P Andrew Futreal

List of Publications by Year in Descending Order

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	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association.. *Nature Communications*, **2022**, 13, 42	17.4	5
216	Abstract P1-22-05: Identifying predictors of invasive recurrence based on molecular profiles of DCIS lesions. *Cancer Research*, **2022**, 82, P1-22-05-P1-22-05	10.1	
215	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold.. *Npj Precision Oncology*, **2022**, 6, 21	9.8	1
214	Distinct molecular and immune hallmarks of inflammatory arthritis induced by immune checkpoint inhibitors for cancer therapy.. *Nature Communications*, **2022**, 13, 1970	17.4	2
213	A functional genomic approach to actionable gene fusions for precision oncology.. *Science Advances* , **2022**, 8, eabm2382	14.3	0
212	The "Great Debate" at Immunotherapy Bridge 2021, December 1st-2nd, 2021.. *Journal of Translational Medicine*, **2022**, 20, 179	8.5	
211	Immunogenomic intertumor heterogeneity across primary and metastatic sites in a patient with lung adenocarcinoma.. *Journal of Experimental and Clinical Cancer Research*, **2022**, 41, 172	12.8	
210	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response.. *Science*, **2021**, 374, 1632-1640	33.3	52
209	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. *Clinical Cancer Research*, **2021**, 27, 5049-5061	12.9	
208	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	17.4	1
207	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	17.4	5
206	Gut Microbiome Features Associated with Liver Fibrosis in Hispanics, a Population at High Risk for Fatty Liver Disease. *Hepatology*, **2021**,	11.2	5
205	An analysis of research biopsy core variability from over 5000 prospectively collected core samples. *Npj Precision Oncology*, **2021**, 5, 94	9.8	0
204	Global analysis of shared T cell specificities in human non-small cell lung cancer enables HLA inference and antigen discovery. *Immunity*, **2021**, 54, 586-602.e8	32.3	16
203	Precision medicine: preliminary results from the Initiative for Molecular Profiling and Advanced Cancer Therapy 2 (IMPACT2) study. *Npj Precision Oncology*, **2021**, 5, 21	9.8	2
202	Pilot Clinical Trial of Perioperative Durvalumab and Tremelimumab in the Treatment of Resectable Colorectal Cancer Liver Metastases. *Clinical Cancer Research*, **2021**, 27, 3039-3049	12.9	3
201	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. *Frontiers in Immunology*, **2021**, 12, 659625	8.4	0

200	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. *Nature Communications*, **2021**, 12, 2607	17.4	13
199	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. *Nature Communications*, **2021**, 12, 2722	17.4	16
198	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. *Nature Communications*, **2021**, 12, 2877	17.4	1
197	Donor clonal hematopoiesis increases risk of acute graft versus host disease after matched sibling transplantation. *Leukemia*, **2021**,	10.7	1
196	Clonal dynamics and clinical implications of postremission clonal hematopoiesis in acute myeloid leukemia. *Blood*, **2021**, 138, 1733-1739	2.2	2
195	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. *Nature Medicine*, **2021**, 27, 1432-1441	50.5	57
194	Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. *Clinical Cancer Research*, **2021**,	12.9	5
193	Summary from the Kidney Cancer Association's Inaugural Think Thank: Coalition for a Cure. *Clinical Genitourinary Cancer*, **2021**, 19, 167-175	3.3	1
192	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. *Clinical Cancer Research*, **2021**, 27, 852-864	12.9	12
191	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	8.9	14
190	Germline DNMT3A mutation in familial acute myeloid leukaemia. *Epigenetics*, **2021**, 16, 567-576	5.7	3
189	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. *Nature Communications*, **2021**, 12, 687	17.4	9
188	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	50.5	105
187	Distinct T□cell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. *IScience*, **2021**, 24, 102053	6.1	1
186	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. *Acta Neuropathologica*, **2021**, 142, 565-590	14.3	0
185	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. *Frontiers in Oncology*, **2021**, 11, 705627	5.3	0
184	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. *Nature Communications*, **2021**, 12, 5606	17.4	12
183	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. *Nature Medicine*, **2021**, 27, 141-151	50.5	30

