

P Andrew Futreal

List of Publications by Year in descending order

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Version: 2024-02-01

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	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. <i>Clinical Cancer Research</i> , 2023, 27, 852-864.	7.0	61
2	Donor clonal hematopoiesis increases risk of acute graft versus host disease after matched sibling transplantation. <i>Leukemia</i> , 2022, 36, 257-262.	7.2	19
3	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.	7.3	25
4	Mouseâ€œIntraDuctalâ€œ (MIND): an <i>in vivo</i> model for studying the underlying mechanisms of DCIS malignancy. <i>Journal of Pathology</i> , 2022, 256, 186-201.	4.5	12
5	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. <i>Nature Communications</i> , 2022, 13, 42.	12.8	27
6	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.	7.2	9
7	Abstract P1-22-05: Identifying predictors of invasive recurrence based on molecular profiles of DCIS lesions. <i>Cancer Research</i> , 2022, 82, P1-22-05-P1-22-05.	0.9	0
8	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. <i>Npj Precision Oncology</i> , 2022, 6, 21.	5.4	7
9	Assessment of Clinical Response Following Atezolizumab and Bevacizumab Treatment in Patients With Neuroendocrine Tumors. <i>JAMA Oncology</i> , 2022, 8, 904.	7.1	13
10	Distinct molecular and immune hallmarks of inflammatory arthritis induced by immune checkpoint inhibitors for cancer therapy. <i>Nature Communications</i> , 2022, 13, 1970.	12.8	34
11	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	10.3	9
12	The â€œGreat Debateâ€œ at Immunotherapy Bridge 2021, December 1stâ€œ2nd, 2021. <i>Journal of Translational Medicine</i> , 2022, 20, 179.	4.4	0
13	Immunogenomic intertumor heterogeneity across primary and metastatic sites in a patient with lung adenocarcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 172.	8.6	2
14	A cellular hierarchy framework for understanding heterogeneity and predicting drug response in acute myeloid leukemia. <i>Nature Medicine</i> , 2022, 28, 1212-1223.	30.7	104
15	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. <i>Nature Communications</i> , 2022, 13, .	12.8	14
16	Androgen receptor blockade promotes response to BRAF/MEK-targeted therapy. <i>Nature</i> , 2022, 606, 797-803.	27.8	54
17	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. <i>Nature Biotechnology</i> , 2022, 40, 1624-1633.	17.5	31
18	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. <i>Nature Genetics</i> , 2022, 54, 850-860.	21.4	34

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19	Multi-modal molecular programs regulate melanoma cell state. <i>Nature Communications</i> , 2022, 13, .	12.8	9
20	Summary from the Kidney Cancer Association's Inaugural Think Thank: Coalition for a Cure. <i>Clinical Genitourinary Cancer</i> , 2021, 19, 167-175.	1.9	4
21	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.	1.1	48
22	Germline DNMT3A mutation in familial acute myeloid leukaemia. <i>Epigenetics</i> , 2021, 16, 567-576.	2.7	9
23	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. <i>Nature Communications</i> , 2021, 12, 687.	12.8	30
24	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.	30.7	357
25	Distinct T cell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. <i>Science</i> , 2021, 24, 102053.	4.1	6
26	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.	14.3	80
27	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.	5.4	12
28	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.	7.0	28
29	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. <i>Frontiers in Immunology</i> , 2021, 12, 659625.	4.8	6
30	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2607.	12.8	61
31	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. <i>Nature Communications</i> , 2021, 12, 2722.	12.8	74
32	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. <i>Nature Communications</i> , 2021, 12, 2877.	12.8	35
33	Clonal dynamics and clinical implications of postremission clonal hematopoiesis in acute myeloid leukemia. <i>Blood</i> , 2021, 138, 1733-1739.	1.4	19
34	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021, 27, 1432-1441.	30.7	216
35	Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 5365-5375.	7.0	29
36	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. <i>Acta Neuropathologica</i> , 2021, 142, 565-590.	7.7	12

