEOSTAR trial. <i>Nature Medicine</i> , 2021, 27, 504-514.	15.2	357
28	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13081-13086.	3.3	320
29	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. <i>Lancet Oncology</i> , The, 2017, 18, 100-111.	5.1	296
30	Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 5361.	5.8	294
31	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. <i>Cell Stem Cell</i> , 2018, 23, 700-713.e6.	5.2	272
32	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. <i>Genome Biology</i> , 2016, 17, 178.	3.8	231
33	Molecular Profiling Reveals Unique Immune and Metabolic Features of Melanoma Brain Metastases. <i>Cancer Discovery</i> , 2019, 9, 628-645.	7.7	231
34	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021, 27, 1432-1441.	15.2	216
35	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. <i>Nature Communications</i> , 2020, 11, 5327.	5.8	208
36	The SMARCA2/4 ATPase Domain Surpasses the Bromodomain as a Drug Target in SWI/SNF-Mutant Cancers: Insights from cDNA Rescue and PFI-3 Inhibitor Studies. <i>Cancer Research</i> , 2015, 75, 3865-3878.	0.4	202

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37	Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma. <i>Nature Medicine</i> , 2020, 26, 1845-1851.	15.2	193
38	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	9.4	180
39	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	5.8	179
40	High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics. <i>Genome Research</i> , 2018, 28, 1345-1352.	2.4	175
41	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. <i>Nature Medicine</i> , 2018, 24, 1047-1057.	15.2	175
42	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. <i>Cancer Cell</i> , 2018, 33, 1128-1141.e7.	7.7	169
43	Novel MYBL1 Gene Rearrangements with Recurrent MYBL1-NFIB Fusions in Salivary Adenoid Cystic Carcinomas Lacking t(6;9) Translocations. <i>Clinical Cancer Research</i> , 2016, 22, 725-733.	3.2	167
44	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	161
45	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. <i>Cancer Discovery</i> , 2017, 7, 1088-1097.	7.7	160
46	Clearance of Somatic Mutations at Remission and the Risk of Relapse in Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , 2018, 36, 1788-1797.	0.8	156
47	Immuno-genomic landscape of osteosarcoma. <i>Nature Communications</i> , 2020, 11, 1008.	5.8	143
48	Comprehensive T cell repertoire characterization of non-small cell lung cancer. <i>Nature Communications</i> , 2020, 11, 603.	5.8	140
49	Oncogenic Kras drives invasion and maintains metastases in colorectal cancer. <i>Genes and Development</i> , 2017, 31, 370-382.	2.7	137
50	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	15.2	134
51	Genomic heterogeneity of multiple synchronous lung cancer. <i>Nature Communications</i> , 2016, 7, 13200.	5.8	132
52	Circulating tumor DNA analysis depicts subclonal architecture and genomic evolution of small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3114.	5.8	122
53	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. <i>Npj Genomic Medicine</i> , 2017, 2, .	1.7	120
54	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	5.8	119

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55	The driver landscape of sporadic chordoma. <i>Nature Communications</i> , 2017, 8, 890.	5.8	115
56	Programmed Death-Ligand 1 Heterogeneity and Its Impact on Benefit From Immune Checkpoint Inhibitors in NSCLC. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1449-1459.	0.5	109
57	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	108
58	Novel algorithmic approach predicts tumor mutation load and correlates with immunotherapy clinical outcomes using a defined gene mutation set. <i>BMC Medicine</i> , 2016, 14, 168.	2.3	106
59	A cellular hierarchy framework for understanding heterogeneity and predicting drug response in acute myeloid leukemia. <i>Nature Medicine</i> , 2022, 28, 1212-1223.	15.2	104
60	Deep sequencing of circulating tumor DNA detects molecular residual disease and predicts recurrence in gastric cancer. <i>Cell Death and Disease</i> , 2020, 11, 346.	2.7	102
61	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. <i>Gut</i> , 2020, 69, 18-31.	6.1	94
62	Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. <i>Cancer Research</i> , 2017, 77, 6119-6130.	0.4	92
63	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 2978.	5.8	91
64	A survey of homozygous deletions in human cancer genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4542-4547.	3.3	90
65	Clinical implications of TP53 mutations in myelodysplastic syndromes treated with hypomethylating agents. <i>Oncotarget</i> , 2016, 7, 14172-14187.	0.8	86
66	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. <i>Cancer Letters</i> , 2015, 357, 179-185.	3.2	81
67	The Prognostic and Therapeutic Role of Genomic Subtyping by Sequencing Tumor or Cell-Free DNA in Pulmonary Large-Cell Neuroendocrine Carcinoma. <i>Clinical Cancer Research</i> , 2020, 26, 892-901.	3.2	80
68	Global analysis of shared T cell specificities in human non-small cell lung cancer enables HLA inference and antigen discovery. <i>Immunity</i> , 2021, 54, 586-602.e8.	6.6	80
69	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. <i>Nature Communications</i> , 2018, 9, 2670.	5.8	79
70	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	9.4	79
71	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , 2021, 12, 5606.	5.8	76
72	Evaluation of Patients and Families With Concern for Predispositions to Hematologic Malignancies Within the Hereditary Hematologic Malignancy Clinic (HHMC). <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2016, 16, 417-428.e2.	0.2	74

