P Andrew Futreal

List of Publications by Year
in descending order

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220 papers	63,386 citations	12330 69 h-index	2629 194 g-index
249 all docs	249 docs citations	249 times ranked	70912 citing authors

#	Article	IF	Citations
1	Mutations of the BRAF gene in human cancer. Nature, 2002, 417, 949-954.	27.8	9,374
2	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
3	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892.	27.0	6,769
4	Gut microbiome modulates response to antiâ€“PD-1 immunotherapy in melanoma patients. Science, 2018, 359, 97-103.	12.6	3,126
5	The cancer genome. Nature, 2009, 458, 719-724.	27.8	2,904
6	A census of human cancer genes. Nature Reviews Cancer, 2004, 4, 177-183.	28.4	2,868
7	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	28.9	2,020
8	COSMIC: mining complete cancer genomes in the Catalogue of Somatic Mutations in Cancer. Nucleic Acids Research, 2011, 39, D945-D950.	14.5	2,015
9	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
10	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
11	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
12	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
13	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. Nature, 2010, 467, 1109-1113.	27.8	1,200
14	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. Nature Genetics, 2014, 46, 225-233.	21.4	1,103
15	Loss of IFN-Î³ Pathway Genes in Tumor Cells as a Mechanism of Resistance to Anti-CTLA-4 Therapy. Cell, 2016, 167, 397-404.e9.	28.9	1,009
16	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	27.8	972
17	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. Science, 2014, 346, 256-259.	12.6	834
18	Analysis of Immune Signatures in Longitudinal Tumor Samples Yields Insight into Biomarkers of Response and Mechanisms of Resistance to Immune Checkpoint Blockade. Cancer Discovery, 2016, 6, 827-837.	9.4	785

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19	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
20	Co-occurring Genomic Alterations Define Major Subsets of KRAS-Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. Cancer Discovery, 2015, 5, 860-877.	9.4	696
21	Integrated molecular analysis of tumor biopsies on sequential CTLA-4 and PD-1 blockade reveals markers of response and resistance. Science Translational Medicine, 2017, 9, .	12.4	689
22	Intratumor Heterogeneity: Seeing the Wood for the Trees. Science Translational Medicine, 2012, 4, 127ps10.	12.4	443
23	Emerging patterns of somatic mutations in cancer. Nature Reviews Genetics, 2013, 14, 703-718.	16.3	442
24	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	28.9	398
25	Chromosomal Instability Confers Intrinsic Multidrug Resistance. Cancer Research, 2011, 71, 1858-1870.	0.9	391
26	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. Science, 2021, 374, 1632-1640.	12.6	369
27	Neoadjuvant nivolumab or nivolumab plus ipilimumab in operable non-small cell lung cancer: the phase 2 randomized NEOSTAR trial. Nature Medicine, 2021, 27, 504-514.	30.7	357
28	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13081-13086.	7.1	320
29	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. Lancet Oncology, The, 2017, 18, 100-111.	10.7	296
30	Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. Nature Communications, 2018, 9, 5361.	12.8	294
31	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. Cell Stem Cell, 2018, 23, 700-713.e6.	11.1	272
32	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. Genome Biology, 2016, 17, 178.	8.8	231
33	Molecular Profiling Reveals Unique Immune and Metabolic Features of Melanoma Brain Metastases. Cancer Discovery, 2019, 9, 628-645.	9.4	231
34	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. Nature Medicine, 2021, 27, 1432-1441.	30.7	216
35	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. Nature Communications, 2020, 11, 5327.	12.8	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. Cancer Research, 2015, 75, 3865-3878.	0.9	202

