Ahmet Zehir

List of Publications by Year
in descending order

217 papers	28,156 citations	17405 63 h-index	6630 156 g-index
230 all docs	230 docs citations	230 times ranked	34221 citing authors

#	Article	IF	Citations
1	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. Nature Genetics, 2019, 51, 202-206.	9.4	2,702
2	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	15.2	2,473
3	Memorial Sloan Kettering-Integrated Mutation Profiling of Actionable Cancer Targets (MSK-IMPACT). Journal of Molecular Diagnostics, 2015, 17, 251-264.	1.2	1,566
4	OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	1,266
5	AACR Project GENIE: Powering Precision Medicine through an International Consortium. Cancer Discovery, 2017, 7, 818-831.	7.7	1,235
6	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205
7	Molecular Determinants of Response to Antiâ€“Programmed Cell Death (PD)-1 and Antiâ€“Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Nonâ€“Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. Journal of Clinical Oncology, 2018, 36, 633-641.	0.8	1,109
8	Patient HLA class I genotype influences cancer response to checkpoint blockade immunotherapy. Science, 2018, 359, 582-587.	6.0	834
9	Variant Review with the Integrative Genomics Viewer. Cancer Research, 2017, 77, e31-e34.	0.4	798
10	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	7.7	633
11	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	7.7	589
12	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.	5.2	578
13	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.	7.7	490
14	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. JAMA Oncology, 2019, 5, 471.	3.4	426
15	Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.	9.4	411
16	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. Journal of Clinical Oncology, 2019, 37, 286-295.	0.8	397
17	Genetic diversity of tumors with mismatch repair deficiency influences antiâ€“PD-1 immunotherapy response. Science, 2019, 364, 485-491.	6.0	395
18	NTRK fusion detection across multiple assays and 33,997 cases: diagnostic implications and pitfalls. Modern Pathology, 2020, 33, 38-46.	2.9	373

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19	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	9.4	367
20	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.	3.8	366
21	Pan-Trk Immunohistochemistry Is an Efficient and Reliable Screen for the Detection of NTRK Fusions. American Journal of Surgical Pathology, 2017, 41, 1547-1551.	2.1	353
22	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. Clinical Cancer Research, 2018, 24, 4154-4161.	3.2	348
23	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, e000147.		329
24	Single-cell mutation analysis of clonal evolution in myeloid malignancies. Nature, 2020, 587, 477-482.	13.7	304
25	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	13.7	295
26	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.	3.2	292
27	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, 1-16.	1.5	286
28	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	7.7	275
29	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	7.7	275
30	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. JAMA Oncology, 2016, 2, 104.	3.4	270
31	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. European Urology, 2017, 72, 952-959.	0.9	263
32	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	13.5	223
33	Pretreatment neutrophil-to-lymphocyte ratio and mutational burden as biomarkers of tumor response to immune checkpoint inhibitors. Nature Communications, 2021, 12, 729.	5.8	212
34	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. JCO Precision Oncology, 2017, 2017, 1-17.	1.5	209
35	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.	3.2	200
36	The Molecular Landscape of Recurrent and Metastatic Head and Neck Cancers. JAMA Oncology, 2017, 3, 244.	3.4	191

