Garrett M Frampton

List of Publications by Year
in descending order

163	31,062	13865 67	7518 151
papers	citations	h-index	g-index

164	164	164	44427
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Histone H3K27ac separates active from poised enhancers and predicts developmental state. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21931-21936.	7.1	3,446
2	Atezolizumab in patients with locally advanced and metastatic urothelial carcinoma who have progressed following treatment with platinum-based chemotherapy: a single-arm, multicentre, phase 2 trial. Lancet, The, 2016, 387, 1909-1920.	13.7	3,077
3	Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden. Genome Medicine, 2017, 9, 34.	8.2	2,480
4	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	17.5	1,785
5	Tumor Mutational Burden as an Independent Predictor of Response to Immunotherapy in Diverse Cancers. Molecular Cancer Therapeutics, 2017, 16, 2598-2608.	4.1	1,779
6	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. Cell, 2008, 134, 521-533.	28.9	1,332
7	STK11/LKB1 Mutations and PD-1 Inhibitor Resistance in KRAS-Mutant Lung Adenocarcinoma. Cancer Discovery, 2018, 8, 822-835.	9.4	1,108
8	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. Cell, 2011, 144, 296-309.	28.9	843
9	Identification of new ALK and RET gene fusions from colorectal and lung cancer biopsies. Nature Medicine, 2012, 18, 382-384.	30.7	782
10	Co-occurring Genomic Alterations Define Major Subsets of KRAS-Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. Cancer Discovery, 2015, 5, 860-877.	9.4	696
11	Foxp3 occupancy and regulation of key target genes during T-cell stimulation. Nature, 2007, 445, 931-935.	27.8	644
12	Activation of MET via Diverse Exon 14 Splicing Alterations Occurs in Multiple Tumor Types and Confers Clinical Sensitivity to MET Inhibitors. Cancer Discovery, 2015, 5, 850-859.	9.4	632
13	Emergence of Constitutively Active Estrogen Receptor-Î± Mutations in Pretreated Advanced Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2014, 20, 1757-1767.	7.0	529
14	Enhancer decommissioning by LSD1 during embryonic stem cell differentiation. Nature, 2012, 482, 221-225.	27.8	527
15	Targeted Next Generation Sequencing Identifies Markers of Response to PD-1 Blockade. Cancer Immunology Research, 2016, 4, 959-967.	3.4	428
16	Chromatin Structure and Gene Expression Programs of Human Embryonic and Induced Pluripotent Stem Cells. Cell Stem Cell, 2010, 7, 249-257.	11.1	405
17	Targeted Next-generation Sequencing of Advanced Prostate Cancer Identifies Potential Therapeutic Targets and Disease Heterogeneity. European Urology, 2013, 63, 920-926.	1.9	379
18	Mechanisms and therapeutic implications of hypermutation in gliomas. Nature, 2020, 580, 517-523.	27.8	374

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19	Association of Patient Characteristics and Tumor Genomics With Clinical Outcomes Among Patients With Nonâ€“Small Cell Lung Cancer Using a Clinicogenomic Database. JAMA - Journal of the American Medical Association, 2019, 321, 1391.	7.4	370
20	Derivation of Pre-X Inactivation Human Embryonic Stem Cells under Physiological Oxygen Concentrations. Cell, 2010, 141, 872-883.	28.9	367
21	PD-L1 expression and tumor mutational burden are independent biomarkers in most cancers. JCI Insight, 2019, 4, .	5.0	345
22	SetDB1 contributes to repression of genes encoding developmental regulators and maintenance of ES cell state. Genes and Development, 2009, 23, 2484-2489.	5.9	292
23	Characterization of 298 Patients with Lung Cancer Harboring MET Exon 14 Skipping Alterations. Journal of Thoracic Oncology, 2016, 11, 1493-1502.	1.1	288
24	Transcriptional role of cyclin D1 in development revealed by a geneticâ€“proteomic screen. Nature, 2010, 463, 374-378.	27.8	247
25	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood, 2016, 127, 3004-3014.	1.4	244
26	Aberrant chromatin at genes encoding stem cell regulators in human mixed-lineage leukemia. Genes and Development, 2008, 22, 3403-3408.	5.9	237
27	Tumor Mutational Burden as a Predictive Biomarker for Response to Immune Checkpoint Inhibitors: A Review of Current Evidence. Oncologist, 2020, 25, e147-e159.	3.7	220
28	Prevalence of PDL1 Amplification and Preliminary Response to Immune Checkpoint Blockade in Solid Tumors. JAMA Oncology, 2018, 4, 1237.	7.1	214
29	Beyond microsatellite testing: assessment of tumor mutational burden identifies subsets of colorectal cancer who may respond to immune checkpoint inhibition. Journal of Gastrointestinal Oncology, 2018, 9, 610-617.	1.4	192
30	A computational approach to distinguish somatic vs. germline origin of genomic alterations from deep sequencing of cancer specimens without a matched normal. PLoS Computational Biology, 2018, 14, e1005965.	3.2	191
31	Microsatellite-Stable Tumors with High Mutational Burden Benefit from Immunotherapy. Cancer Immunology Research, 2019, 7, 1570-1573.	3.4	190
32	Targeted next-generation sequencing of head and neck squamous cell carcinoma identifies novel genetic alterations in HPV+ and HPV- tumors. Genome Medicine, 2013, 5, 49.	8.2	188
33	Comprehensive Genomic Profiling of 282 Pediatric Low- and High-Grade Gliomas Reveals Genomic Drivers, Tumor Mutational Burden, and Hypermutation Signatures. Oncologist, 2017, 22, 1478-1490.	3.7	176
34	Next-Generation Sequencing Reveals High Concordance of Recurrent Somatic Alterations Between Primary Tumor and Metastases From Patients With Nonâ€“Small-Cell Lung Cancer. Journal of Clinical Oncology, 2013, 31, 2167-2172.	1.6	170
35	Genomic alterations in head and neck squamous cell carcinoma determined by cancer gene-targeted sequencing. Annals of Oncology, 2015, 26, 1216-1223.	1.2	163
36	Diverse EGFR Exon 20 Insertions and Co-Occurring Molecular Alterations Identified by Comprehensive Genomic Profiling of NSCLC. Journal of Thoracic Oncology, 2018, 13, 1560-1568.	1.1	158