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37	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7411.	4.1	3
38	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 705627.	2.8	7
39	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , 2021, 12, 5606.	12.8	76
40	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	30.7	134
41	Genetic determinants of immune-related adverse events in patients with melanoma receiving immune checkpoint inhibitors. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 1939-1949.	4.2	27
42	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.	12.8	44
43	An analysis of research biopsy core variability from over 5000 prospectively collected core samples. <i>Npj Precision Oncology</i> , 2021, 5, 94.	5.4	4
44	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	7.0	0
45	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.	12.8	24
46	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	12.6	369
47	Statistical tests for intra-tumour clonal co-occurrence and exclusivity. <i>PLoS Computational Biology</i> , 2021, 17, e1009036.	3.2	6
48	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , 2021, 12, 7081.	12.8	16
49	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	7.0	6
50	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.	7.0	80
51	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.	5.1	55
52	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.	12.1	94
53	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.	0.8	27
54	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.	7.0	30

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55	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.	5.9	29
56	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.	7.0	31
57	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. <i>Nature Communications</i> , 2020, 11, 5327.	12.8	208
58	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.	30.7	193
59	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	21.4	79
60	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.	1.3	6
61	Fidelity of peripheral blood for monitoring genomics and tumor immune microenvironment in myelodysplastic syndromes. <i>EJHaem</i> , 2020, 1, 552-557.	1.0	3
62	Effect of Antibiotics on Gut and Vaginal Microbiomes Associated with Cervical Cancer Development in Mice. <i>Cancer Prevention Research</i> , 2020, 13, 997-1006.	1.5	9
63	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. <i>Clinical Cancer Research</i> , 2020, 26, 5477-5486.	7.0	15
64	Multiomics 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.	8.8	36
65	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.	6.3	102
66	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. <i>PLoS ONE</i> , 2020, 15, e0234505.	2.5	25
67	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	108
68	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020, 12, 1952-1959.	1.4	6
69	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.	7.2	14
70	Immuno-genomic landscape of osteosarcoma. <i>Nature Communications</i> , 2020, 11, 1008.	12.8	143
71	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	21.4	180
72	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2020, 31, 107502.	6.4	69

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73	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.	0.7	14
74	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. <i>Nature Communications</i> , 2020, 11, 1839.	12.8	15
75	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.	5.2	43
76	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.	4.8	21
77	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.	1.1	109
78	Comprehensive T cell repertoire characterization of non-small cell lung cancer. <i>Nature Communications</i> , 2020, 11, 603.	12.8	140
79	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846.	8.2	58
80	Extensive Changes of the Immune Microenvironment Are Associated with Progression from Precursor Stages to Multiple Myeloma. <i>Blood</i> , 2020, 136, 37-38.	1.4	2
81	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. <i>Oncotarget</i> , 2020, 11, 1-14.	1.8	1
82	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2020, 18, 1300-1304.	4.9	4
83	Single-Cell Characterization of Acute Myeloid Leukemia (AML) and Its Microenvironment Identifies Signatures of Resistance to PD-1 Blockade Based Therapy. <i>Blood</i> , 2020, 136, 29-31.	1.4	0
84	Immunologic Predictors for Clinical Responses in Patients with Myelodysplastic Syndromes Treated with Immune Checkpoint Blockade. <i>Blood</i> , 2020, 136, 4-4.	1.4	0
85	Prognostic Significance of Genetic Alterations in Patients with Philadelphia Chromosome-Positive Acute Lymphoblastic Leukemia Treated with Hyper-CVAD Plus Dasatinib or Hyper-CVAD Plus Ponatinib. <i>Blood</i> , 2020, 136, 40-41.	1.4	2
86	Hypomethylating Agents Do Not Alter Novel Splicing Events in Myeloid Neoplasms. <i>Blood</i> , 2020, 136, 37-38.	1.4	0
87	Single Cell Transcriptomic Evolution and Resistance Mechanisms of BTK and BCL-2 Inhibition in Mantle Cell Lymphoma. <i>Blood</i> , 2020, 136, 33-34.	1.4	0
88	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. , 2020, 15, e0234505.		0
89	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. , 2020, 15, e0234505.		0
90	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. , 2020, 15, e0234505.		0