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37	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.	0.5	182
38	Prospective Evaluation of Germline Alterations in Patients With Exocrine Pancreatic Neoplasms. Journal of the National Cancer Institute, 2018, 110, 1067-1074.	3.0	170
39	Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. Clinical Cancer Research, 2017, 23, 6094-6100.	3.2	161
40	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.	1.2	161
41	Prevalence of Clonal Hematopoiesis Mutations in Tumor-Only Clinical Genomic Profiling of Solid Tumors. JAMA Oncology, 2018, 4, 1589.	3.4	139
42	The association between tumor mutational burden and prognosis is dependent on treatment context. Nature Genetics, 2021, 53, 11-15.	9.4	139
43	Isoform Switching as a Mechanism of Acquired Resistance to Mutant Isocitrate Dehydrogenase Inhibition. Cancer Discovery, 2018, 8, 1540-1547.	7.7	138
44	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.	3.9	134
45	Response Rates to Antiâ€“PD-1 Immunotherapy in Microsatellite-Stable Solid Tumors With 10 or More Mutations per Megabase. JAMA Oncology, 2021, 7, 739.	3.4	125
46	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.	2.0	124
47	Dicer is required for survival of differentiating neural crest cells. Developmental Biology, 2010, 340, 459-467.	0.9	121
48	Colorectal Carcinomas Containing Hypermethylated MLH1 Promoter and Wild-Type BRAF/KRAS Are Enriched for Targetable Kinase Fusions. Cancer Research, 2019, 79, 1047-1053.	0.4	112
49	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.	0.7	111
50	Improved prediction of immune checkpoint blockade efficacy across multiple cancer types. Nature Biotechnology, 2022, 40, 499-506.	9.4	110
51	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. Clinical Cancer Research, 2019, 25, 5537-5547.	3.2	107
52	Genomic Differences Between â€œPrimaryâ€•and â€œSecondaryâ€•Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. European Urology, 2019, 75, 231-239.	0.9	104
53	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. Clinical Cancer Research, 2018, 24, 5939-5947.	3.2	100
54	Next-Generation Assessment of Human Epidermal Growth Factor Receptor 2 (ERBB2) Amplification Status. Journal of Molecular Diagnostics, 2017, 19, 244-254.	1.2	96

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55	BMP signaling regulates sympathetic nervous system development through Smad4-dependent and -independent pathways. Development (Cambridge), 2009, 136, 3575-3584.	1.2	91
56	The value of cellâ€free DNA for molecular pathology. Journal of Pathology, 2018, 244, 616-627.	2.1	91
57	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.	0.6	86
58	Identification of Clonal Hematopoiesis Mutations in Solid Tumor Patients Undergoing Unpaired Next-Generation Sequencing Assays. Clinical Cancer Research, 2018, 24, 5918-5924.	3.2	84
59	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. Journal of Clinical Oncology, 2021, 39, 2698-2709.	0.8	83
60	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	5.8	81
61	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. Annals of Oncology, 2017, 28, 3015-3021.	0.6	79
62	Clinical Genomic Sequencing of Pediatric and Adult Osteosarcoma Reveals Distinct Molecular Subsets with Potentially Targetable Alterations. Clinical Cancer Research, 2019, 25, 6346-6356.	3.2	75
63	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. Nature Cancer, 2021, 2, 357-365.	5.7	74
64	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. Cancer Cell, 2018, 34, 852-862.e4.	7.7	73
65	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.	1.2	69
66	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.	5.8	68
67	Pancreatic intraductal tubulopapillary neoplasm is genetically distinct from intraductal papillary mucinous neoplasm and ductal adenocarcinoma. Modern Pathology, 2017, 30, 1760-1772.	2.9	67
68	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncology, 2020, 6, 84.	3.4	66
69	Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. Nature Communications, 2021, 12, 338.	5.8	64
70	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .	5.8	63
71	Majority of B2M-Mutant and -Deficient Colorectal Carcinomas Achieve Clinical Benefit From Immune Checkpoint Inhibitor Therapy and Are Microsatellite Instability-High. JCO Precision Oncology, 2019, 3, 1-14.	1.5	61
72	Managing Clonal Hematopoiesis in Patients With Solid Tumors. Journal of Clinical Oncology, 2019, 37, 7-11.	0.8	60