182	Genetic determinants of immune-related adverse events in patients with melanoma receiving immune checkpoint inhibitors. *Cancer Immunology, Immunotherapy*, **2021**, 70, 1939-1949	7.4	5
181	Statistical tests for intra-tumour clonal co-occurrence and exclusivity.. *PLoS Computational Biology*, **2021**, 17, e1009036	5	1
180	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. *Nature Communications*, **2021**, 12, 7081	17.4	1
179	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. *Clinical Cancer Research*, **2021**, 27, 5049-5061	12.9	2
178	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	18.3	13
177	Deep sequencing of circulating tumor DNA detects molecular residual disease and predicts recurrence in gastric cancer. *Cell Death and Disease*, **2020**, 11, 346	9.8	32
176	Comparative genomics of high grade neuroendocrine carcinoma of the cervix. *PLoS ONE*, **2020**, 15, e0234505	3.7	5
175	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. *Science Translational Medicine*, **2020**, 12,	17.5	54
174	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. *Journal of Thoracic Disease*, **2020**, 12, 1952-1959	2.6	4
173	T(6;14)(q25;q32) involves BCL11B and is highly associated with mixed-phenotype acute leukemia, T/myeloid. *Leukemia*, **2020**, 34, 2509-2512	10.7	6
172	Immuno-genomic landscape of osteosarcoma. *Nature Communications*, **2020**, 11, 1008	17.4	77
171	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. *Nature Genetics*, **2020**, 52, 294-305	36.3	81
170	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	12.9	34
169	Single-Cell Characterization of Acute Myeloid Leukemia (AML) and Its Microenvironment Identifies Signatures of Resistance to PD-1 Blockade Based Therapy. *Blood*, **2020**, 136, 29-31	2.2	
168	Immunologic Predictors for Clinical Responses in Patients with Myelodysplastic Syndromes Treated with Immune Checkpoint Blockade. *Blood*, **2020**, 136, 4-4	2.2	
167	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. *Blood*, **2020**, 136, 40-41	2.2	0
166	Hypomethylating Agents Do Not Alter Novel Splicing Events in Myeloid Neoplasms. *Blood*, **2020**, 136, 37-38	2.2	
165	Single Cell Transcriptomic Evolution and Resistance Mechanisms of BTK and BCL-2 Inhibition in Mantle Cell Lymphoma. *Blood*, **2020**, 136, 33-34	2.2	

164	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. *Journal of Clinical Investigation*, **2020**, 130, 5833-5846	15.9	22
163	Extensive Changes of the Immune Microenvironment Are Associated with Progression from Precursor Stages to Multiple Myeloma. *Blood*, **2020**, 136, 37-38	2.2	1
162	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. *Oncotarget*, **2020**, 11, 1-14	3.3	0
161	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	7.3	2
160	Programmed Death-Ligand 1 Heterogeneity and Its Impact on Benefit From Immune Checkpoint Inhibitors in NSCLC. *Journal of Thoracic Oncology*, **2020**, 15, 1449-1459	8.9	49
159	Comprehensive T cell repertoire characterization of non-small cell lung cancer. *Nature Communications*, **2020**, 11, 603	17.4	67
158	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	4	15
157	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. *Clinical Cancer Research*, **2020**, 26, 2908-2920	12.9	12
156	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	9.2	15
155	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	12.9	17
154	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. *Nature Communications*, **2020**, 11, 5327	17.4	75
153	Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma. *Nature Medicine*, **2020**, 26, 1845-1851	50.5	72
152	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. *Nature Genetics*, **2020**, 52, 1178-1188	36.3	25
151	Acute promyelocytic leukemia (APL) with an fusion transcript: an aggressive APL variant. *Leukemia and Lymphoma*, **2020**, 61, 3018-3020	1.9	4
150	Fidelity of peripheral blood for monitoring genomics and tumor immune-microenvironment in myelodysplastic syndromes. *EJHaem*, **2020**, 1, 552-557	0.9	
149	Effect of Antibiotics on Gut and Vaginal Microbiomes Associated with Cervical Cancer Development in Mice. *Cancer Prevention Research*, **2020**, 13, 997-1006	3.2	2
148	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. *Clinical Cancer Research*, **2020**, 26, 5477-5486	12.9	12
147	Assessing tumor heterogeneity using ctDNA to predict and monitor therapeutic response in metastatic breast cancer. *International Journal of Cancer*, **2020**, 146, 1359-1368	7.5	30