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91	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. , 2020, 15, e0234505.		0
92	MYC protein expression is an important prognostic factor in acute myeloid leukemia. Leukemia and Lymphoma, 2019, 60, 37-48.	1.3	54
93	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. Nature Communications, 2019, 10, 2978.	12.8	91
94	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
95	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemiaâ€“initiating cells. Blood, 2019, 134, 614-625.	1.4	16
96	Identification of predictors of drug sensitivity using patient-derived models of esophageal squamous cell carcinoma. Nature Communications, 2019, 10, 5076.	12.8	30
97	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
98	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. Science Translational Medicine, 2019, 11, .	12.4	161
99	MAGE-A3 Is a Clinically Relevant Target in Undifferentiated Pleomorphic Sarcoma/Myxofibrosarcoma. Cancers, 2019, 11, 677.	3.7	20
100	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. EBioMedicine, 2019, 42, 296-303.	6.1	15
101	Managing Clonal Hematopoiesis in Patients With Solid Tumors. Journal of Clinical Oncology, 2019, 37, 7-11.	1.6	60
102	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
103	Molecular Profiling Reveals Unique Immune and Metabolic Features of Melanoma Brain Metastases. Cancer Discovery, 2019, 9, 628-645.	9.4	231
104	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
105	Applying Artificial Intelligence to Address the Knowledge Gaps in Cancer Care. Oncologist, 2019, 24, 772-782.	3.7	38
106	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
107	Donor Clonal Hematopoiesis Increases Risk of Acute Graft Versus Host Disease after Matched Related Transplantation in AML and MDS Patients. Blood, 2019, 134, 47-47.	1.4	2
108	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). Blood, 2019, 134, 458-458.	1.4	4

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109	Genetic determinants of adverse events in cancer patients receiving immune checkpoint inhibitors.. Journal of Clinical Oncology, 2019, 37, 2586-2586.	1.6	2
110	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
111	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
112	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
113	Tracking circulating cell-free tumor DNA in gastric cancer to detect early disease recurrence.. Journal of Clinical Oncology, 2019, 37, e14571-e14571.	1.6	0
114	Metagenomic discovery of a distinct inflammatory subtype of human angiosarcoma associated with human herpesvirus 7.. Journal of Clinical Oncology, 2019, 37, 11047-11047.	1.6	0
115	cfDNA analysis to reveal association of genomic features with chemotherapy response and survival in patients with pulmonary large-cell neuroendocrine carcinoma.. Journal of Clinical Oncology, 2019, 37, e14555-e14555.	1.6	0
116	Prognostic Significance of IKZF1, PAX5, and CDKN2A Deletions in Patients with Philadelphia Chromosome-Positive Acute Lymphoblastic Leukemia Treated with Hyper-CVAD/MA with Dasatinib or Ponatinib. Blood, 2019, 134, 2753-2753.	1.4	0
117	Clonal Dynamics and Clinical Implications of Post-Remission Clonal Hematopoiesis in Acute Myeloid Leukemia (AML). Blood, 2019, 134, 17-17.	1.4	0
118	Characterization of Changes in the T-Cell Receptor Repertoire in Patients with Acute Myeloid Leukemia with Durable Remission Following Allogeneic Stem Cell Transplant. Blood, 2019, 134, 5186-5186.	1.4	0
119	Identification of Gene Expression Signatures in Leukemia Stem Cells and Minimal Residual Disease Following Treatment of Adverse Risk Acute Myeloid Leukemia. Blood, 2019, 134, 2717-2717.	1.4	1
120	Transcriptomic Heterogeneity and Clonal Evolution Associated with Therapeutic Resistance in Mantle Cell Lymphoma Revealed By Single Cell RNA-Seq. Blood, 2019, 134, 5217-5217.	1.4	0
121	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. Cancer Discovery, 2018, 8, 556-567.	9.4	55
122	Improving the detection of patients with inherited predispositions to hematologic malignancies using next-generation sequencing-based leukemia prognostication panels. Cancer, 2018, 124, 2704-2713.	4.1	39
123	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
124	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	28.9	398
125	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
126	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

