

# Ahmet Zehir

## 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.

184  
papers

15,642  
citations

51  
h-index

124  
g-index

230  
ext. papers

22,516  
ext. citations

9.2  
avg, IF

6.62  
L-index

#	Paper	IF	Citations
184	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , <b>2017</b> , 23, 703-713	50.5	1638
183	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. <i>Nature Genetics</i> , <b>2019</b> , 51, 202-206	36.3	1435
182	Memorial Sloan Kettering-Integrated Mutation Profiling of Actionable Cancer Targets (MSK-IMPACT): A Hybridization Capture-Based Next-Generation Sequencing Clinical Assay for Solid Tumor Molecular Oncology. <i>Journal of Molecular Diagnostics</i> , <b>2015</b> , 17, 251-64	5.1	1066
181	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , <b>2016</b> , 375, 443-53	59.2	791
180	Molecular Determinants of Response to Anti-Programmed Cell Death (PD)-1 and Anti-Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Non-Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. <i>Journal of Clinical Oncology</i> , <b>2018</b> , 36, 633-641	2.2	730
179	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	699
178	AACR Project GENIE: Powering Precision Medicine through an International Consortium. <i>Cancer Discovery</i> , <b>2017</b> , 7, 818-831	24.4	629
177	Patient HLA class I genotype influences cancer response to checkpoint blockade immunotherapy. <i>Science</i> , <b>2018</b> , 359, 582-587	33.3	500
176	Variant Review with the Integrative Genomics Viewer. <i>Cancer Research</i> , <b>2017</b> , 77, e31-e34	10.1	386
175	Therapy-Related Clonal Hematopoiesis in Patients with Non-hematologic Cancers Is Common and Associated with Adverse Clinical Outcomes. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 374-382.e4	18	339
174	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 34, 427-438.e4	24.6	339
173	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 125-136.e3	24.3	338
172	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , <b>2017</b> , 7, 596-609	24.4	317
171	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. <i>JAMA Oncology</i> , <b>2019</b> , 5, 471-478	13.4	257
170	Mutation Detection in Patients With Advanced Cancer by Universal Sequencing of Cancer-Related Genes in Tumor and Normal DNA vs Guideline-Based Germline Testing. <i>JAMA - Journal of the American Medical Association</i> , <b>2017</b> , 318, 825-835	27.4	235
169	Pan-Trk Immunohistochemistry Is an Efficient and Reliable Screen for the Detection of NTRK Fusions. <i>American Journal of Surgical Pathology</i> , <b>2017</b> , 41, 1547-1551	6.7	231
168	Genetic diversity of tumors with mismatch repair deficiency influences anti-PD-1 immunotherapy response. <i>Science</i> , <b>2019</b> , 364, 485-491	33.3	228

167	Genome doubling shapes the evolution and prognosis of advanced cancers. <i>Nature Genetics</i> , <b>2018</b> , 50, 1189-1195	36.3	208
166	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 286-295	2.2	203
165	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. <i>JAMA Oncology</i> , <b>2016</b> , 2, 104-11	13.4	198
164	NTRK fusion detection across multiple assays and 33,997 cases: diagnostic implications and pitfalls. <i>Modern Pathology</i> , <b>2020</b> , 33, 38-46	9.8	187
163	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 4154-4161	12.9	182
162	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 49-58	24.4	180
161	High Yield of RNA Sequencing for Targetable Kinase Fusions in Lung Adenocarcinomas with No Mitogenic Driver Alteration Detected by DNA Sequencing and Low Tumor Mutation Burden. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 4712-4722	12.9	170
160	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , <b>2019</b> , 571, 576-579	50.4	170
159	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. <i>European Urology</i> , <b>2017</b> , 72, 952-959	10.2	168
158	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 174-183	24.4	162
157	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	151
156	The Molecular Landscape of Recurrent and Metastatic Head and Neck Cancers: Insights From a Precision Oncology Sequencing Platform. <i>JAMA Oncology</i> , <b>2017</b> , 3, 244-255	13.4	141
155	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	128
154	Establishing guidelines to harmonize tumor mutational burden (TMB): in silico assessment of variation in TMB quantification across diagnostic platforms: phase I of the Friends of Cancer Research TMB Harmonization Project <b>2020</b> , 8,		125
153	Concurrent Alterations in EGFR-Mutant Lung Cancers Associated with Resistance to EGFR Kinase Inhibitors and Characterization of MTOR as a Mediator of Resistance. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 3108-3118	12.9	123
152	Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 6094-6100	12.9	107
151	Single-cell mutation analysis of clonal evolution in myeloid malignancies. <i>Nature</i> , <b>2020</b> , 587, 477-482	50.4	107
150	Prospective Evaluation of Germline Alterations in Patients With Exocrine Pancreatic Neoplasms. <i>Journal of the National Cancer Institute</i> , <b>2018</b> , 110, 1067-1074	9.7	103