146	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. *Gut*, **2020**, 69, 18-31	19.2	39
145	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. *Cell Reports*, **2020**, 31, 107502	10.6	28
144	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	4.3	9
143	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. *Nature Communications*, **2020**, 11, 1839	17.4	9
142	Genomic profiles and clinical outcomes of de novo blastoid/pleomorphic MCL are distinct from those of transformed MCL. *Blood Advances*, **2020**, 4, 1038-1050	7.8	25
141	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	8.4	5
140	Comparative genomics of high grade neuroendocrine carcinoma of the cervix **2020**, 15, e0234505		
139	Comparative genomics of high grade neuroendocrine carcinoma of the cervix **2020**, 15, e0234505		
138	Comparative genomics of high grade neuroendocrine carcinoma of the cervix **2020**, 15, e0234505		
137	Comparative genomics of high grade neuroendocrine carcinoma of the cervix **2020**, 15, e0234505		
136	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. *Cell Reports*, **2019**, 26, 1518-1532.e9	10.6	36
135	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. *Science Translational Medicine*, **2019**, 11,	17.5	77
134	MAGE-A3 is a Clinically Relevant Target in Undifferentiated Pleomorphic Sarcoma/Myxofibrosarcoma. *Cancers*, **2019**, 11,	6.6	12
133	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. *EBioMedicine*, **2019**, 42, 296-303	8.8	8
132	Managing Clonal Hematopoiesis in Patients With Solid Tumors. *Journal of Clinical Oncology*, **2019**, 37, 7-11	2.2	33
131	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	9.8	27
130	MYC protein expression is an important prognostic factor in acute myeloid leukemia. *Leukemia and Lymphoma*, **2019**, 60, 37-48	1.9	33
129	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. *Nature Communications*, **2019**, 10, 2978	17.4	43

128	The landscape of genetic mutations in patients with chronic lymphocytic leukaemia and complex karyotype. *British Journal of Haematology*, **2019**, 187, e1-e4	4.5	2
127	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemia-initiating cells. *Blood*, **2019**, 134, 614-625	2.2	10
126	Identification of predictors of drug sensitivity using patient-derived models of esophageal squamous cell carcinoma. *Nature Communications*, **2019**, 10, 5076	17.4	17
125	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	2.2	2
124	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). *Blood*, **2019**, 134, 458-458	2.2	2
123	Genetic determinants of adverse events in cancer patients receiving immune checkpoint inhibitors.. *Journal of Clinical Oncology*, **2019**, 37, 2586-2586	2.2	2
122	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	2.2	2
121	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	2.2	3
120	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	2.2	1
119	Tracking circulating cell-free tumor DNA in gastric cancer to detect early disease recurrence.. *Journal of Clinical Oncology*, **2019**, 37, e14571-e14571	2.2	
118	Metagenomic discovery of a distinct inflammatory subtype of human angiosarcoma associated with human herpesvirus 7.. *Journal of Clinical Oncology*, **2019**, 37, 11047-11047	2.2	
117	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	2.2	
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	2.2	
115	Clonal Dynamics and Clinical Implications of Post-Remission Clonal Hematopoiesis in Acute Myeloid Leukemia (AML). *Blood*, **2019**, 134, 17-17	2.2	
114	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	2.2	
113	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	2.2	
112	Transcriptomic Heterogeneity and Clonal Evolution Associated with Therapeutic Resistance in Mantle Cell Lymphoma Revealed By Single Cell RNA-Seq. *Blood*, **2019**, 134, 5217-5217	2.2	
111	Molecular Profiling Reveals Unique Immune and Metabolic Features of Melanoma Brain Metastases. *Cancer Discovery*, **2019**, 9, 628-645	24.4	124