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73	Genomic Profiling Identifies Association of IDH1/IDH2 Mutation with Longer Relapse-Free and Metastasis-Free Survival in High-Grade Chondrosarcoma. Clinical Cancer Research, 2020, 26, 419-427.	3.2	60
74	Genomic aberrations frequently alter chromatin regulatory genes in chordoma. Genes Chromosomes and Cancer, 2016, 55, 591-600.	1.5	58
75	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Nonâ€“Small-Cell Lung Cancer. JCO Precision Oncology, 2019, 3, 1-12.	1.5	58
76	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.	2.9	58
77	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. Blood, 2021, 137, 2103-2113.	0.6	57
78	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.	2.9	57
79	OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.	1.0	51
80	Preâ€clinical efficacy of PUâ€H71, a novel HSP90 inhibitor, alone and in combination with bortezomib in Ewing sarcoma. Molecular Oncology, 2014, 8, 323-336.	2.1	48
81	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.	1.5	46
82	Consistent copy number changes and recurrent <scp>PRKAR1A</scp> mutations distinguish <scp>M</scp>elanotic <scp>S</scp>chwannomas from <scp>M</scp>elanomas: <scp>SNP</scp>â€array and next generation sequencing analysis. Genes Chromosomes and Cancer, 2015, 54, 463-471.	1.5	44
83	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
84	The Clinical Management of Clonal Hematopoiesis. Hematology/Oncology Clinics of North America, 2020, 34, 357-367.	0.9	42
85	The repertoire of genetic alterations in salivary duct carcinoma including a novel HNRNPH3-ALK rearrangement. Human Pathology, 2019, 88, 66-77.	1.1	38
86	Plasma DNA-Based Molecular Diagnosis, Prognostication, and Monitoring of Patients With EWSR1 Fusion-Positive Sarcomas. JCO Precision Oncology, 2017, 2017, 1-11.	1.5	36
87	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.	1.6	35
88	Fragment Size Analysis May Distinguish Clonal Hematopoiesis from Tumor-Derived Mutations in Cell-Free DNA. Clinical Chemistry, 2020, 66, 616-618.	1.5	35
89	MET Exon 14â€“altered Lung Cancers and MET Inhibitor Resistance. Clinical Cancer Research, 2021, 27, 799-806.	3.2	35
90	Structureâ€“function analysis of oncogenic EGFR Kinase Domain Duplication reveals insights into activation and a potential approach for therapeutic targeting. Nature Communications, 2021, 12, 1382.	5.8	34

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91	Radioactive Iodineâ€“Related Clonal Hematopoiesis in Thyroid Cancer Is Common and Associated With Decreased Survival. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4216-4223.	1.8	33
92	Successful Targeted Therapy of Refractory Pediatric ETV6-NTRK3 Fusion-Positive Secretory Breast Carcinoma. JCO Precision Oncology, 2017, 2017, 1-8.	1.5	31
93	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers. Nature Communications, 2022, 13, 2485.	5.8	31
94	Functional landscapes of POLE and POLD1 mutations in checkpoint blockade-dependent antitumor immunity. Nature Genetics, 2022, 54, 996-1012.	9.4	30
95	BRCA Mutations, Homologous DNA Repair Deficiency, Tumor Mutational Burden, and Response to Immune Checkpoint Inhibition in Recurrent Ovarian Cancer. JCO Precision Oncology, 2020, 4, 665-679.	1.5	29
96	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, 177-184.	1.5	28
97	Ampullary cancer: Evaluation of somatic and germline genetic alterations and association with clinical outcomes. Cancer, 2019, 125, 1441-1448.	2.0	28
98	Detection of Mutations in Myeloid Malignancies through Paired-Sample Analysis of Microdroplet-PCR Deep Sequencing Data. Journal of Molecular Diagnostics, 2014, 16, 504-518.	1.2	26
99	Recurrent, truncating SOX9 mutations are associated with SOX9 overexpression, KRAS mutation, and TP53 wild type status in colorectal carcinoma. Oncotarget, 2016, 7, 50875-50882.	0.8	26
100	Harnessing Clinical Sequencing Data for Survival Stratification of Patients With Metastatic Lung Adenocarcinomas. JCO Precision Oncology, 2019, 3, 1-9.	1.5	26
101	Tumor fraction-guided cell-free DNA profiling in metastatic solid tumor patients. Genome Medicine, 2021, 13, 96.	3.6	26
102	Fumarate hydrataseFHc.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. Human Mutation, 2020, 41, 103-109.	1.1	25
103	Reliable Clinical MLH1 Promoter Hypermethylation Assessment Using a High-Throughput Genome-Wide Methylation Array Platform. Journal of Molecular Diagnostics, 2020, 22, 368-375.	1.2	25
104	The molecular landscape of extraskeletal osteosarcoma: A clinicopathological and molecular biomarker study. Journal of Pathology: Clinical Research, 2016, 2, 9-20.	1.3	24
105	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.	1.5	24
106	MET inhibitor resistance in patients with MET exon 14-altered lung cancers.. Journal of Clinical Oncology, 2019, 37, 9006-9006.	0.8	24
107	Characterization and Clinical Outcomes of DNA Mismatch Repairâ€“deficient Small Bowel Adenocarcinoma. Clinical Cancer Research, 2021, 27, 1429-1437.	3.2	23
108	Binimetinib plus Gemcitabine and Cisplatin Phase I/II Trial in Patients with Advanced Biliary Cancers. Clinical Cancer Research, 2019, 25, 937-945.	3.2	22

