Ahmet Zehir

List of Publications by Year in Descending Order

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	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients.. *Cell*, **2022**, 185, 563-575.e11	56.2	11
183	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer.. *JCO Precision Oncology*, **2022**, 6, e2100365	3.6	
182	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers.. *Nature Communications*, **2022**, 13, 2485	17.4	4
181	The context-specific role of germline pathogenicity in tumorigenesis. *Nature Genetics*, **2021**, 53, 1577-1586	36.3	6
180	A quick guide for clinical oncology.. *Nature Cancer*, **2021**, 2, 998-999	15.4	1
179	Clonal hematopoiesis is associated with risk of severe Covid-19. *Nature Communications*, **2021**, 12, 5975	17.4	12
178	Improved prediction of immune checkpoint blockade efficacy across multiple cancer types. *Nature Biotechnology*, **2021**,	44.5	10
177	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. *Molecular Cancer Research*, **2021**, 19, 1146-1155	6.6	3
176	OncoTree: A Cancer Classification System for Precision Oncology. *JCO Clinical Cancer Informatics*, **2021**, 5, 221-230	5.2	11
175	Structure-function analysis of oncogenic EGFR Kinase Domain Duplication reveals insights into activation and a potential approach for therapeutic targeting. *Nature Communications*, **2021**, 12, 1382	17.4	8
174	Mesonephric and mesonephric-like carcinomas of the female genital tract: molecular characterization including cases with mixed histology and matched metastases. *Modern Pathology*, **2021**, 34, 1570-1587	9.8	12
173	Genetic and molecular subtype heterogeneity in newly diagnosed early- and advanced-stage endometrial cancer. *Gynecologic Oncology*, **2021**, 161, 535-544	4.9	0
172	Tumor fraction-guided cell-free DNA profiling in metastatic solid tumor patients. *Genome Medicine*, **2021**, 13, 96	14.4	8
171	Response Rates to Anti-PD-1 Immunotherapy in Microsatellite-Stable Solid Tumors With 10 or More Mutations per Megabase. *JAMA Oncology*, **2021**, 7, 739-743	13.4	40
170	Clinical Experience of Cerebrospinal Fluid-Based Liquid Biopsy Demonstrates Superiority of Cell-Free DNA over Cell Pellet Genomic DNA for Molecular Profiling. *Journal of Molecular Diagnostics*, **2021**, 23, 742-752	5.1	1
169	Enhanced specificity of clinical high-sensitivity tumor mutation profiling in cell-free DNA via paired normal sequencing using MSK-ACCESS. *Nature Communications*, **2021**, 12, 3770	17.4	10
168	The clinical implications of clonal hematopoiesis in hematopoietic cell transplantation. *Blood Reviews*, **2021**, 46, 100744	11.1	5

167	Characterization and Clinical Outcomes of DNA Mismatch Repair-deficient Small Bowel Adenocarcinoma. *Clinical Cancer Research*, **2021**, 27, 1429-1437	12.9	9
166	A Pan-Cancer Study of Somatic TERT Promoter Mutations and Amplification in 30,773 Tumors Profiled by Clinical Genomic Sequencing. *Journal of Molecular Diagnostics*, **2021**, 23, 253-263	5.1	4
165	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. *Blood*, **2021**, 137, 2103-2113	2.2	19
164	Exon 14-altered Lung Cancers and MET Inhibitor Resistance. *Clinical Cancer Research*, **2021**, 27, 799-806	12.9	11
163	Genotypic correlation between post discharge Clostridiodes difficile infection (CDI) and previous unit-based contacts. *Journal of Hospital Infection*, **2021**, 109, 96-100	6.9	
162	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. *Histopathology*, **2021**, 78, 498-507	7.3	3
161	Evaluation of a Combined Multilocus Sequence Typing and Whole-Genome Sequencing Two-Step Algorithm for Routine Typing of. *Journal of Clinical Microbiology*, **2021**, 59,	9.7	2
160	The association between tumor mutational burden and prognosis is dependent on treatment context. *Nature Genetics*, **2021**, 53, 11-15	36.3	38