149	Dicer is required for survival of differentiating neural crest cells. <i>Developmental Biology</i> , <b>2010</b> , 340, 459-671	103
148	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. <i>Nature Genetics</i> , <b>2020</b> , 52, 1219-1226	103
147	Prevalence of Clonal Hematopoiesis Mutations in Tumor-Only Clinical Genomic Profiling of Solid Tumors. <i>JAMA Oncology</i> , <b>2018</b> , 4, 1589-1593	13.4 91
146	Detection of Tumor NTRK Gene Fusions to Identify Patients Who May Benefit from Tyrosine Kinase (TRK) Inhibitor Therapy. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 553-571	5.1 86
145	Isoform Switching as a Mechanism of Acquired Resistance to Mutant Isocitrate Dehydrogenase Inhibition. <i>Cancer Discovery</i> , <b>2018</b> , 8, 1540-1547	24.4 86
144	Multicolor Flow Cytometry and Multigene Next-Generation Sequencing Are Complementary and Highly Predictive for Relapse in Acute Myeloid Leukemia after Allogeneic Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , <b>2017</b> , 23, 1064-1071	4.7 83
143	The Promises and Challenges of Tumor Mutation Burden as an Immunotherapy Biomarker: A Perspective from the International Association for the Study of Lung Cancer Pathology Committee. <i>Journal of Thoracic Oncology</i> , <b>2020</b> , 15, 1409-1424	8.9 80
142	Colorectal Carcinomas Containing Hypermethylated MLH1 Promoter and Wild-Type BRAF/KRAS Are Enriched for Targetable Kinase Fusions. <i>Cancer Research</i> , <b>2019</b> , 79, 1047-1053	10.1 73
141	BMP signaling regulates sympathetic nervous system development through Smad4-dependent and -independent pathways. <i>Development (Cambridge)</i> , <b>2009</b> , 136, 3575-84	6.6 70
140	Next-Generation Assessment of Human Epidermal Growth Factor Receptor 2 (ERBB2) Amplification Status: Clinical Validation in the Context of a Hybrid Capture-Based, Comprehensive Solid Tumor Genomic Profiling Assay. <i>Journal of Molecular Diagnostics</i> , <b>2017</b> , 19, 244-254	5.1 66
139	Comprehensive detection of germline variants by MSK-IMPACT, a clinical diagnostic platform for solid tumor molecular oncology and concurrent cancer predisposition testing. <i>BMC Medical Genomics</i> , <b>2017</b> , 10, 33	3.7 64
138	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 4276-4289	15.9 64
137	The value of cell-free DNA for molecular pathology. <i>Journal of Pathology</i> , <b>2018</b> , 244, 616-627	9.4 62
136	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 5939-5947	12.9 60
135	Genomic Differences Between "Primary" and "Secondary" Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. <i>European Urology</i> , <b>2019</b> , 75, 231-239	10.2 53
134	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. <i>Annals of Oncology</i> , <b>2017</b> , 28, 3015-3021	10.3 52
133	Identification of Clonal Hematopoiesis Mutations in Solid Tumor Patients Undergoing Unpaired Next-Generation Sequencing Assays. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 5918-5924	12.9 50
132	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. <i>Cancer Cell</i> , <b>2018</b> , 34, 852-862.e44.3	44.3 50