110	Features of non-activation dendritic state and immune deficiency in blastic plasmacytoid dendritic cell neoplasm (BPDCN). *Blood Cancer Journal*, **2019**, 9, 99	7	15
109	Applying Artificial Intelligence to Address the Knowledge Gaps in Cancer Care. *Oncologist*, **2019**, 24, 772-782	5.7	19
108	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	4.9	19
107	A Preexisting Rare Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in Melanoma and Is Dependent on S6K1 Signaling. *Cancer Discovery*, **2018**, 8, 556-567	24.4	42
106	Improving the detection of patients with inherited predispositions to hematologic malignancies using next-generation sequencing-based leukemia prognostication panels. *Cancer*, **2018**, 124, 2704-2713	6.4	29
105	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,	2.8	26
104	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. *Cell*, **2018**, 173, 611-623.e17	56.2	228
103	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. *Modern Pathology*, **2018**, 31, 947-955	9.8	35
102	Genomic Rearrangement Signatures and Clinical Outcomes in High-Grade Serous Ovarian Cancer. *Journal of the National Cancer Institute*, **2018**, 110,	9.7	22
101	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. *Blood*, **2018**, 131, 1820-1832	2.2	25
100	The somatic mutation landscape of premalignant colorectal adenoma. *Gut*, **2018**, 67, 1299-1305	19.2	33
99	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. *Science*, **2018**, 359, 97-103	33.3	1895
98	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. *Nature Communications*, **2018**, 9, 2496	17.4	16
97	Circulating tumor DNA analysis depicts subclonal architecture and genomic evolution of small cell lung cancer. *Nature Communications*, **2018**, 9, 3114	17.4	73
96	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. *Oncotarget*, **2018**, 9, 29495-29507	3.3	13
95	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. *Nature Communications*, **2018**, 9, 2670	17.4	47
94	Associations of inflammation with symptom burden in patients with acute myeloid leukemia. *Psychoneuroendocrinology*, **2018**, 89, 203-208	5	7
93	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. *PLoS Computational Biology*, **2018**, 14, e1006266	5	7

92	High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics. *Genome Research*, **2018**, 28, 1345-1352	9.7	102
91	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. *Nature Medicine*, **2018**, 24, 1047-1057	50.5	99
90	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	2.2	3
89	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. *Blood*, **2018**, 132, 1801-1801	2.2	2
88	Association of the T-cell receptor landscape with survival in non-small cell lung cancer.. *Journal of Clinical Oncology*, **2018**, 36, 140-140	2.2	2
87	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	3.3	42
86	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. *Oncotarget*, **2018**, 9, 19891-19899	3.3	19
85	Patient-reported fatigue prior to treatment is prognostic of survival in patients with acute myeloid leukemia. *Oncotarget*, **2018**, 9, 31244-31252	3.3	9
84	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
83	High Prevalence of PPM1D Mutations in Therapy-Related AML/MDS Is Due to Context-Specific Clonal Hematopoiesis. *Blood*, **2018**, 132, 746-746	2.2	
82	Clinical Heterogeneity of AML Is Associated with Mutational Heterogeneity. *Blood*, **2018**, 132, 5240-5240	2.2	0
81	Combination of Lenalidomide and Rituximab in Patients with Treatment-Naïve and Relapsed Chronic Lymphocytic Leukemia: Treatment Results and Predictive Factors of Response. *Blood*, **2018**, 132, 295-295	2.2	
80	Single-Cell Atlas of Driver Mutations in Acute Myeloid Leukemia (AML). *Blood*, **2018**, 132, 88-88	2.2	
79	Distinct Gene Expression Patterns of Minimal Residual Disease (MRD) Cells in High-Risk AML Patients Identified By RNA-Sequencing. *Blood*, **2018**, 132, 2757-2757	2.2	
78	Clearance of Somatic Mutations at Remission and the Risk of Relapse in Acute Myeloid Leukemia. *Journal of Clinical Oncology*, **2018**, 36, 1788-1797	2.2	111
77	Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. *Nature Communications*, **2018**, 9, 5361	17.4	145
76	High Prevalence of Hereditary Cancer Syndromes and Outcomes in Adults with Early-Onset Pancreatic Cancer. *Cancer Prevention Research*, **2018**, 11, 679-686	3.2	11
75	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. *Cell Stem Cell*, **2018**, 23, 700-713.e6	18	147