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37	Comprehensive Genomic Profiling of Pancreatic Acinar Cell Carcinomas Identifies Recurrent RAF Fusions and Frequent Inactivation of DNA Repair Genes. Cancer Discovery, 2014, 4, 1398-1405.	9.4	151
38	Targeting HER2 in colorectal cancer: The landscape of amplification and short variant mutations in ERBB2 and ERBB3. Cancer, 2018, 124, 1358-1373.	4.1	151
39	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
40	Analytical Validation of a Hybrid Captureâ€"Based Next-Generation Sequencing Clinical Assay for Genomic Profiling of Cell-Free Circulating Tumor DNA. Journal of Molecular Diagnostics, 2018, 20, 686-702.	2.8	149
41	A Novel Next-Generation Sequencing Approach to Detecting Microsatellite Instability and Pan-Tumor Characterization of 1000 Microsatellite Instabilityâ€"High Cases in 67,000 Patient Samples. Journal of Molecular Diagnostics, 2019, 21, 1053-1066.	2.8	147
42	Pan-Cancer Landscape and Analysis of ERBB2 Mutations Identifies Poziotinib as a Clinically Active Inhibitor and Enhancer of T-DM1 Activity. Cancer Cell, 2019, 36, 444-457.e7.	16.8	145
43	Somatic HLA Class I Loss Is a Widespread Mechanism of Immune Evasion Which Refines the Use of Tumor Mutational Burden as a Biomarker of Checkpoint Inhibitor Response. Cancer Discovery, 2021, 11, 282-292.	9.4	132
44	Comprehensive characterization of RAS mutations in colon and rectal cancers in old and young patients. Nature Communications, 2019, 10, 3722.	12.8	131
45	Pulmonary Sarcomatoid Carcinomas Commonly Harbor Either Potentially Targetable Genomic Alterations or High Tumor Mutational Burden as Observed by Comprehensive Genomic Profiling. Journal of Thoracic Oncology, 2017, 12, 932-942.	1.1	129
46	A High Frequency of Activating Extracellular Domain ERBB2 (HER2) Mutation in Micropapillary Urothelial Carcinoma. Clinical Cancer Research, 2014, 20, 68-75.	7.0	120
47	Comprehensive Genomic Profiling Identifies a Subset of Crizotinib-Responsive ALK-Rearranged Non-Small Cell Lung Cancer Not Detected by Fluorescence In Situ Hybridization. Oncologist, 2016, 21, 762-770.	3.7	119
48	The Genomic Landscape of Merkel Cell Carcinoma and Clinicogenomic Biomarkers of Response to Immune Checkpoint Inhibitor Therapy. Clinical Cancer Research, 2019, 25, 5961-5971.	7.0	118
49	Comprehensive Genomic Landscapes in Early and Later Onset Colorectal Cancer. Clinical Cancer Research, 2019, 25, 5852-5858.	7.0	116
50	Ronin/Hcf-1 binds to a hyperconserved enhancer element and regulates genes involved in the growth of embryonic stem cells. Genes and Development, 2010, 24, 1479-1484.	5.9	106
51	Concordance of Genomic Alterations between Primary and Recurrent Breast Cancer. Molecular Cancer Therapeutics, 2014, 13, 1382-1389.	4.1	104
52	Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. Blood, 2011, 118, e128-e138.	1.4	103
53	Metastatic basal cell carcinoma with amplification of PD-L1: exceptional response to anti-PD1 therapy. Npj Genomic Medicine, 2016, 1, .	3.8	103
54	Pan-Cancer Analysis of BRCA1 and BRCA2 Genomic Alterations and Their Association With Genomic Instability as Measured by Genome-Wide Loss of Heterozygosity. JCO Precision Oncology, 2020, 4, 442-465.	3.0	103