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73	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. <i>Nature Communications</i> , 2021, 12, 2722.	5.8	74
74	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. <i>Cell Reports</i> , 2019, 26, 1518-1532.e9.	2.9	70
75	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2020, 31, 107502.	2.9	69
76	Overexpressed PRAME is a potential immunotherapy target in sarcoma subtypes. <i>Clinical Sarcoma Research</i> , 2017, 7, 11.	2.3	61
77	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. <i>Clinical Cancer Research</i> , 2023, 27, 852-864.	3.2	61
78	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2607.	5.8	61
79	Managing Clonal Hematopoiesis in Patients With Solid Tumors. <i>Journal of Clinical Oncology</i> , 2019, 37, 7-11.	0.8	60
80	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846.	3.9	58
81	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. <i>Modern Pathology</i> , 2018, 31, 947-955.	2.9	56
82	Impact of the number of mutations in survival and response outcomes to hypomethylating agents in patients with myelodysplastic syndromes or myelodysplastic/myeloproliferative neoplasms. <i>Oncotarget</i> , 2018, 9, 9714-9727.	0.8	56
83	A Preexisting Rare <i>PIK3CA</i> E545K Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in <i>NRAS</i> Melanoma and Is Dependent on S6K1 Signaling. <i>Cancer Discovery</i> , 2018, 8, 556-567.	7.7	55
84	Assessing tumor heterogeneity using ctDNA to predict and monitor therapeutic response in metastatic breast cancer. <i>International Journal of Cancer</i> , 2020, 146, 1359-1368.	2.3	55
85	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014, 124, 3110-3117.	0.6	54
86	MYC protein expression is an important prognostic factor in acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 37-48.	0.6	54
87	Androgen receptor blockade promotes response to BRAF/MEK-targeted therapy. <i>Nature</i> , 2022, 606, 797-803.	13.7	54
88	The somatic mutation landscape of premalignant colorectal adenoma. <i>Gut</i> , 2018, 67, 1299-1305.	6.1	52
89	Neoadjuvant Chemotherapy Increases Cytotoxic T Cell, Tissue Resident Memory T Cell, and B Cell Infiltration in Resectable NSCLC. <i>Journal of Thoracic Oncology</i> , 2021, 16, 127-139.	0.5	48
90	Identification of a Novel Fusion Gene, IRF2BP2-RARA, in Acute Promyelocytic Leukemia. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2015, 13, 19-22.	2.3	46