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37	Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma. Nature Medicine, 2020, 26, 1845-1851.	30.7	193
38	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	21.4	180
39	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. Nature Communications, 2017, 8, 15936.	12.8	179
40	High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics. Genome Research, 2018, 28, 1345-1352.	5.5	175
41	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. Nature Medicine, 2018, 24, 1047-1057.	30.7	175
42	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 1128-1141.e7.	16.8	169
43	Novel MYBL1 Gene Rearrangements with Recurrent MYBL1â€“NFIB Fusions in Salivary Adenoid Cystic Carcinomas Lacking t(6;9) Translocations. Clinical Cancer Research, 2016, 22, 725-733.	7.0	167
44	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. Science Translational Medicine, 2019, 11, .	12.4	161
45	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. Cancer Discovery, 2017, 7, 1088-1097.	9.4	160
46	Clearance of Somatic Mutations at Remission and the Risk of Relapse in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2018, 36, 1788-1797.	1.6	156
47	Immuno-genomic landscape of osteosarcoma. Nature Communications, 2020, 11, 1008.	12.8	143
48	Comprehensive T cell repertoire characterization of non-small cell lung cancer. Nature Communications, 2020, 11, 603.	12.8	140
49	Oncogenic Kras drives invasion and maintains metastases in colorectal cancer. Genes and Development, 2017, 31, 370-382.	5.9	137
50	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	30.7	134
51	Genomic heterogeneity of multiple synchronous lung cancer. Nature Communications, 2016, 7, 13200.	12.8	132
52	Circulating tumor DNA analysis depicts subclonal architecture and genomic evolution of small cell lung cancer. Nature Communications, 2018, 9, 3114.	12.8	122
53	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. Npj Genomic Medicine, 2017, 2, .	3.8	120
54	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	12.8	119

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55	The driver landscape of sporadic chordoma. Nature Communications, 2017, 8, 890.	12.8	115
56	Programmed Death-Ligand 1 Heterogeneity and Its Impact on Benefit From Immune Checkpoint Inhibitors in NSCLC. Journal of Thoracic Oncology, 2020, 15, 1449-1459.	1.1	109
57	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. Science Translational Medicine, 2020, 12, .	12.4	108
58	Novel algorithmic approach predicts tumor mutation load and correlates with immunotherapy clinical outcomes using a defined gene mutation set. BMC Medicine, 2016, 14, 168.	5.5	106
59	A cellular hierarchy framework for understanding heterogeneity and predicting drug response in acute myeloid leukemia. Nature Medicine, 2022, 28, 1212-1223.	30.7	104
60	Deep sequencing of circulating tumor DNA detects molecular residual disease and predicts recurrence in gastric cancer. Cell Death and Disease, 2020, 11, 346.	6.3	102
61	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. Gut, 2020, 69, 18-31.	12.1	94
62	Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. Cancer Research, 2017, 77, 6119-6130.	0.9	92
63	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. Nature Communications, 2019, 10, 2978.	12.8	91
64	A survey of homozygous deletions in human cancer genomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4542-4547.	7.1	90
65	Clinical implications of TP53 mutations in myelodysplastic syndromes treated with hypomethylating agents. Oncotarget, 2016, 7, 14172-14187.	1.8	86
66	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. Cancer Letters, 2015, 357, 179-185.	7.2	81
67	The Prognostic and Therapeutic Role of Genomic Subtyping by Sequencing Tumor or Cell-Free DNA in Pulmonary Large-Cell Neuroendocrine Carcinoma. Clinical Cancer Research, 2020, 26, 892-901.	7.0	80
68	Global analysis of shared TÂcell specificities in human non-small cell lung cancer enables HLA inference and antigen discovery. Immunity, 2021, 54, 586-602.e8.	14.3	80
69	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. Nature Communications, 2018, 9, 2670.	12.8	79
70	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	21.4	79
71	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. Nature Communications, 2021, 12, 5606.	12.8	76
72	Evaluation of Patients and Families With Concern for Predispositions to Hematologic Malignancies Within the Hereditary Hematologic Malignancy Clinic (HHMC). Clinical Lymphoma, Myeloma and Leukemia, 2016, 16, 417-428.e2.	0.4	74