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109	Cancer-Causative Mutations Occurring in Early Embryogenesis. Cancer Discovery, 2022, 12, 949-957.	7.7	21
110	E-cadherin immunohistochemical expression in invasive lobular carcinoma of the breast: correlation with morphology and CDH1 somatic alterations. Human Pathology, 2020, 102, 44-53.	1.1	20
111	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.	1.2	20
112	Clinical, genomic, and transcriptomic correlates of response to immune checkpoint blockade-based therapy in a cohort of patients with angiosarcoma treated at a single center. , 2022, 10, e004149.		20
113	Next-Generation Sequencingâ€“Based Assessment of JAK2, PD-L1, and PD-L2 Copy Number Alterations at 9p24.1 in Breast Cancer. Journal of Molecular Diagnostics, 2019, 21, 307-317.	1.2	19
114	Universal screening for microsatellite instability in colorectal cancer in the clinical genomics era: new recommendations, methods, and considerations. Familial Cancer, 2017, 16, 525-529.	0.9	18
115	Ultrarapid EGFR Mutation Screening Followed by Comprehensive Next-Generation Sequencing: AÂFeasible, Informative Approach for Lung Carcinoma Cytology Specimens With a High Success Rate. JTO Clinical and Research Reports, 2020, 1, 100077.	0.6	18
116	Comprehensive assessment of germline pathogenic variant detection in tumor-only sequencing. Annals of Oncology, 2022, 33, 426-433.	0.6	18
117	A FISH assay efficiently screens for BRAF gene rearrangements in pancreatic acinar-type neoplasms. Modern Pathology, 2018, 31, 132-140.	2.9	17
118	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.	0.6	17
119	Clinical Experience of Cerebrospinal Fluidâ€“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.	1.2	17
120	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.	0.8	17
121	The clinical implications of clonal hematopoiesis in hematopoietic cell transplantation. Blood Reviews, 2021, 46, 100744.	2.8	16
122	Genetic and molecular subtype heterogeneity in newly diagnosed early- and advanced-stage endometrial cancer. Gynecologic Oncology, 2021, 161, 535-544.	0.6	16
123	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.	0.6	16
124	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.	1.1	14
125	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. Molecular Cancer Research, 2021, 19, 1146-1155.	1.5	14
126	Distance in cancer gene expression from stem cells predicts patient survival. PLoS ONE, 2017, 12, e0173589.	1.1	12