74	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. *Cancer Cell*, **2018**, 33, 1128-1141.e7	24.3	100
73	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,	17.5	409
72	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. *Lancet Oncology, The*, **2017**, 18, 100-111	21.7	189
71	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	17
70	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. *Nature Communications*, **2017**, 8, 15936	17.4	125
69	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. *Npj Genomic Medicine*, **2017**, 2,	6.2	82
68	Oncogenic drives invasion and maintains metastases in colorectal cancer. *Genes and Development*, **2017**, 31, 370-382	12.6	80
67	Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. *Cancer Research*, **2017**, 77, 6119-6130	10.1	56
66	The driver landscape of sporadic chordoma. *Nature Communications*, **2017**, 8, 890	17.4	64
65	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. *Cancer Discovery*, **2017**, 7, 1088-1097	24.4	105
64	Overexpressed PRAME is a potential immunotherapy target in sarcoma subtypes. *Clinical Sarcoma Research*, **2017**, 7, 11	2.5	32
63	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. *Blood Advances*, **2017**, 1, 1031-1036	7.8	21
62	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. *Oncotarget*, **2017**, 8, 21994-22002	5.3	83
61	Are sarcomas hereditary?. *Lancet Oncology, The*, **2016**, 17, 1179-81	21.7	1
60	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	18.3	120
59	Loss of IFN-Pathway Genes in Tumor Cells as a Mechanism of Resistance to Anti-CTLA-4 Therapy. *Cell*, **2016**, 167, 397-404.e9	56.2	688
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	11.4	87
57	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. *Nature Communications*, **2016**, 7, 12910	17.4	74

56	Genomic heterogeneity of multiple synchronous lung cancer. *Nature Communications*, **2016**, 7, 13200	17.4	85
55	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	2	55
54	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, 827-37	24.4	561
53	Novel MYBL1 Gene Rearrangements with Recurrent MYBL1-NFIB Fusions in Salivary Adenoid Cystic Carcinomas Lacking t(6;9) Translocations. *Clinical Cancer Research*, **2016**, 22, 725-33	12.9	116
52	STAG2 Mutations Are an Independent Prognostic Factor in Patients with Myelodysplastic Syndromes. *Blood*, **2016**, 128, 3182-3182	2.2	1
51	Clinical Relevance of Driver Mutations and Number of Driver Mutations in Patients with Myelodysplastic Syndromes and Chronic Myelomonocytic Leukemia. *Blood*, **2016**, 128, 54-54	2.2	0
50	Clinical implications of TP53 mutations in myelodysplastic syndromes treated with hypomethylating agents. *Oncotarget*, **2016**, 7, 14172-87	3.3	59
49	Activity of Hypomethylating Agents in the Treatment of Therapy-Related Myelodysplastic Syndrome. *Blood*, **2016**, 128, 3177-3177	2.2	
48	Impact of Driver Mutations in Patients with Lower-Risk Myelodysplastic Syndromes Classified By the MD Anderson Lower-Risk Prognostic Scoring System. *Blood*, **2016**, 128, 4317-4317	2.2	
47	Impact of the Next-Generation Sequencing Panel on Treatment Choice in Patients with Myelodysplastic Syndrome. *Blood*, **2016**, 128, 4340-4340	2.2	
46	Increased Number of Driver Mutations Is a Predictor of Response to Hypomethylating Agents in Patients with Myelodysplastic Syndromes. *Blood*, **2016**, 128, 51-51	2.2	
45	Clonal Hematopoiesis Increases Risk of Therapy-Related Myeloid Neoplasms. *Blood*, **2016**, 128, 38-38	2.2	
44	Archetypes of AML Defined Using Whole Exome Sequencing and Clinical Characteristics in a Diverse Group of Patients. *Blood*, **2016**, 128, 597-597	2.2	
43	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	30.4	1193
42	Downregulation of Protection of Telomeres 1 expression in myelodysplastic syndromes with 7q deletion. *British Journal of Haematology*, **2016**, 173, 161-5	4.5	4
41	Co-occurring genomic alterations define major subsets of KRAS-mutant lung adenocarcinoma with distinct biology, immune profiles, and therapeutic vulnerabilities. *Cancer Discovery*, **2015**, 5, 860-77	24.4	476
40	Cancer Genomics in Clinical Context. *Trends in Cancer*, **2015**, 1, 36-43	12.5	5
39	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	10.1	146