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73	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. Nature Communications, 2021, 12, 2722.	12.8	74
74	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. Cell Reports, 2019, 26, 1518-1532.e9.	6.4	70
75	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. Cell Reports, 2020, 31, 107502.	6.4	69
76	Overexpressed PRAME is a potential immunotherapy target in sarcoma subtypes. Clinical Sarcoma Research, 2017, 7, 11.	2.3	61
77	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. Clinical Cancer Research, 2023, 27, 852-864.	7.0	61
78	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. Nature Communications, 2021, 12, 2607.	12.8	61
79	Managing Clonal Hematopoiesis in Patients With Solid Tumors. Journal of Clinical Oncology, 2019, 37, 7-11.	1.6	60
80	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. Journal of Clinical Investigation, 2020, 130, 5833-5846.	8.2	58
81	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. Modern Pathology, 2018, 31, 947-955.	5.5	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. Oncotarget, 2018, 9, 9714-9727.	1.8	56
83	A Preexisting Rare PIK3CAE545K Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in NRAS Melanoma and Is Dependent on S6K1 Signaling. Cancer Discovery, 2018, 8, 556-567.	9.4	55
84	Assessing tumor heterogeneity using ctDNA to predict and monitor therapeutic response in metastatic breast cancer. International Journal of Cancer, 2020, 146, 1359-1368.	5.1	55
85	Differential and limited expression of mutant alleles in multiple myeloma. Blood, 2014, 124, 3110-3117.	1.4	54
86	MYC protein expression is an important prognostic factor in acute myeloid leukemia. Leukemia and Lymphoma, 2019, 60, 37-48.	1.3	54
87	Androgen receptor blockade promotes response to BRAF/MEK-targeted therapy. Nature, 2022, 606, 797-803.	27.8	54
88	The somatic mutation landscape of premalignant colorectal adenoma. Gut, 2018, 67, 1299-1305.	12.1	52
89	Neoadjuvant Chemotherapy Increases Cytotoxic T Cell, Tissue Resident Memory T Cell, and B Cell Infiltration in Resectable NSCLC. Journal of Thoracic Oncology, 2021, 16, 127-139.	1.1	48
90	Identification of a Novel Fusion Gene,IRF2BP2-RARA, in Acute Promyelocytic Leukemia. Journal of the National Comprehensive Cancer Network: JNCCN, 2015, 13, 19-22.	4.9	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. Journal of Physical Education and Sports Management, 2018, 4, a002386.	1.2	45
92	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. Nature Communications, 2021, 12, 6071.	12.8	44
93	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. Genome Medicine, 2010, 2, 53.	8.2	43
94	Genomic profiles and clinical outcomes of de novo blastoid/pleomorphic MCL are distinct from those of transformed MCL. Blood Advances, 2020, 4, 1038-1050.	5.2	43
95	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. Blood, 2018, 131, 1820-1832.	1.4	40
96	Prevalence of recurrent oncogenic fusion in mismatch repair-deficient colorectal carcinoma with hypermethylated MLH1 and wild-type BRAF and KRAS. Modern Pathology, 2019, 32, 1053-1064.	5.5	40
97	Improving the detection of patients with inherited predispositions to hematologic malignancies using nextâ€generation sequencingâ€based leukemia prognostication panels. Cancer, 2018, 124, 2704-2713.	4.1	39
98	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. Nature Communications, 2018, 9, 2496.	12.8	39
99	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. Oncotarget, 2017, 8, 21994-22002.	1.8	39
100	Applying Artificial Intelligence to Address the Knowledge Gaps in Cancer Care. Oncologist, 2019, 24, 772-782.	3.7	38
101	Targeted Tissue and Cell-Free Tumor DNA Sequencing of Advanced Lung Squamous-Cell Carcinoma Reveals Clinically Significant Prevalence of Actionable Alterations. Clinical Lung Cancer, 2019, 20, 30-36.e3.	2.6	37
102	Multiomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. Genome Biology, 2020, 21, 271.	8.8	36
103	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. Nature Communications, 2021, 12, 2877.	12.8	35
104	Distinct molecular and immune hallmarks of inflammatory arthritis induced by immune checkpoint inhibitors for cancer therapy. Nature Communications, 2022, 13, 1970.	12.8	34
105	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	21.4	34
106	Genomic Rearrangement Signatures and Clinical Outcomes in High-Grade Serous Ovarian Cancer. Journal of the National Cancer Institute, 2018, 110, 265-272.	6.3	31
107	Germline DNA Sequencing Reveals Novel Mutations Predictive of Overall Survival in a Cohort of Patients with Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 1385-1394.	7.0	31
108	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. Nature Biotechnology, 2022, 40, 1624-1633.	17.5	31