159	Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. *Nature Communications*, **2021**, 12, 338	17.4	21
158	Pretreatment neutrophil-to-lymphocyte ratio and mutational burden as biomarkers of tumor response to immune checkpoint inhibitors. *Nature Communications*, **2021**, 12, 729	17.4	44
157	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. *Nature Cancer*, **2021**, 2, 357-365	15.4	23
156	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. *Journal of Clinical Oncology*, **2021**, 39, 2698-2709	2.2	16
155	Spectrum of Mutations and Gene Rearrangements in Ovarian Serous Carcinoma. *JCO Precision Oncology*, **2021**, 5,	3.6	3
154	Multicenter Analysis of Genomically Targeted Single Patient Use Requests for Pediatric Neoplasms. *Journal of Clinical Oncology*, **2021**, 39, 3822-3828	2.2	0
153	Somatic intronic TP53 c.375+5G mutations are a recurrent but under-recognized mode of TP53 inactivation. *Journal of Pathology: Clinical Research*, **2021**,	5.3	1
152	Aligning tumor mutational burden (TMB) quantification across diagnostic platforms: phase II of the Friends of Cancer Research TMB Harmonization Project. *Annals of Oncology*, **2021**, 32, 1626-1636	10.3	7
151	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. *JCO Precision Oncology*, **2020**, 4,	3.6	4
150	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. *Journal of Thoracic Oncology*, **2020**, 15, 1409-1424	8.9	80

149	Mutations, Homologous DNA Repair Deficiency, Tumor Mutational Burden, and Response to Immune Checkpoint Inhibition in Recurrent Ovarian Cancer. *JCO Precision Oncology*, **2020**, 4,	3.6	12
148	Fragment Size Analysis May Distinguish Clonal Hematopoiesis from Tumor-Derived Mutations in Cell-Free DNA. *Clinical Chemistry*, **2020**, 66, 616-618	5.5	14
147	E-cadherin immunohistochemical expression in invasive lobular carcinoma of the breast: correlation with morphology and CDH1 somatic alterations. *Human Pathology*, **2020**, 102, 44-53	3.7	7
146	The Clinical Management of Clonal Hematopoiesis: Creation of a Clonal Hematopoiesis Clinic. *Hematology/Oncology Clinics of North America*, **2020**, 34, 357-367	3.1	17
145	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 **2020**, 8,		125
144	Clonal Hematopoiesis and COVID-19 Severity in Cancer Patients. *Blood*, **2020**, 136, 37-38	2.2	1
143	Interplay between Chromosomal Alterations and Gene Mutations Shapes the Evolutionary Trajectory of Clonal Hematopoiesis. *Blood*, **2020**, 136, 29-30	2.2	
142	Germline Contributions to Clonal Hematopoiesis in Solid Cancer Patients. *Blood*, **2020**, 136, 30-31	2.2	
141	Creating a Variant Database for the American Society of Hematalogy By Consensus Variant Classification of Common Genes Associated with Hematologic Malignancies. *Blood*, **2020**, 136, 4-5	2.2	0
140	Microsatellite instability (MSI-H) in metastatic urothelial carcinoma (mUC): A biomarker of divergent responses to systemic therapy.. *Journal of Clinical Oncology*, **2020**, 38, 566-566	2.2	0
139	Ultrarapid Mutation Screening Followed by Comprehensive Next-Generation Sequencing: A Feasible, Informative Approach for Lung Carcinoma Cytology Specimens With a High Success Rate. *JTO Clinical and Research Reports*, **2020**, 1,	1.4	8
138	Clonal hematopoiesis is associated with risk of severe Covid-19 **2020**,		10
137	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. *JAMA Oncology*, **2020**, 6, 84-91	13.4	33
136	Reliable Clinical MLH1 Promoter Hypermethylation Assessment Using a High-Throughput Genome-Wide Methylation Array Platform. *Journal of Molecular Diagnostics*, **2020**, 22, 368-375	5.1	8