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91	Genomic profiling of dedifferentiated liposarcoma compared to matched well-differentiated liposarcoma reveals higher genomic complexity and a common origin. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002386.	0.5	45
92	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. <i>Nature Communications</i> , 2021, 12, 6071.	5.8	44
93	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010, 2, 53.	3.6	43
94	Genomic profiles and clinical outcomes of de novo blastoid/pleomorphic MCL are distinct from those of transformed MCL. <i>Blood Advances</i> , 2020, 4, 1038-1050.	2.5	43
95	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. <i>Blood</i> , 2018, 131, 1820-1832.	0.6	40
96	Prevalence of recurrent oncogenic fusion in mismatch repair-deficient colorectal carcinoma with hypermethylated MLH1 and wild-type BRAF and KRAS. <i>Modern Pathology</i> , 2019, 32, 1053-1064.	2.9	40
97	Improving the detection of patients with inherited predispositions to hematologic malignancies using next-generation sequencing-based leukemia prognostication panels. <i>Cancer</i> , 2018, 124, 2704-2713.	2.0	39
98	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. <i>Nature Communications</i> , 2018, 9, 2496.	5.8	39
99	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. <i>Oncotarget</i> , 2017, 8, 21994-22002.	0.8	39
100	Applying Artificial Intelligence to Address the Knowledge Gaps in Cancer Care. <i>Oncologist</i> , 2019, 24, 772-782.	1.9	38
101	Targeted Tissue and Cell-Free Tumor DNA Sequencing of Advanced Lung Squamous-Cell Carcinoma Reveals Clinically Significant Prevalence of Actionable Alterations. <i>Clinical Lung Cancer</i> , 2019, 20, 30-36.e3.	1.1	37
102	Multomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. <i>Genome Biology</i> , 2020, 21, 271.	3.8	36
103	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. <i>Nature Communications</i> , 2021, 12, 2877.	5.8	35
104	Distinct molecular and immune hallmarks of inflammatory arthritis induced by immune checkpoint inhibitors for cancer therapy. <i>Nature Communications</i> , 2022, 13, 1970.	5.8	34
105	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. <i>Nature Genetics</i> , 2022, 54, 850-860.	9.4	34
106	Genomic Rearrangement Signatures and Clinical Outcomes in High-Grade Serous Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2018, 110, 265-272.	3.0	31
107	Germline DNA Sequencing Reveals Novel Mutations Predictive of Overall Survival in a Cohort of Patients with Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1385-1394.	3.2	31
108	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. <i>Nature Biotechnology</i> , 2022, 40, 1624-1633.	9.4	31

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109	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. <i>Blood Advances</i> , 2017, 1, 1031-1036.	2.5	30
110	Identification of predictors of drug sensitivity using patient-derived models of esophageal squamous cell carcinoma. <i>Nature Communications</i> , 2019, 10, 5076.	5.8	30
111	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. <i>Clinical Cancer Research</i> , 2020, 26, 2908-2920.	3.2	30
112	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. <i>Nature Communications</i> , 2021, 12, 687.	5.8	30
113	Distinct co-acquired alterations and genomic evolution during TKI treatment in non-small-cell lung cancer patients with or without acquired T790M mutation. <i>Oncogene</i> , 2020, 39, 1846-1859.	2.6	29
114	Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 5365-5375.	3.2	29
115	Pilot Clinical Trial of Perioperative Durvalumab and Tremelimumab in the Treatment of Resectable Colorectal Cancer Liver Metastases. <i>Clinical Cancer Research</i> , 2021, 27, 3039-3049.	3.2	28
116	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. <i>Oncotarget</i> , 2018, 9, 19891-19899.	0.8	28
117	Immune and Circulating Tumor DNA Profiling After Radiation Treatment for Oligometastatic Non-Small Cell Lung Cancer: Translational Correlatives from a Mature Randomized Phase II Trial. <i>International Journal of Radiation Oncology Biology Physics</i> , 2020, 106, 349-357.	0.4	27
118	Genetic determinants of immune-related adverse events in patients with melanoma receiving immune checkpoint inhibitors. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 1939-1949.	2.0	27
119	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. <i>Nature Communications</i> , 2022, 13, 42.	5.8	27
120	Features of non-activation dendritic state and immune deficiency in blastic plasmacytoid dendritic cell neoplasm (BPDCN). <i>Blood Cancer Journal</i> , 2019, 9, 99.	2.8	26
121	High Prevalence of Hereditary Cancer Syndromes and Outcomes in Adults with Early-Onset Pancreatic Cancer. <i>Cancer Prevention Research</i> , 2018, 11, 679-686.	0.7	25
122	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. <i>PLoS ONE</i> , 2020, 15, e0234505.	1.1	25
123	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. <i>Hepatology</i> , 2022, 75, 955-967.	3.6	25
124	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. <i>Nature Communications</i> , 2021, 12, 6655.	5.8	24
125	Distinct Immunophenotypes of T Cells in Bronchoalveolar Lavage Fluid From Leukemia Patients With Immune Checkpoint Inhibitors-Related Pulmonary Complications. <i>Frontiers in Immunology</i> , 2020, 11, 590494.	2.2	21
126	MAGE-A3 Is a Clinically Relevant Target in Undifferentiated Pleomorphic Sarcoma/Myxofibrosarcoma. <i>Cancers</i> , 2019, 11, 677.	1.7	20