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127	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. <i>Blood</i> , 2018, 131, 1820-1832.	1.4	40
128	The somatic mutation landscape of premalignant colorectal adenoma. <i>Gut</i> , 2018, 67, 1299-1305.	12.1	52
129	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	12.6	3,126
130	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.	1.6	156
131	Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 5361.	12.8	294
132	High Prevalence of Hereditary Cancer Syndromes and Outcomes in Adults with Early-Onset Pancreatic Cancer. <i>Cancer Prevention Research</i> , 2018, 11, 679-686.	1.5	25
133	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. <i>Cell Stem Cell</i> , 2018, 23, 700-713.e6.	11.1	272
134	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. <i>Cancer Cell</i> , 2018, 33, 1128-1141.e7.	16.8	169
135	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. <i>Nature Communications</i> , 2018, 9, 2496.	12.8	39
136	Circulating tumor DNA analysis depicts subclonal architecture and genomic evolution of small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3114.	12.8	122
137	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. <i>Oncotarget</i> , 2018, 9, 29495-29507.	1.8	18
138	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. <i>Nature Communications</i> , 2018, 9, 2670.	12.8	79
139	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. <i>Psychoneuroendocrinology</i> , 2018, 89, 203-208.	2.7	10
140	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. <i>PLoS Computational Biology</i> , 2018, 14, e1006266.	3.2	8
141	High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics. <i>Genome Research</i> , 2018, 28, 1345-1352.	5.5	175
142	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. <i>Nature Medicine</i> , 2018, 24, 1047-1057.	30.7	175
143	Abstract 4686: T cell repertoire evolution from the normal lung to invasive lung adenocarcinoma. , 2018, , .		2
144	Comprehensive Genomic Analysis of IDH Inhibitor-Treated AML Samples Delineates Molecular Mechanisms of Differentiation and Heterogeneous Patterns of Acquired Resistance. <i>Blood</i> , 2018, 132, 441-441.	1.4	3

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145	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. <i>Blood</i> , 2018, 132, 1801-1801.	1.4	4
146	Association of the T-cell receptor landscape with survival in non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2018, 36, 140-140.	1.6	4
147	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.	1.8	56
148	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. <i>Oncotarget</i> , 2018, 9, 19891-19899.	1.8	28
149	Patient-reported fatigue prior to treatment is prognostic of survival in patients with acute myeloid leukemia. <i>Oncotarget</i> , 2018, 9, 31244-31252.	1.8	17
150	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
151	High Prevalence of PPM1D Mutations in Therapy-Related AML/MDS Is Due to Context-Specific Clonal Hematopoiesis. <i>Blood</i> , 2018, 132, 746-746.	1.4	0
152	Clinical Heterogeneity of AML Is Associated with Mutational Heterogeneity. <i>Blood</i> , 2018, 132, 5240-5240.	1.4	2
153	Combination of Lenalidomide and Rituximab in Patients with Treatment-Naïve and Relapsed Chronic Lymphocytic Leukemia: Treatment Results and Predictive Factors of Response. <i>Blood</i> , 2018, 132, 295-295.	1.4	0
154	Single-Cell Atlas of Driver Mutations in Acute Myeloid Leukemia (AML). <i>Blood</i> , 2018, 132, 88-88.	1.4	1
155	Distinct Gene Expression Patterns of Minimal Residual Disease (MRD) Cells in High-Risk AML Patients Identified By RNA-Sequencing. <i>Blood</i> , 2018, 132, 2757-2757.	1.4	0
156	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, .	12.4	689
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