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109	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. Blood Advances, 2017, 1, 1031-1036.	5.2	30
110	Identification of predictors of drug sensitivity using patient-derived models of esophageal squamous cell carcinoma. Nature Communications, 2019, 10, 5076.	12.8	30
111	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. Clinical Cancer Research, 2020, 26, 2908-2920.	7.0	30
112	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. Nature Communications, 2021, 12, 687.	12.8	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. Oncogene, 2020, 39, 1846-1859.	5.9	29
114	Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. Clinical Cancer Research, 2021, 27, 5365-5375.	7.0	29
115	Pilot Clinical Trial of Perioperative Durvalumab and Tremelimumab in the Treatment of Resectable Colorectal Cancer Liver Metastases. Clinical Cancer Research, 2021, 27, 3039-3049.	7.0	28
116	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. Oncotarget, 2018, 9, 19891-19899.	1.8	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. International Journal of Radiation Oncology Biology Physics, 2020, 106, 349-357.	0.8	27
118	Genetic determinants of immune-related adverse events in patients with melanoma receiving immune checkpoint inhibitors. Cancer Immunology, Immunotherapy, 2021, 70, 1939-1949.	4.2	27
119	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. Nature Communications, 2022, 13, 42.	12.8	27
120	Features of non-activation dendritic state and immune deficiency in blastic plasmacytoid dendritic cell neoplasm (BPDCN). Blood Cancer Journal, 2019, 9, 99.	6.2	26
121	High Prevalence of Hereditary Cancer Syndromes and Outcomes in Adults with Early-Onset Pancreatic Cancer. Cancer Prevention Research, 2018, 11, 679-686.	1.5	25
122	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. PLoS ONE, 2020, 15, e0234505.	2.5	25
123	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. Hepatology, 2022, 75, 955-967.	7.3	25
124	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. Nature Communications, 2021, 12, 6655.	12.8	24
125	Distinct Immunophenotypes of T Cells in Bronchoalveolar Lavage Fluid From Leukemia Patients With Immune Checkpoint Inhibitors-Related Pulmonary Complications. Frontiers in Immunology, 2020, 11, 590494.	4.8	21
126	MAGE-A3 Is a Clinically Relevant Target in Undifferentiated Pleomorphic Sarcoma/Myxofibrosarcoma. Cancers, 2019, 11, 677.	3.7	20

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127	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. Journal of the National Cancer Institute, 2017, 109, .	6.3	19
128	Donor clonal hematopoiesis increases risk of acute graft versus host disease after matched sibling transplantation. Leukemia, 2022, 36, 257-262.	7.2	19
129	Clonal dynamics and clinical implications of postremission clonal hematopoiesis in acute myeloid leukemia. Blood, 2021, 138, 1733-1739.	1.4	19
130	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. Oncotarget, 2018, 9, 29495-29507.	1.8	18
131	Patient-reported fatigue prior to treatment is prognostic of survival in patients with acute myeloid leukemia. Oncotarget, 2018, 9, 31244-31252.	1.8	17
132	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemiaâ€“initiating cells. Blood, 2019, 134, 614-625.	1.4	16
133	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. Nature Communications, 2021, 12, 7081.	12.8	16
134	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. EBioMedicine, 2019, 42, 296-303.	6.1	15
135	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. Clinical Cancer Research, 2020, 26, 5477-5486.	7.0	15
136	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. Nature Communications, 2020, 11, 1839.	12.8	15
137	T(6;14)(q25;q32) involves BCL11B and is highly associated with mixed-phenotype acute leukemia, T/myeloid. Leukemia, 2020, 34, 2509-2512.	7.2	14
138	T-Cell Repertoire in Combination with T-Cell Density Predicts Clinical Outcomes in Patients with Merkel Cell Carcinoma. Journal of Investigative Dermatology, 2020, 140, 2146-2156.e4.	0.7	14
139	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. Nature Communications, 2022, 13, .	12.8	14
140	Assessment of Clinical Response Following Atezolizumab and Bevacizumab Treatment in Patients With Neuroendocrine Tumors. JAMA Oncology, 2022, 8, 904.	7.1	13
141	Precision medicine: preliminary results from the Initiative for Molecular Profiling and Advanced Cancer Therapy 2 (IMPACT2) study. Npj Precision Oncology, 2021, 5, 21.	5.4	12
142	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. Acta Neuropathologica, 2021, 142, 565-590.	7.7	12
143	<scp>Mouseâ€ŠNtraDuctal</scp> (<scp>MIND</scp>): an in vivo model for studying the underlying mechanisms of <scp>DCIS</scp> malignancy. Journal of Pathology, 2022, 256, 186-201.	4.5	12
144	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. Psychoneuroendocrinology, 2018, 89, 203-208.	2.7	10