131	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 5537-5547	12.9	48
130	Pretreatment neutrophil-to-lymphocyte ratio and mutational burden as biomarkers of tumor response to immune checkpoint inhibitors. <i>Nature Communications</i> , <b>2021</b> , 12, 729	17.4	44
129	Response Rates to Anti-PD-1 Immunotherapy in Microsatellite-Stable Solid Tumors With 10 or More Mutations per Megabase. <i>JAMA Oncology</i> , <b>2021</b> , 7, 739-743	13.4	40
128	Establishment of Immunoglobulin Heavy (IGH) Chain Clonality Testing by Next-Generation Sequencing for Routine Characterization of B-Cell and Plasma Cell Neoplasms. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 330-342	5.1	40
127	Clinical Genomic Sequencing of Pediatric and Adult Osteosarcoma Reveals Distinct Molecular Subsets with Potentially Targetable Alterations. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 6346-6356	12.9	39
126	Pancreatic intraductal tubulopapillary neoplasm is genetically distinct from intraductal papillary mucinous neoplasm and ductal adenocarcinoma. <i>Modern Pathology</i> , <b>2017</b> , 30, 1760-1772	9.8	39
125	The association between tumor mutational burden and prognosis is dependent on treatment context. <i>Nature Genetics</i> , <b>2021</b> , 53, 11-15	36.3	38
124	Pre-clinical efficacy of PU-H71, a novel HSP90 inhibitor, alone and in combination with bortezomib in Ewing sarcoma. <i>Molecular Oncology</i> , <b>2014</b> , 8, 323-36	7.9	37
123	Genomic aberrations frequently alter chromatin regulatory genes in chordoma. <i>Genes Chromosomes and Cancer</i> , <b>2016</b> , 55, 591-600	5	37
122	Identification of Targetable Kinase Alterations in Patients with Colorectal Carcinoma That are Preferentially Associated with Wild-Type RAS/RAF. <i>Molecular Cancer Research</i> , <b>2016</b> , 14, 296-301	6.6	34
121	Managing Clonal Hematopoiesis in Patients With Solid Tumors. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 7-11	2.2	33
120	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. <i>JAMA Oncology</i> , <b>2020</b> , 6, 84-91	13.4	33
119	Majority of -Mutant and -Deficient Colorectal Carcinomas Achieve Clinical Benefit From Immune Checkpoint Inhibitor Therapy and Are Microsatellite Instability-High. <i>JCO Precision Oncology</i> , <b>2019</b> , 3,	3.6	32
118	Genomic Profiling Identifies Association of Mutation with Longer Relapse-Free and Metastasis-Free Survival in High-Grade Chondrosarcoma. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 419-427	12.9	32
117	Consistent copy number changes and recurrent PRKAR1A mutations distinguish Melanotic Schwannomas from Melanomas: SNP-array and next generation sequencing analysis. <i>Genes Chromosomes and Cancer</i> , <b>2015</b> , 54, 463-471	5	30
116	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Non-Small-Cell Lung Cancer. <i>JCO Precision Oncology</i> , <b>2019</b> , 3,	3.6	27
115	Plasma DNA-based molecular diagnosis, prognostication, and monitoring of patients with fusion-positive sarcomas. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	24
114	Novel oncogene and tumor suppressor mutations in KIT and PDGFRA wild type gastrointestinal stromal tumors revealed by next generation sequencing. <i>Genes Chromosomes and Cancer</i> , <b>2015</b> , 54, 177-84	5	23

