

P Andrew Futreal

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.

217
papers

46,597
citations

57
h-index

215
g-index

249
ext. papers

56,647
ext. citations

14
avg, IF

6.53
L-index

#	Paper	IF	Citations
217	Mutations of the BRAF gene in human cancer. <i>Nature</i> , 2002 , 417, 949-54	50.4	7962
216	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
215	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. <i>New England Journal of Medicine</i> , 2012 , 366, 883-892	59.2	5559
214	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004 , 4, 177-83	31.3	2424
213	The cancer genome. <i>Nature</i> , 2009 , 458, 719-24	50.4	2272
212	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018 , 359, 97-103	33.3	1895
211	COSMIC: mining complete cancer genomes in the Catalogue of Somatic Mutations in Cancer. <i>Nucleic Acids Research</i> , 2011 , 39, D945-50	20.1	1774
210	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. <i>Cell</i> , 2011 , 144, 27-40	56.2	1628
209	Mutational processes molding the genomes of 21 breast cancers. <i>Cell</i> , 2012 , 149, 979-93	56.2	1279
208	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012 , 486, 400-4	50.4	1264
207	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
206	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. <i>Nature</i> , 2010 , 467, 1109-13	50.4	1013
205	The life history of 21 breast cancers. <i>Cell</i> , 2012 , 149, 994-1007	56.2	979
204	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. <i>Nature Genetics</i> , 2014 , 46, 225-233	36.3	866
203	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010 , 463, 184-90	50.4	852
202	Loss of IFN- γ Pathway Genes in Tumor Cells as a Mechanism of Resistance to Anti-CTLA-4 Therapy. <i>Cell</i> , 2016 , 167, 397-404.e9	56.2	688
201	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. <i>Science</i> , 2014 , 346, 256-9	33.3	659

200	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014 , 5, 2997	17.4	564
199	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, 827-37	24.4	561
198	Co-occurring genomic alterations define major subsets of KRAS-mutant lung adenocarcinoma with distinct biology, immune profiles, and therapeutic vulnerabilities. <i>Cancer Discovery</i> , 2015 , 5, 860-77	24.4	476
197	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,	17.5	409
196	Intratumor heterogeneity: seeing the wood for the trees. <i>Science Translational Medicine</i> , 2012 , 4, 127ps107.5	10.5	375
195	Emerging patterns of somatic mutations in cancer. <i>Nature Reviews Genetics</i> , 2013 , 14, 703-18	30.1	366
194	Chromosomal instability confers intrinsic multidrug resistance. <i>Cancer Research</i> , 2011 , 71, 1858-70	10.1	309
193	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, 13081-6	11.5	283
192	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018 , 173, 611-623.e17	56.2	228
191	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. <i>Lancet Oncology, The</i> , 2017 , 18, 100-111	21.7	189
190	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. <i>Cell Stem Cell</i> , 2018 , 23, 700-713.e6	18	147
189	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	10.1	146
188	Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. <i>Nature Communications</i> , 2018 , 9, 5361	17.4	145
187	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017 , 8, 15936	17.4	125
186	Molecular Profiling Reveals Unique Immune and Metabolic Features of Melanoma Brain Metastases. <i>Cancer Discovery</i> , 2019 , 9, 628-645	24.4	124
185	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	18.3	120
184	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, 725-33	12.9	116
183	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	2.2	111

182	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	24.4	105
181	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	50.5	105
180	High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics. <i>Genome Research</i> , 2018 , 28, 1345-1352	9.7	102
179	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. <i>Cancer Cell</i> , 2018 , 33, 1128-1141.e7	24.3	100
178	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. <i>Nature Medicine</i> , 2018 , 24, 1047-1057	50.5	99
177	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	11.4	87
176	Genomic heterogeneity of multiple synchronous lung cancer. <i>Nature Communications</i> , 2016 , 7, 13200	17.4	85
175	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. <i>Npj Genomic Medicine</i> , 2017 , 2,	6.2	82
174	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020 , 52, 294-305	36.3	81
173	Oncogenic drives invasion and maintains metastases in colorectal cancer. <i>Genes and Development</i> , 2017 , 31, 370-382	12.6	80
172	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	77
171	Immuno-genomic landscape of osteosarcoma. <i>Nature Communications</i> , 2020 , 11, 1008	17.4	77
170	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. <i>Nature Communications</i> , 2020 , 11, 5327	17.4	75
169	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016 , 7, 12910	17.4	74
168	Circulating tumor DNA analysis depicts subclonal architecture and genomic evolution of small cell lung cancer. <i>Nature Communications</i> , 2018 , 9, 3114	17.4	73
167	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	50.5	72
166	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, 4542-7	11.5	70
165	iTALK: an R Package to Characterize and Illustrate Intercellular Communication		70