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145	Effect of Antibiotics on Gut and Vaginal Microbiomes Associated with Cervical Cancer Development in Mice. Cancer Prevention Research, 2020, 13, 997-1006.	1.5	9
146	Germline DNMT3A mutation in familial acute myeloid leukaemia. Epigenetics, 2021, 16, 567-576.	2.7	9
147	Genetic correlates in patients with Philadelphia chromosome-positive acute lymphoblastic leukemia treated with Hyper-CVAD plus dasatinib or ponatinib. Leukemia, 2022, 36, 1253-1260.	7.2	9
148	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	10.3	9
149	Multi-modal molecular programs regulate melanoma cell state. Nature Communications, 2022, 13, .	12.8	9
150	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. PLoS Computational Biology, 2018, 14, e1006266.	3.2	8
151	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. Frontiers in Oncology, 2021, 11, 705627.	2.8	7
152	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. Npj Precision Oncology, 2022, 6, 21.	5.4	7
153	Cancer Genomics in Clinical Context. Trends in Cancer, 2015, 1, 36-43.	7.4	6
154	Acute promyelocytic leukemia (APL) with an IRF2BP2-RARA fusion transcript: an aggressive APL variant. Leukemia and Lymphoma, 2020, 61, 3018-3020.	1.3	6
155	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. Journal of Thoracic Disease, 2020, 12, 1952-1959.	1.4	6
156	Distinct TÂcell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. IScience, 2021, 24, 102053.	4.1	6
157	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. Frontiers in Immunology, 2021, 12, 659625.	4.8	6
158	Statistical tests for intra-tumour clonal co-occurrence and exclusivity. PLoS Computational Biology, 2021, 17, e1009036.	3.2	6
159	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. Clinical Cancer Research, 2021, 27, 5049-5061.	7.0	6
160	Presence of 4 or More Driver Mutations Predicts Poor Response to Hypomethylating Agent (HMA) Therapy and Poor Overall Survival in MDS. Blood, 2015, 126, 1663-1663.	1.4	5
161	Comprehensive multiplexed immune profiling of the ductal carcinoma in situ immune microenvironment regarding subsequent ipsilateral invasive breast cancer risk. British Journal of Cancer, 0, , .	6.4	5
162	Clonal evolution of acute myeloid leukemia relapsed after 19 years of remission. American Journal of Hematology, 2015, 90, E134-5.	4.1	4

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163	Downregulation of Protection of Telomeres 1 expression in myelodysplastic syndromes with 7q deletion. British Journal of Haematology, 2016, 173, 161-165.	2.5	4
164	The landscape of genetic mutations in patients with chronic lymphocytic leukaemia and complex karyotype. British Journal of Haematology, 2019, 187, e1-e4.	2.5	4
165	Summary from the Kidney Cancer Associationâ€™s Inaugural Think Thank: Coalition for a Cure. Clinical Genitourinary Cancer, 2021, 19, 167-175.	1.9	4
166	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. Blood, 2018, 132, 1801-1801.	1.4	4
167	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). Blood, 2019, 134, 458-458.	1.4	4
168	Association of the T-cell receptor landscape with survival in non-small cell lung cancer.. Journal of Clinical Oncology, 2018, 36, 140-140.	1.6	4
169	T cell repertoire analysis of non-small cell lung cancer patients treated with neoadjuvant nivolumab alone or in combination with ipilimumab (NEOSTAR trial).. Journal of Clinical Oncology, 2019, 37, 8532-8532.	1.6	4
170	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. Journal of the National Comprehensive Cancer Network: JNCCN, 2020, 18, 1300-1304.	4.9	4
171	An analysis of research biopsy core variability from over 5000 prospectively collected core samples. Npj Precision Oncology, 2021, 5, 94.	5.4	4
172	Fidelity of peripheral blood for monitoring genomics and tumor immuneâ€microenvironment in myelodysplastic syndromes. EJHaem, 2020, 1, 552-557.	1.0	3
173	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. International Journal of Molecular Sciences, 2021, 22, 7411.	4.1	3
174	Comprehensive Genomic Analysis of IDH Inhibitor-Treated AML Samples Delineates Molecular Mechanisms of Differentiation and Heterogeneous Patterns of Acquired Resistance. Blood, 2018, 132, 441-441.	1.4	3
175	Delineating longitudinal patterns of response to neoadjuvant systemic therapy (NAST) in triple-negative breast cancer (TNBC): Profiling results from a randomized, TNBC enrolling trial to confirm molecular profiling improves survival (ARTEMIS; NCT02276443).. Journal of Clinical Oncology, 2019, 37, 586-586.	1.6	3
176	Building a data foundation: How MD Anderson and Palantir are partnering to accelerate research and improve patient care.. Journal of Clinical Oncology, 2019, 37, e18077-e18077.	1.6	3
177	Abstract 213: Exome sequencing of paired primary and relapsed small cell lung cancers reveals increased copy number aberration complexity to be associated with disease relapse. , 2018, , .		3
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