113	Retained mismatch repair protein expression occurs in approximately 6% of microsatellite instability-high cancers and is associated with missense mutations in mismatch repair genes. <i>Modern Pathology</i> , <b>2020</b> , 33, 871-879	9.8	23
112	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. <i>Nature Cancer</i> , <b>2021</b> , 2, 357-365	15.4	23
111	Detection of mutations in myeloid malignancies through paired-sample analysis of microdroplet-PCR deep sequencing data. <i>Journal of Molecular Diagnostics</i> , <b>2014</b> , 16, 504-518	5.1	22
110	The repertoire of genetic alterations in salivary duct carcinoma including a novel HNRNPH3-ALK rearrangement. <i>Human Pathology</i> , <b>2019</b> , 88, 66-77	3.7	21
109	Successful Targeted Therapy of Refractory Pediatric Fusion-Positive Secretory Breast Carcinoma. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	21
108	Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. <i>Nature Communications</i> , <b>2021</b> , 12, 338	17.4	21
107	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. <i>Blood</i> , <b>2021</b> , 137, 2103-2113	2.2	19
106	Radioactive Iodine-Related Clonal Hematopoiesis in Thyroid Cancer Is Common and Associated With Decreased Survival. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2018</b> , 103, 4216-4223	5.6	18
105	The Clinical Management of Clonal Hematopoiesis: Creation of a Clonal Hematopoiesis Clinic. <i>Hematology/Oncology Clinics of North America</i> , <b>2020</b> , 34, 357-367	3.1	17
104	MET inhibitor resistance in patients with MET exon 14-altered lung cancers.. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 9006-9006	2.2	17
103	The molecular landscape of extraskeletal osteosarcoma: A clinicopathological and molecular biomarker study. <i>Journal of Pathology: Clinical Research</i> , <b>2016</b> , 2, 9-20	5.3	17
102	Next-Generation Sequencing-Based Assessment of JAK2, PD-L1, and PD-L2 Copy Number Alterations at 9p24.1 in Breast Cancer: Potential Implications for Clinical Management. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 307-317	5.1	17
101	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. <i>Journal of Clinical Oncology</i> , <b>2021</b> , 39, 2698-2709	2.2	16
100	Recurrent, truncating SOX9 mutations are associated with SOX9 overexpression, KRAS mutation, and TP53 wild type status in colorectal carcinoma. <i>Oncotarget</i> , <b>2016</b> , 7, 50875-50882	3.3	15
99	Binimetinib plus Gemcitabine and Cisplatin Phase I/II Trial in Patients with Advanced Biliary Cancers. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 937-945	12.9	15
98	Universal screening for microsatellite instability in colorectal cancer in the clinical genomics era: new recommendations, methods, and considerations. <i>Familial Cancer</i> , <b>2017</b> , 16, 525-529	3	14
97	Fragment Size Analysis May Distinguish Clonal Hematopoiesis from Tumor-Derived Mutations in Cell-Free DNA. <i>Clinical Chemistry</i> , <b>2020</b> , 66, 616-618	5.5	14
96	Enrichment of kinase fusions in ESR1 wild-type, metastatic breast cancer revealed by a systematic analysis of 4854 patients. <i>Annals of Oncology</i> , <b>2020</b> , 31, 991-1000	10.3	14