164	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	9.9	68
163	Comprehensive T cell repertoire characterization of non-small cell lung cancer. <i>Nature Communications</i> , 2020 , 11, 603	17.4	67
162	The driver landscape of sporadic chordoma. <i>Nature Communications</i> , 2017 , 8, 890	17.4	64
161	Clinical implications of TP53 mutations in myelodysplastic syndromes treated with hypomethylating agents. <i>Oncotarget</i> , 2016 , 7, 14172-87	3.3	59
160	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021 , 27, 1432-1441	50.5	57
159	Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. <i>Cancer Research</i> , 2017 , 77, 6119-6130	10.1	56
158	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	2	55
157	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	54
156	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response.. <i>Science</i> , 2021 , 374, 1632-1640	33.3	52
155	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	8.9	49
154	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. <i>Nature Communications</i> , 2018 , 9, 2670	17.4	47
153	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. <i>Nature Communications</i> , 2019 , 10, 2978	17.4	43
152	A Preexisting Rare Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in Melanoma and Is Dependent on S6K1 Signaling. <i>Cancer Discovery</i> , 2018 , 8, 556-567	24.4	42
151	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014 , 124, 3110-7	2.2	42
150	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	3.3	42
149	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	19.2	39
148	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	7.3	38
147	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. <i>Cell Reports</i> , 2019 , 26, 1518-1532.e9	10.6	36

146	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010 , 2, 53	14.4	36
145	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. <i>Modern Pathology</i> , 2018 , 31, 947-955	9.8	35
144	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	12.9	34
143	Managing Clonal Hematopoiesis in Patients With Solid Tumors. <i>Journal of Clinical Oncology</i> , 2019 , 37, 7-11	2.2	33
142	The somatic mutation landscape of premalignant colorectal adenoma. <i>Gut</i> , 2018 , 67, 1299-1305	19.2	33
141	MYC protein expression is an important prognostic factor in acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2019 , 60, 37-48	1.9	33
140	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	9.8	32
139	Overexpressed PRAME is a potential immunotherapy target in sarcoma subtypes. <i>Clinical Sarcoma Research</i> , 2017 , 7, 11	2.5	32
138	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	7.5	30
137	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021 , 27, 141-151	50.5	30
136	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	6.4	29
135	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2020 , 31, 107502	10.6	28
134	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	9.8	27
133	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,	2.8	26
132	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. <i>Blood</i> , 2018 , 131, 1820-1832	2.2	25
131	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020 , 52, 1178-1188	36.3	25
130	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	7.8	25
129	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. <i>Oncotarget</i> , 2017 , 8, 21994-22003	9.4	23

128	Genomic Rearrangement Signatures and Clinical Outcomes in High-Grade Serous Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2018 , 110,	9.7	22
127	Multioomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020 , 130, 5833-5846	15.9	22
126	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. <i>Blood Advances</i> , 2017 , 1, 1031-1036	7.8	21
125	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. <i>Oncotarget</i> , 2018 , 9, 19891-19899	3.3	19
124	Applying Artificial Intelligence to Address the Knowledge Gaps in Cancer Care. <i>Oncologist</i> , 2019 , 24, 772-782	5.82	19
123	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	4.9	19
122	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	17
121	Identification of predictors of drug sensitivity using patient-derived models of esophageal squamous cell carcinoma. <i>Nature Communications</i> , 2019 , 10, 5076	17.4	17
120	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	12.9	17
119	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. <i>Nature Communications</i> , 2018 , 9, 2496	17.4	16
118	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	32.3	16
117	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. <i>Nature Communications</i> , 2021 , 12, 2722	17.4	16
116	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	4	15
115	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	9.2	15
114	Features of non-activation dendritic state and immune deficiency in blastic plasmacytoid dendritic cell neoplasm (BPDCN). <i>Blood Cancer Journal</i> , 2019 , 9, 99	7	15
113	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	8.9	14
112	Multioomics 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	18.3	13
111	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. <i>Oncotarget</i> , 2018 , 9, 29495-29507	3.3	13

110	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. <i>Nature Communications</i> , 2021 , 12, 2607	17.4	13
109	MAGE-A3 is a Clinically Relevant Target in Undifferentiated Pleomorphic Sarcoma/Myxofibrosarcoma. <i>Cancers</i> , 2019 , 11,	6.6	12
108	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	12.8	12
107	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. <i>Clinical Cancer Research</i> , 2020 , 26, 5477-5486	12.9	12
106	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. <i>Clinical Cancer Research</i> , 2021 , 27, 852-864	12.9	12
105	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , 2021 , 12, 5606	17.4	12
104	High Prevalence of Hereditary Cancer Syndromes and Outcomes in Adults with Early-Onset Pancreatic Cancer. <i>Cancer Prevention Research</i> , 2018 , 11, 679-686	3.2	11
103	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemia-initiating cells. <i>Blood</i> , 2019 , 134, 614-625	2.2	10
102	Patient-reported fatigue prior to treatment is prognostic of survival in patients with acute myeloid leukemia. <i>Oncotarget</i> , 2018 , 9, 31244-31252	3.3	9
101	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	4.3	9
100	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. <i>Nature Communications</i> , 2020 , 11, 1839	17.4	9
99	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. <i>Nature Communications</i> , 2021 , 12, 687	17.4	9
98	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. <i>EBioMedicine</i> , 2019 , 42, 296-303	8.8	8
97	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. <i>Psychoneuroendocrinology</i> , 2018 , 89, 203-208	5	7
96	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. <i>PLoS Computational Biology</i> , 2018 , 14, e1006266	5	7
95	Clonal Evolution of Acute Myeloid Leukemia Revealed by High-Throughput Single-Cell Genomics		7
94	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	10.7	6
93	Cancer Genomics in Clinical Context. <i>Trends in Cancer</i> , 2015 , 1, 36-43	12.5	5