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127	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	19
128	Donor clonal hematopoiesis increases risk of acute graft versus host disease after matched sibling transplantation. <i>Leukemia</i> , 2022, 36, 257-262.	3.3	19
129	Clonal dynamics and clinical implications of postremission clonal hematopoiesis in acute myeloid leukemia. <i>Blood</i> , 2021, 138, 1733-1739.	0.6	19
130	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. <i>Oncotarget</i> , 2018, 9, 29495-29507.	0.8	18
131	Patient-reported fatigue prior to treatment is prognostic of survival in patients with acute myeloid leukemia. <i>Oncotarget</i> , 2018, 9, 31244-31252.	0.8	17
132	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemia-initiating cells. <i>Blood</i> , 2019, 134, 614-625.	0.6	16
133	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , 2021, 12, 7081.	5.8	16
134	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. <i>EBioMedicine</i> , 2019, 42, 296-303.	2.7	15
135	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. <i>Clinical Cancer Research</i> , 2020, 26, 5477-5486.	3.2	15
136	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. <i>Nature Communications</i> , 2020, 11, 1839.	5.8	15
137	T(6;14)(q25;q32) involves BCL11B and is highly associated with mixed-phenotype acute leukemia, T/myeloid. <i>Leukemia</i> , 2020, 34, 2509-2512.	3.3	14
138	T-Cell Repertoire in Combination with T-Cell Density Predicts Clinical Outcomes in Patients with Merkel Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2146-2156.e4.	0.3	14
139	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. <i>Nature Communications</i> , 2022, 13, .	5.8	14
140	Assessment of Clinical Response Following Atezolizumab and Bevacizumab Treatment in Patients With Neuroendocrine Tumors. <i>JAMA Oncology</i> , 2022, 8, 904.	3.4	13
141	Precision medicine: preliminary results from the Initiative for Molecular Profiling and Advanced Cancer Therapy 2 (IMPACT2) study. <i>Npj Precision Oncology</i> , 2021, 5, 21.	2.3	12
142	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. <i>Acta Neuropathologica</i> , 2021, 142, 565-590.	3.9	12
143	Mouse IntraDuctal (MIND): an <i>in vivo</i> model for studying the underlying mechanisms of DCIS malignancy. <i>Journal of Pathology</i> , 2022, 256, 186-201.	2.1	12
144	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. <i>Psychoneuroendocrinology</i> , 2018, 89, 203-208.	1.3	10

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145	Effect of Antibiotics on Gut and Vaginal Microbiomes Associated with Cervical Cancer Development in Mice. <i>Cancer Prevention Research</i> , 2020, 13, 997-1006.	0.7	9
146	Germline DNMT3A mutation in familial acute myeloid leukaemia. <i>Epigenetics</i> , 2021, 16, 567-576.	1.3	9
147	Genetic correlates in patients with Philadelphia chromosome-positive acute lymphoblastic leukemia treated with Hyper-CVAD plus dasatinib or ponatinib. <i>Leukemia</i> , 2022, 36, 1253-1260.	3.3	9
148	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	4.7	9
149	Multi-modal molecular programs regulate melanoma cell state. <i>Nature Communications</i> , 2022, 13, .	5.8	9
150	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. <i>PLoS Computational Biology</i> , 2018, 14, e1006266.	1.5	8
151	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 705627.	1.3	7
152	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. <i>Npj Precision Oncology</i> , 2022, 6, 21.	2.3	7
153	Cancer Genomics in Clinical Context. <i>Trends in Cancer</i> , 2015, 1, 36-43.	3.8	6
154	Acute promyelocytic leukemia (APL) with an <i>IRF2BP2-RARA</i> fusion transcript: an aggressive APL variant. <i>Leukemia and Lymphoma</i> , 2020, 61, 3018-3020.	0.6	6
155	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020, 12, 1952-1959.	0.6	6
156	Distinct T cell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. <i>IScience</i> , 2021, 24, 102053.	1.9	6
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