135	Retained mismatch repair protein expression occurs in approximately 6% of microsatellite instability-high cancers and is associated with missense mutations in mismatch repair genes. *Modern Pathology*, **2020**, 33, 871-879	9.8	23
134	Machine learning-based prediction of microsatellite instability and high tumor mutation burden from contrast-enhanced computed tomography in endometrial cancers. *Scientific Reports*, **2020**, 10, 17769	4.9	7
133	Genomic Alterations as Potential Therapeutic Targets in Extramammary Paget's Disease of the Vulva. *JCO Precision Oncology*, **2020**, 4,	3.6	6
132	Molecular profiling and analysis of genetic aberrations aimed at identifying potential therapeutic targets in fibrolamellar carcinoma of the liver. *Cancer*, **2020**, 126, 4126-4135	6.4	0

131	Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. *JCO Clinical Cancer Informatics*, **2020**, 4, 691-699	5.2	1
130	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. *Nature Genetics*, **2020**, 52, 1219-1226	38.3	103
129	Single-cell mutation analysis of clonal evolution in myeloid malignancies. *Nature*, **2020**, 587, 477-482	50.4	107
128	Enrichment of kinase fusions in ESR1 wild-type, metastatic breast cancer revealed by a systematic analysis of 4854 patients. *Annals of Oncology*, **2020**, 31, 991-1000	10.3	14
127	Genomic Profiling Identifies Association of Mutation with Longer Relapse-Free and Metastasis-Free Survival in High-Grade Chondrosarcoma. *Clinical Cancer Research*, **2020**, 26, 419-427	12.9	32
126	NTRK fusion detection across multiple assays and 33,997 cases: diagnostic implications and pitfalls. *Modern Pathology*, **2020**, 33, 38-46	9.8	187
125	Fumarate hydratase FH c.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. *Human Mutation*, **2020**, 41, 103-109	4.7	11
124	Clinical Genomic Sequencing of Pediatric and Adult Osteosarcoma Reveals Distinct Molecular Subsets with Potentially Targetable Alterations. *Clinical Cancer Research*, **2019**, 25, 6346-6356	12.9	39
123	Detection of Tumor NTRK Gene Fusions to Identify Patients Who May Benefit from Tyrosine Kinase (TRK) Inhibitor Therapy. *Journal of Molecular Diagnostics*, **2019**, 21, 553-571	5.1	86
122	Genetic diversity of tumors with mismatch repair deficiency influences anti-PD-1 immunotherapy response. *Science*, **2019**, 364, 485-491	33.3	228
121	Majority of -Mutant and -Deficient Colorectal Carcinomas Achieve Clinical Benefit From Immune Checkpoint Inhibitor Therapy and Are Microsatellite Instability-High. *JCO Precision Oncology*, **2019**, 3,	3.6	32
120	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. *Clinical Cancer Research*, **2019**, 25, 4712-4722	12.9	170
119	Managing Clonal Hematopoiesis in Patients With Solid Tumors. *Journal of Clinical Oncology*, **2019**, 37, 7-11	2.2	33
118	The repertoire of genetic alterations in salivary duct carcinoma including a novel HNRNPH3-ALK rearrangement. *Human Pathology*, **2019**, 88, 66-77	3.7	21
117	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. *Journal of Clinical Oncology*, **2019**, 37, 286-295	2.2	203
116	Somatic HNF1A mutations in the malignant transformation of hepatocellular adenomas: a retrospective analysis of data from MSK-IMPACT and TCGA. *Human Pathology*, **2019**, 83, 1-6	3.7	7
115	Tumour lineage shapes BRCA-mediated phenotypes. *Nature*, **2019**, 571, 576-579	50.4	170
114	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. *Clinical Cancer Research*, **2019**, 25, 5537-5547	12.9	48

113	Prevalence and Preliminary Validation of Screening Criteria to Identify Carriers of Germline BAP1 Mutations. *Journal of Thoracic Oncology*, **2019**, 14, 1989-1994	8.9	5
112	Abstract 1387: Tracking minimal residual disease in post-operative cell-free DNA using MSK-ACCESS **2019**,		2
111	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. *Journal of Clinical Investigation* , **2019**, 129, 4276-4289	15.9	64