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127	Genomic Alterations as Potential Therapeutic Targets in Extramammary Pagetâ€™s Disease of the Vulva. JCO Precision Oncology, 2020, 4, 1054-1060.	1.5	12
128	Defining Novel DNA Virus-Tumor Associations and Genomic Correlates Using Prospective Clinical Tumor/Normal Matched Sequencing Data. Journal of Molecular Diagnostics, 2022, 24, 515-528.	1.2	12
129	Prevalence and Preliminary Validation of Screening Criteria to Identify Carriers of Germline BAP1 Mutations. Journal of Thoracic Oncology, 2019, 14, 1989-1994.	0.5	10
130	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.	2.9	10
131	Germline Pathogenic Variants Impact Clinicopathology of Advanced Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1450-1459.	1.1	10
132	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. JCO Precision Oncology, 2020, 4, 1307-1320.	1.5	9
133	Evaluation of a Combined Multilocus Sequence Typing and Whole-Genome Sequencing Two-Step Algorithm for Routine Typing of Clostridioides difficile. Journal of Clinical Microbiology, 2021, 59, .	1.8	8
134	Spectrum of BRAF Mutations and Gene Rearrangements in Ovarian Serous Carcinoma. JCO Precision Oncology, 2021, 5, 1480-1492.	1.5	8
135	Electronic Health Records and Genomics. Journal of Molecular Diagnostics, 2022, 24, 1-17.	1.2	8
136	Comprehensive Genomic Analysis of Metastatic Nonâ€“Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. JCO Precision Oncology, 2019, 3, 1-18.	1.5	7
137	Nextâ€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.	1.6	7
138	Multiple Primary Cancers in Patients Undergoing Tumor-Normal Sequencing Define Novel Associations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 362-371.	1.1	7
139	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Clinics in Laboratory Medicine, 2016, 36, 153-181.	0.7	6
140	Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. JCO Precision Oncology, 2019, 3, 1-13.	1.5	6
141	Paired Tumor-Normal Sequencing Provides Insights into TP53-Related Cancer Spectrum in Li-Fraumeni Patients. Journal of the National Cancer Institute, 2021, , .	3.0	6
142	Somatic intronic <scp>TP53</scp> c.375+<scp>5G</scp> mutations are a recurrent but underâ€recognized mode of <scp>TP53</scp> inactivation. Journal of Pathology: Clinical Research, 2022, 8, 14-18.	1.3	6
143	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.	0.8	6
144	Evaluation of Initial Telomere Length and Changes after Transplantation in Adult Double-Unit Cord Blood Transplant Recipients. Biology of Blood and Marrow Transplantation, 2015, 21, 1334-1336.	2.0	5

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145	Molecular profiling and analysis of genetic aberrations aimed at identifying potential therapeutic targets in fibrolamellar carcinoma of the liver. Cancer, 2020, 126, 4126-4135.	2.0	5
146	Comprehensive detection of targetable fusions in lung adenocarcinomas by complementary targeted DNAseq and RNAseq assays.. Journal of Clinical Oncology, 2018, 36, 12076-12076.	0.8	5
147	Multicenter Analysis of Genomically Targeted Single Patient Use Requests for Pediatric Neoplasms. Journal of Clinical Oncology, 2021, 39, 3822-3828.	0.8	4
148	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.. Journal of Clinical Oncology, 2015, 33, 604-604.	0.8	4
149	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.	0.8	4
150	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.	0.8	4
151	Bone Marrow Surveillance of Pediatric Cancer Survivors Identifies Clones that Predict Therapy-Related Leukemia. Clinical Cancer Research, 2022, 28, 1614-1627.	3.2	4
152	Oncologic Therapy for Solid Tumors Alters the Risk of Clonal Hematopoiesis. Blood, 2018, 132, 747-747.	0.6	3
153	Tumor relevant germline findings in targeted tumor sequencing using matched normal DNA of 1,570 unselected cases.. Journal of Clinical Oncology, 2015, 33, 1509-1509.	0.8	3
154	The clinical impact of performing routine next generation sequencing (NGS) in gastrointestinal stromal tumors (GIST).. Journal of Clinical Oncology, 2017, 35, 11010-11010.	0.8	3
155	Defining the DNA damage repair (DDR) genomic landscape of urothelial carcinoma of the bladder (UCB).. Journal of Clinical Oncology, 2018, 36, 502-502.	0.8	3
156	Abstract 3409: MSK-IMPACT Heme: Validation and clinical experience of a comprehensive molecular profiling platform for hematologic malignancies. , 2019, , .		3
157	Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. Blood, 2019, 134, 2148-2148.	0.6	3
158	Matched Molecular Profiling of Cell-Free DNA and Tumor Tissue in Patients With Advanced Clear Cell Renal Cell Carcinoma. JCO Precision Oncology, 2022, , .	1.5	3
159	Intracardiac Low-grade Sarcoma Following Treatment for Ewing Sarcoma. Journal of Pediatric Hematology/Oncology, 2017, 39, e443-e445.	0.3	2
160	Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. JCO Clinical Cancer Informatics, 2020, 4, 691-699.	1.0	2
161	Abstract 1387: Tracking minimal residual disease in post-operative cell-free DNA using MSK-ACCESS. , 2019, , .		2
162	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.	0.8	2

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163	Frequency of actionable cancer predisposing germline mutations in patients with lung cancers.. Journal of Clinical Oncology, 2018, 36, 1504-1504.	0.8	2
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