38	Identification of a novel fusion gene, IRF2BP2-RARA, in acute promyelocytic leukemia. *Journal of the National Comprehensive Cancer Network: JNCCN*, **2015**, 13, 19-22	7.3	38
37	Clonal evolution of acute myeloid leukemia relapsed after 19 years of remission. *American Journal of Hematology*, **2015**, 90, E134-5	7.1	4
36	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. *Cancer Letters*, **2015**, 357, 179-185	9.9	68
35	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	2.2	5
34	TP53 Mutated MDS Patients Respond Equally to Hypomethylating Agents but Have Significantly Shorter Response Duration Compared to Patients with Wild Type TP53. *Blood*, **2015**, 126, 1681-1681	2.2	2
33	Clinico-Pathological Characteristics, Treatments and Outcomes of Patients with Dendritic Cell Sarcoma (DS). *Blood*, **2015**, 126, 2700-2700	2.2	2
32	IKZF3 p.L162R Is a Recurrent Hotspot Mutation in Chronic Lymphocytic Leukemia (CLL). *Blood*, **2015** , 126, 4136-4136	2.2	
31	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications*, **2014**, 5, 2997	17.4	564
30	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. *Science*, **2014**, 346, 256-9	33.3	659
29	Differential and limited expression of mutant alleles in multiple myeloma. *Blood*, **2014**, 124, 3110-7	2.2	42
28	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. *Nature Genetics*, **2014**, 46, 225-233	36.3	866
27	Author response: Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer **2014**,		3
26	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
25	Emerging patterns of somatic mutations in cancer. *Nature Reviews Genetics*, **2013**, 14, 703-18	30.1	366
24	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
23	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *New England Journal of Medicine*, **2012**, 366, 883-892	59.2	5559
22	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
21	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979

20	Intratumor heterogeneity: seeing the wood for the trees. *Science Translational Medicine*, **2012**, 4, 127ps10	17.5	375
19	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. *Cell*, **2011**, 144, 27-40	56.2	1628
18	Chromosomal instability confers intrinsic multidrug resistance. *Cancer Research*, **2011**, 71, 1858-70	10.1	309
17	COSMIC: mining complete cancer genomes in the Catalogue of Somatic Mutations in Cancer. *Nucleic Acids Research*, **2011**, 39, D945-50	20.1	1774
16	A small-cell lung cancer genome with complex signatures of tobacco exposure. *Nature*, **2010**, 463, 184-90	30.4	852
15	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. *Nature*, **2010**, 467, 1109-13	50.4	1013
14	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. *Genome Medicine*, **2010**, 2, 53	14.4	36
13	The cancer genome. *Nature*, **2009**, 458, 719-24	50.4	2272
12	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, 13081-6	11.5	283
11	A survey of homozygous deletions in human cancer genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 4542-7	11.5	70
10	A census of human cancer genes. *Nature Reviews Cancer*, **2004**, 4, 177-83	31.3	2424
9	Mutations of the BRAF gene in human cancer. *Nature*, **2002**, 417, 949-54	50.4	7962
8	Clonal Evolution of Acute Myeloid Leukemia Revealed by High-Throughput Single-Cell Genomics		7
7	A computational network approach to identify predictive biomarkers and therapeutic combinations for anti-PD-1 immunotherapy in cancer		1
6	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features		2
5	Single-cell Characterization of Acute Myeloid Leukemia and its Microenvironment Following PD-1 Blockade Based Therapy		1
4	Tumor cell total mRNA expression shapes the molecular and clinical phenotype of cancer		2
3	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia		2

2	iTALK: an R Package to Characterize and Illustrate Intercellular Communication	70
1	Accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling for sequencing data	1