110	Single Cell DNA Sequencing Identifies Combinatorial Mutation Patterns and Clonal Architecture in Myeloid Malignancies. *Blood*, **2019**, 134, 913-913	2.2	1
109	TMB standardization by alignment to reference standards: Phase II of the Friends of Cancer Research TMB Harmonization Project.. *Journal of Clinical Oncology*, **2019**, 37, 2624-2624	2.2	11
108	MET inhibitor resistance in patients with MET exon 14-altered lung cancers.. *Journal of Clinical Oncology*, **2019**, 37, 9006-9006	2.2	17
107	Tumor mutational burden reference materials for assay standardization.. *Journal of Clinical Oncology*, **2019**, 37, e14746-e14746	2.2	1
106	Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. *Blood*, **2019**, 134, 2148-2148	2.2	0
105	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. *Blood*, **2019**, 134, 633-633	2.2	
104	Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. *JCO Precision Oncology*, **2019**, 3,	3.6	3
103	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Non-Small-Cell Lung Cancer. *JCO Precision Oncology*, **2019**, 3,	3.6	27
102	Comprehensive Genomic Analysis of Metastatic Non-Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. *JCO Precision Oncology*, **2019**, 3,	3.6	4
101	Harnessing Clinical Sequencing Data for Survival Stratification of Patients with Metastatic Lung Adenocarcinomas. *JCO Precision Oncology*, **2019**, 3,	3.6	13
100	Immunohistochemical analysis of estrogen receptor in breast cancer with ESR1 mutations detected by hybrid capture-based next-generation sequencing. *Modern Pathology*, **2019**, 32, 81-87	9.8	6
99	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. *Journal of Molecular Diagnostics*, **2019**, 21, 307-317	5.1	17
98	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. *JAMA Oncology*, **2019**, 5, 471-478	13.4	257
97	Establishment of Immunoglobulin Heavy (IGH) Chain Clonality Testing by Next-Generation Sequencing for Routine Characterization of B-Cell and Plasma Cell Neoplasms. *Journal of Molecular Diagnostics*, **2019**, 21, 330-342	5.1	40
96	Binimetinib plus Gemcitabine and Cisplatin Phase I/II Trial in Patients with Advanced Biliary Cancers. *Clinical Cancer Research*, **2019**, 25, 937-945	12.9	15

95	Ampullary cancer: Evaluation of somatic and germline genetic alterations and association with clinical outcomes. *Cancer*, **2019**, 125, 1441-1448	6.4	8
94	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. *Nature Genetics*, **2019**, 51, 202-206	36.3	1435
93	Colorectal Carcinomas Containing Hypermethylated MLH1 Promoter and Wild-Type BRAF/KRAS Are Enriched for Targetable Kinase Fusions. *Cancer Research*, **2019**, 79, 1047-1053	10.1	73
92	Genomic Differences Between "Primary" and "Secondary" Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. *European Urology*, **2019**, 75, 231-239	10.2	53
91	Prospective Evaluation of Germline Alterations in Patients With Exocrine Pancreatic Neoplasms. *Journal of the National Cancer Institute*, **2018**, 110, 1067-1074	9.7	103
90	The value of cell-free DNA for molecular pathology. *Journal of Pathology*, **2018**, 244, 616-627	9.4	62
89	Accelerating Discovery of Functional Mutant Alleles in Cancer. *Cancer Discovery*, **2018**, 8, 174-183	24.4	162
88	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. *Cancer Cell*, **2018**, 33, 125-136.e3	24.3	338
87	Concurrent Alterations in EGFR-Mutant Lung Cancers Associated with Resistance to EGFR Kinase Inhibitors and Characterization of MTOR as a Mediator of Resistance. *Clinical Cancer Research*, **2018**, 24, 3108-3118	12.9	123
86	A FISH assay efficiently screens for BRAF gene rearrangements in pancreatic acinar-type neoplasms. *Modern Pathology*, **2018**, 31, 132-140	9.8	9