95	Harnessing Clinical Sequencing Data for Survival Stratification of Patients with Metastatic Lung Adenocarcinomas. <i>JCO Precision Oncology</i> , <b>2019</b> , 3,	3.6	13
94	Mutations, Homologous DNA Repair Deficiency, Tumor Mutational Burden, and Response to Immune Checkpoint Inhibition in Recurrent Ovarian Cancer. <i>JCO Precision Oncology</i> , <b>2020</b> , 4,	3.6	12
93	Clonal hematopoiesis is associated with risk of severe Covid-19. <i>Nature Communications</i> , <b>2021</b> , 12, 5975	17.4	12
92	Mesonephric and mesonephric-like carcinomas of the female genital tract: molecular characterization including cases with mixed histology and matched metastases. <i>Modern Pathology</i> , <b>2021</b> , 34, 1570-1587	9.8	12
91	Chromosome 20q Amplification Defines a Subtype of Microsatellite Stable, Left-Sided Colon Cancers with Wild-type RAS/RAF and Better Overall Survival. <i>Molecular Cancer Research</i> , <b>2017</b> , 15, 708-713	6.6	11
90	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients.. <i>Cell</i> , <b>2022</b> , 185, 563-575.e11	56.2	11
89	TMB standardization by alignment to reference standards: Phase II of the Friends of Cancer Research TMB Harmonization Project.. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 2624-2624	2.2	11
88	OncoTree: A Cancer Classification System for Precision Oncology. <i>JCO Clinical Cancer Informatics</i> , <b>2021</b> , 5, 221-230	5.2	11
87	Fumarate hydratase FH c.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. <i>Human Mutation</i> , <b>2020</b> , 41, 103-109	4.7	11
86	Exon 14-altered Lung Cancers and MET Inhibitor Resistance. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 799-806	12.9	11
85	Improved prediction of immune checkpoint blockade efficacy across multiple cancer types. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	10
84	Clonal hematopoiesis is associated with risk of severe Covid-19 <b>2020</b> ,		10
83	Enhanced specificity of clinical high-sensitivity tumor mutation profiling in cell-free DNA via paired normal sequencing using MSK-ACCESS. <i>Nature Communications</i> , <b>2021</b> , 12, 3770	17.4	10
82	A FISH assay efficiently screens for BRAF gene rearrangements in pancreatic acinar-type neoplasms. <i>Modern Pathology</i> , <b>2018</b> , 31, 132-140	9.8	9
81	Characterization and Clinical Outcomes of DNA Mismatch Repair-deficient Small Bowel Adenocarcinoma. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 1429-1437	12.9	9
80	Ultrarapid Mutation Screening Followed by Comprehensive Next-Generation Sequencing: A Feasible, Informative Approach for Lung Carcinoma Cytology Specimens With a High Success Rate. <i>JTO Clinical and Research Reports</i> , <b>2020</b> , 1,	1.4	8
79	Reliable Clinical MLH1 Promoter Hypermethylation Assessment Using a High-Throughput Genome-Wide Methylation Array Platform. <i>Journal of Molecular Diagnostics</i> , <b>2020</b> , 22, 368-375	5.1	8
78	Structure-function analysis of oncogenic EGFR Kinase Domain Duplication reveals insights into activation and a potential approach for therapeutic targeting. <i>Nature Communications</i> , <b>2021</b> , 12, 1382	17.4	8