92	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. <i>PLoS ONE</i> , 2020 , 15, e0234505	4.5	5
91	Presence of 4 or More Driver Mutations Predicts Poor Response to Hypomethylating Agent (HMA) Therapy and Poor Overall Survival in MDS. <i>Blood</i> , 2015 , 126, 1663-1663	2.2	5
90	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association.. <i>Nature Communications</i> , 2022 , 13, 42	17.4	5
89	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	17.4	5
88	Gut Microbiome Features Associated with Liver Fibrosis in Hispanics, a Population at High Risk for Fatty Liver Disease. <i>Hepatology</i> , 2021 ,	11.2	5
87	Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021 ,	12.9	5
86	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	8.4	5
85	Genetic determinants of immune-related adverse events in patients with melanoma receiving immune checkpoint inhibitors. <i>Cancer Immunology, Immunotherapy</i> , 2021 , 70, 1939-1949	7.4	5
84	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020 , 12, 1952-1959	2.6	4
83	Clonal evolution of acute myeloid leukemia relapsed after 19 years of remission. <i>American Journal of Hematology</i> , 2015 , 90, E134-5	7.1	4
82	Acute promyelocytic leukemia (APL) with an fusion transcript: an aggressive APL variant. <i>Leukemia and Lymphoma</i> , 2020 , 61, 3018-3020	1.9	4
81	Downregulation of Protection of Telomeres 1 expression in myelodysplastic syndromes with 7q deletion. <i>British Journal of Haematology</i> , 2016 , 173, 161-5	4.5	4
80	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	2.2	3
79	T cell repertoire analysis of non-small cell lung cancer patients treated with neoadjuvant nivolumab alone or in combination with ipilimumab (NEOSTAR trial).. <i>Journal of Clinical Oncology</i> , 2019 , 37, 8532-8532	2.2	3
78	Author response: Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer 2014 ,		3
77	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	12.9	3
76	Germline DNMT3A mutation in familial acute myeloid leukaemia. <i>Epigenetics</i> , 2021 , 16, 567-576	5.7	3
75	The landscape of genetic mutations in patients with chronic lymphocytic leukaemia and complex karyotype. <i>British Journal of Haematology</i> , 2019 , 187, e1-e4	4.5	2

74	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. <i>Blood</i> , 2018 , 132, 1801-1801	2.2	2
73	Donor Clonal Hematopoiesis Increases Risk of Acute Graft Versus Host Disease after Matched Related Transplantation in AML and MDS Patients. <i>Blood</i> , 2019 , 134, 47-47	2.2	2
72	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). <i>Blood</i> , 2019 , 134, 458-458	2.2	2
71	TP53 Mutated MDS Patients Respond Equally to Hypomethylating Agents but Have Significantly Shorter Response Duration Compared to Patients with Wild Type TP53. <i>Blood</i> , 2015 , 126, 1681-1681	2.2	2
70	Clinico-Pathological Characteristics, Treatments and Outcomes of Patients with Dendritic Cell Sarcoma (DS). <i>Blood</i> , 2015 , 126, 2700-2700	2.2	2
69	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	2.2	2
68	Genetic determinants of adverse events in cancer patients receiving immune checkpoint inhibitors.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 2586-2586	2.2	2
67	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).. <i>Journal of Clinical Oncology</i> , 2019 , 37, 101-101	2.2	2
66	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	7.3	2
65	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 ,		2
64	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features		2
63	Tumor cell total mRNA expression shapes the molecular and clinical phenotype of cancer		2
62	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia		2
61	Effect of Antibiotics on Gut and Vaginal Microbiomes Associated with Cervical Cancer Development in Mice. <i>Cancer Prevention Research</i> , 2020 , 13, 997-1006	3.2	2
60	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	9.8	2
59	Clonal dynamics and clinical implications of postremission clonal hematopoiesis in acute myeloid leukemia. <i>Blood</i> , 2021 , 138, 1733-1739	2.2	2
58	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	12.9	2
57	Distinct molecular and immune hallmarks of inflammatory arthritis induced by immune checkpoint inhibitors for cancer therapy.. <i>Nature Communications</i> , 2022 , 13, 1970	17.4	2

56	Are sarcomas hereditary?. <i>Lancet Oncology, The</i> , 2016 , 17, 1179-81	21.7	1
55	Extensive Changes of the Immune Microenvironment Are Associated with Progression from Precursor Stages to Multiple Myeloma. <i>Blood</i> , 2020 , 136, 37-38	2.2	1
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