85	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. *Clinical Cancer Research*, **2018**, 24, 5939-5947	12.9	60
84	Genome doubling shapes the evolution and prognosis of advanced cancers. *Nature Genetics*, **2018**, 50, 1189-1195	36.3	208
83	Prevalence of Clonal Hematopoiesis Mutations in Tumor-Only Clinical Genomic Profiling of Solid Tumors. *JAMA Oncology*, **2018**, 4, 1589-1593	13.4	91
82	Identification of Clonal Hematopoiesis Mutations in Solid Tumor Patients Undergoing Unpaired Next-Generation Sequencing Assays. *Clinical Cancer Research*, **2018**, 24, 5918-5924	12.9	50
81	Oncologic Therapy for Solid Tumors Alters the Risk of Clonal Hematopoiesis. *Blood*, **2018**, 132, 747-747	2.2	2
80	Comprehensive detection of targetable fusions in lung adenocarcinomas by complementary targeted DNAseq and RNAseq assays.. *Journal of Clinical Oncology*, **2018**, 36, 12076-12076	2.2	3
79	Frequency of actionable cancer predisposing germline mutations in patients with lung cancers.. *Journal of Clinical Oncology*, **2018**, 36, 1504-1504	2.2	2
78	PRECISE: A clinical-grade automated molecular eligibility screening and just-in-time (JIT) physician decision support solution for molecularly-selected oncology trials.. *Journal of Clinical Oncology*, **2018**, 36, 6507-6507	2.2	1

77	Defining the DNA damage repair (DDR) genomic landscape of urothelial carcinoma of the bladder (UCB).. *Journal of Clinical Oncology*, **2018**, 36, 502-502	2.2	1
76	Refining actionable HER2 alterations in lung cancers through next generation sequencing (NGS).. *Journal of Clinical Oncology*, **2018**, 36, e24181-e24181	2.2	
75	Confounding effects of clonal hematopoiesis in clinical genomic profiling of solid tumors.. *Journal of Clinical Oncology*, **2018**, 36, 12004-12004	2.2	
74	Prognostic relevance of tumor sequencing in metastatic lung adenocarcinomas.. *Journal of Clinical Oncology*, **2018**, 36, 9049-9049	2.2	
73	Identification of clonal hematopoiesis mutations in solid tumor patients undergoing unpaired commercial next-generation sequencing assays.. *Journal of Clinical Oncology*, **2018**, 36, 12068-12068	2.2	0
72	Patient HLA class I genotype influences cancer response to checkpoint blockade immunotherapy. *Science*, **2018**, 359, 582-587	33.3	500
71	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. *Cancer Discovery*, **2018**, 8, 49-58	24.4	180
70	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. *Journal of Clinical Oncology*, **2018**, 36, 633-641	2.2	730
69	Isoform Switching as a Mechanism of Acquired Resistance to Mutant Isocitrate Dehydrogenase Inhibition. *Cancer Discovery*, **2018**, 8, 1540-1547	24.4	86
68	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. *Cancer Cell*, **2018**, 34, 852-862.e4	24.3	50
67	Radioactive Iodine-Related Clonal Hematopoiesis in Thyroid Cancer Is Common and Associated With Decreased Survival. *Journal of Clinical Endocrinology and Metabolism*, **2018**, 103, 4216-4223	5.6	18
66	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. *Cancer Cell*, **2018**, 34, 427-438.e6	24.3	339
65	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. *Clinical Cancer Research*, **2018**, 24, 4154-4161	12.9	182
64	Chromosome 20q Amplification Defines a Subtype of Microsatellite Stable, Left-Sided Colon Cancers with Wild-type RAS/RAF and Better Overall Survival. *Molecular Cancer Research*, **2017**, 15, 708-713	6.6	11
63	Universal screening for microsatellite instability in colorectal cancer in the clinical genomics era: new recommendations, methods, and considerations. *Familial Cancer*, **2017**, 16, 525-529	3	14
62	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. *Nature Medicine*, **2017**, 23, 703-713	50.5	1638
61	AACR Project GENIE: Powering Precision Medicine through an International Consortium. *Cancer Discovery*, **2017**, 7, 818-831	24.4	629