77	Tumor fraction-guided cell-free DNA profiling in metastatic solid tumor patients. <i>Genome Medicine</i> , <b>2021</b> , 13, 96	14.4	8
76	Ampullary cancer: Evaluation of somatic and germline genetic alterations and association with clinical outcomes. <i>Cancer</i> , <b>2019</b> , 125, 1441-1448	6.4	8
75	E-cadherin immunohistochemical expression in invasive lobular carcinoma of the breast: correlation with morphology and CDH1 somatic alterations. <i>Human Pathology</i> , <b>2020</b> , 102, 44-53	3.7	7
74	Distance in cancer gene expression from stem cells predicts patient survival. <i>PLoS ONE</i> , <b>2017</b> , 12, e0173589	3.7	7
73	Somatic HNF1A mutations in the malignant transformation of hepatocellular adenomas: a retrospective analysis of data from MSK-IMPACT and TCGA. <i>Human Pathology</i> , <b>2019</b> , 83, 1-6	3.7	7
72	Oncologic therapy shapes the fitness landscape of clonal hematopoiesis		7
71	Machine learning-based prediction of microsatellite instability and high tumor mutation burden from contrast-enhanced computed tomography in endometrial cancers. <i>Scientific Reports</i> , <b>2020</b> , 10, 17769	4.9	7
70	Aligning tumor mutational burden (TMB) quantification across diagnostic platforms: phase II of the Friends of Cancer Research TMB Harmonization Project. <i>Annals of Oncology</i> , <b>2021</b> , 32, 1626-1636	10.3	7
69	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , <b>2021</b> , 53, 1577-1583	5.3	6
68	Single cell mutational profiling delineates clonal trajectories in myeloid malignancies		6
67	Genomic Alterations as Potential Therapeutic Targets in Extramammary Paget Disease of the Vulva. <i>JCO Precision Oncology</i> , <b>2020</b> , 4,	3.6	6
66	Immunohistochemical analysis of estrogen receptor in breast cancer with ESR1 mutations detected by hybrid capture-based next-generation sequencing. <i>Modern Pathology</i> , <b>2019</b> , 32, 81-87	9.8	6
65	Prevalence and Preliminary Validation of Screening Criteria to Identify Carriers of Germline BAP1 Mutations. <i>Journal of Thoracic Oncology</i> , <b>2019</b> , 14, 1989-1994	8.9	5
64	Correlation of benefit from immune checkpoint inhibitors with next gen sequencing (NGS) profiles in esophagogastric cancer (EGC) patients.. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 4025-4025	2.2	5
63	The clinical implications of clonal hematopoiesis in hematopoietic cell transplantation. <i>Blood Reviews</i> , <b>2021</b> , 46, 100744	11.1	5
62	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. <i>JCO Precision Oncology</i> , <b>2020</b> , 4,	3.6	4
61	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. <i>Clinics in Laboratory Medicine</i> , <b>2016</b> , 36, 153-81	2.1	4
60	Molecular determinants of response and resistance to anti-PD-(L)1 blockade in patients with NSCLC profiled with targeted next-generation sequencing (NGS).. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 9015-9015	2.2	4



59	Comprehensive Genomic Analysis of Metastatic Non-Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. <i>JCO Precision Oncology</i> , <b>2019</b> , 3,	3.6	4
58	A Pan-Cancer Study of Somatic TERT Promoter Mutations and Amplification in 30,773 Tumors Profiled by Clinical Genomic Sequencing. <i>Journal of Molecular Diagnostics</i> , <b>2021</b> , 23, 253-263	5.1	4
57	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers.. <i>Nature Communications</i> , <b>2022</b> , 13, 2485	17.4	4
56	Tumor relevant germline findings in targeted tumor sequencing using matched normal DNA of 1,570 unselected cases.. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 1509-1509	2.2	3
55	The clinical utility of ERBB2 amplification detection in breast carcinoma using a 341 gene hybrid capture-based next generation sequencing (NGS) assay: Comparison with standard immunohistochemistry (IHC) and Fluorescence In Situ Hybridization (FISH) assays.. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 604-604	2.2	3
54	The clinical impact of performing routine next generation sequencing (NGS) in gastrointestinal stromal tumors (GIST).. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 11010-11010	2.2	3
53	Comprehensive detection of targetable fusions in lung adenocarcinomas by complementary targeted DNaseq and RNAseq assays.. <i>Journal of Clinical Oncology</i> , <b>2018</b> , 36, 12076-12076	2.2	3
52	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. <i>Molecular Cancer Research</i> , <b>2021</b> , 19, 1146-1155	6.6	3
51	Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. <i>JCO Precision Oncology</i> , <b>2019</b> , 3,	3.6	3
50	Next-generation assessment of human epidermal growth factor receptor 2 gene (ERBB2) amplification status in invasive breast carcinoma: a focus on Group 4 by use of the 2018 American Society of Clinical Oncology/College of American Pathologists HER2 testing guideline. <i>Histopathology</i> , <b>2021</b> , 78, 498-507	7.3	3
49	Spectrum of Mutations and Gene Rearrangements in Ovarian Serous Carcinoma. <i>JCO Precision Oncology</i> , <b>2021</b> , 5,	3.6	3
48	Evaluation of Initial Telomere Length and Changes after Transplantation in Adult Double-Unit Cord Blood Transplant Recipients. <i>Biology of Blood and Marrow Transplantation</i> , <b>2015</b> , 21, 1334-6	4.7	2
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