60	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. *Cancer Discovery*, **2017**, 7, 596-609	24.4	317

59	Multicolor Flow Cytometry and Multigene Next-Generation Sequencing Are Complementary and Highly Predictive for Relapse in Acute Myeloid Leukemia after Allogeneic Transplantation. *Biology of Blood and Marrow Transplantation*, **2017**, 23, 1064-1071	4.7	83
58	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. *Journal of Molecular Diagnostics*, **2017**, 19, 244-254	5.1	66
57	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. *Annals of Oncology*, **2017**, 28, 3015-3021	10.3	52
56	Distance in cancer gene expression from stem cells predicts patient survival. *PLoS ONE*, **2017**, 12, e0173589	3.7	7
55	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. *European Urology*, **2017**, 72, 952-959	10.2	168
54	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. *JCO Precision Oncology*, **2017**, 2017,	3.6	128
53	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. *JCO Precision Oncology*, **2017**, 2017,	3.6	151
52	OncoKB: A Precision Oncology Knowledge Base. *JCO Precision Oncology*, **2017**, 2017,	3.6	699
51	Plasma DNA-based molecular diagnosis, prognostication, and monitoring of patients with fusion-positive sarcomas. *JCO Precision Oncology*, **2017**, 2017,	3.6	24
50	Successful Targeted Therapy of Refractory Pediatric Fusion-Positive Secretory Breast Carcinoma. *JCO Precision Oncology*, **2017**, 2017,	3.6	21
49	Mutation Detection in Patients With Advanced Cancer by Universal Sequencing of Cancer-Related Genes in Tumor and Normal DNA vs Guideline-Based Germline Testing. *JAMA - Journal of the American Medical Association*, **2017**, 318, 825-835	27.4	235
48	Pan-Trk Immunohistochemistry Is an Efficient and Reliable Screen for the Detection of NTRK Fusions. *American Journal of Surgical Pathology*, **2017**, 41, 1547-1551	6.7	231
47	Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. *Clinical Cancer Research*, **2017**, 23, 6094-6100	12.9	107
46	Therapy-Related Clonal Hematopoiesis in Patients with Non-hematologic Cancers Is Common and Associated with Adverse Clinical Outcomes. *Cell Stem Cell*, **2017**, 21, 374-382.e4	18	339
45	Pancreatic intraductal tubulopapillary neoplasm is genetically distinct from intraductal papillary mucinous neoplasm and ductal adenocarcinoma. *Modern Pathology*, **2017**, 30, 1760-1772	9.8	39
44	Variant Review with the Integrative Genomics Viewer. *Cancer Research*, **2017**, 77, e31-e34	10.1	386
43	Intracardiac Low-grade Sarcoma Following Treatment for Ewing Sarcoma. *Journal of Pediatric Hematology/Oncology*, **2017**, 39, e443-e445	1.2	1
42	Comprehensive detection of germline variants by MSK-IMPACT, a clinical diagnostic platform for solid tumor molecular oncology and concurrent cancer predisposition testing. *BMC Medical Genomics*, **2017**, 10, 33	3.7	64

41	The Molecular Landscape of Recurrent and Metastatic Head and Neck Cancers: Insights From a Precision Oncology Sequencing Platform. *JAMA Oncology*, **2017**, 3, 244-255	13.4	141
40	The clinical impact of performing routine next generation sequencing (NGS) in gastrointestinal stromal tumors (GIST).. *Journal of Clinical Oncology*, **2017**, 35, 11010-11010	2.2	3
39	Correlation of benefit from immune checkpoint inhibitors with next gen sequencing (NGS) profiles in esophagogastric cancer (EGC) patients.. *Journal of Clinical Oncology*, **2017**, 35, 4025-4025	2.2	5
38	Molecular determinants of response and resistance to anti-PD-(L)1 blockade in patients with NSCLC profiled with targeted next-generation sequencing (NGS).. *Journal of Clinical Oncology*, **2017**, 35, 9015-9015	2.2	4
37	Clinical utility of clonality testing by next generation sequencing in the monitoring of B-cell and T-cell malignancies.. *Journal of Clinical Oncology*, **2017**, 35, 72-72	2.2	1
36	Comparison of genomic alterations in bladder urothelial tumors with and without telomerase reverse transcriptase promoter mutation using a next-generation sequencing assay.. *Journal of Clinical Oncology*, **2017**, 35, 310-310	2.2	0
35	Variability in genomic alterations between right- and left-sided microsatellite stable (MSS) metastatic colorectal cancer and impact on survival.. *Journal of Clinical Oncology*, **2017**, 35, 3534-3534	2.2	1
34	Next-generation sequencing (NGS) of tissue and cell free DNA (cfDNA) to identify somatic and germline alterations in advanced prostate cancer.. *Journal of Clinical Oncology*, **2017**, 35, 5010-5010	2.2	2
33	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. *JAMA Oncology*, **2016**, 2, 104-11	13.4	198
32	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. *Clinics in Laboratory Medicine*, **2016**, 36, 153-81	2.1	4
31	Identification of Targetable Kinase Alterations in Patients with Colorectal Carcinoma That are Preferentially Associated with Wild-Type RAS/RAF. *Molecular Cancer Research*, **2016**, 14, 296-301	6.6	34
30	Mutational Analysis of Clonal Hematopoiesis in Solid Tumor Patients Illustrates the Critical Role of Systemic Anti-Cancer Therapies in the Evolution of Somatic Leukemia Disease Alleles. *Blood*, **2016**, 128, 37-37	2.2	2
29	Prevalence of clonal hematopoiesis in patients with advanced cancer.. *Journal of Clinical Oncology*, **2016**, 34, 1511-1511	2.2	
28	Comprehensive molecular profiling and analysis of mutual exclusivity of genetic aberrations (MEGA) of intra- and extrahepatic cholangiocarcinomas (IHC and EHC) evaluation of prognostic features and potential targets for intervention.. *Journal of Clinical Oncology*, **2016**, 34, 4088-4088	2.2	1
27	Use of next generation sequencing and quantitative mass spectrometry to determine HER2 status.. *Journal of Clinical Oncology*, **2016**, 34, e23237-e23237	2.2	
26	Differences in somatic DNA damage repair (DDR) gene alterations between primary and secondary muscle invasive bladder cancer (MIBC).. *Journal of Clinical Oncology*, **2016**, 34, 4519-4519	2.2	
25	Recurrent, truncating SOX9 mutations are associated with SOX9 overexpression, KRAS mutation, and TP53 wild type status in colorectal carcinoma. *Oncotarget*, **2016**, 7, 50875-50882	3.3	15
24	Genomic aberrations frequently alter chromatin regulatory genes in chordoma. *Genes Chromosomes and Cancer*, **2016**, 55, 591-600	5	37

23	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. *New England Journal of Medicine*, **2016**, 375, 443-53	59.2	791
22	The molecular landscape of extraskeletal osteosarcoma: A clinicopathological and molecular biomarker study. *Journal of Pathology: Clinical Research*, **2016**, 2, 9-20	5.3	17
21	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. *Journal of Molecular Diagnostics*, **2015**, 17, 251-64	5.1	1066
20	Novel oncogene and tumor suppressor mutations in KIT and PDGFRA wild type gastrointestinal stromal tumors revealed by next generation sequencing. *Genes Chromosomes and Cancer*, **2015**, 54, 177-84	5	23
19	Consistent copy number changes and recurrent PRKAR1A mutations distinguish Melanotic Schwannomas from Melanomas: SNP-array and next generation sequencing analysis. *Genes Chromosomes and Cancer*, **2015**, 54, 463-471	5	30
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2	Enhanced specificity of high sensitivity somatic variant profiling in cell-free DNA via paired normal sequencing: design, validation, and clinical experience of the MSK-ACCESS liquid biopsy assay		2
1	Oncologic therapy shapes the fitness landscape of clonal hematopoiesis		7