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55	Clinical and analytical validation of FoundationOneÂ®CDx, a comprehensive genomic profiling assay for solid tumors. PLoS ONE, 2022, 17, e0264138.	2.5	100
56	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. Cancer Research, 2017, 77, 2464-2475.	0.9	93
57	Prevalence of High Tumor Mutational Burden and Association With Survival in Patients With Less Common Solid Tumors. JAMA Network Open, 2020, 3, e2025109.	5.9	92
58	Characterization of Clinical Cases of Advanced Papillary Renal Cell Carcinoma via Comprehensive Genomic Profiling. European Urology, 2018, 73, 71-78.	1.9	87
59	Comprehensive Genomic Profiling Facilitates Implementation of the National Comprehensive Cancer Network Guidelines for Lung Cancer Biomarker Testing and Identifies Patients Who May Benefit From Enrollment in Mechanism-Driven Clinical Trials. Oncologist, 2016, 21, 684-691.	3.7	85
60	Comprehensive genomic profiles of metastatic and relapsed salivary gland carcinomas are associated with tumor type and reveal new routes to targeted therapies. Annals of Oncology, 2017, 28, 2539-2546.	1.2	84
61	Comparative analysis of primary tumour and matched metastases in colorectal cancer patients: Evaluation of concordance between genomic and transcriptional profiles. European Journal of Cancer, 2015, 51, 791-799.	2.8	83
62	ALK Fusions in a Wide Variety of Tumor Types Respond to Anti-ALK Targeted Therapy. Oncologist, 2017, 22, 1444-1450.	3.7	81
63	Successful Treatment of HIV-Associated Kaposi Sarcoma with Immune Checkpoint Blockade. Cancer Immunology Research, 2018, 6, 1129-1135.	3.4	81
64	OA20.01 Tumor Mutation Burden (TMB) is Associated with Improved Efficacy of Atezolizumab in 1L and 2L+ NSCLC Patients. Journal of Thoracic Oncology, 2017, 12, S321-S322.	1.1	80
65	Comprehensive genomic profiling of anal squamous cell carcinoma reveals distinct genomically defined classes. Annals of Oncology, 2016, 27, 1336-1341.	1.2	78
66	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. Cancer Research, 2017, 77, 509-519.	0.9	75
67	Recurrent hyperactive ESR1 fusion proteins in endocrine therapy-resistant breast cancer. Annals of Oncology, 2018, 29, 872-880.	1.2	73
68	Analysis of DNA Damage Response Gene Alterations and Tumor Mutational Burden Across 17,486 Tubular Gastrointestinal Carcinomas: Implications for Therapy. Oncologist, 2019, 24, 1340-1347.	3.7	73
69	RET fusions in a small subset of advanced colorectal cancers at risk of being neglected. Annals of Oncology, 2018, 29, 1394-1401.	1.2	72
70	MHC-I genotype and tumor mutational burden predict response to immunotherapy. Genome Medicine, 2020, 12, 45.	8.2	70
71	Oncogenic Alterations in ERBB2/HER2 Represent Potential Therapeutic Targets Across Tumors From Diverse Anatomic Sites of Origin. Oncologist, 2015, 20, 7-12.	3.7	69
72	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	3.7	69

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73	Genomic Profiling of Prostate Cancers from Men with African and European Ancestry. Clinical Cancer Research, 2020, 26, 4651-4660.	7.0	68
74	Hybrid capture-based genomic profiling of circulating tumor DNA from patients with estrogen receptor-positive metastatic breast cancer. Annals of Oncology, 2017, 28, 2866-2873.	1.2	67
75	HER2-Overexpressing Breast Cancers Amplify FGFR Signaling upon Acquisition of Resistance to Dual Therapeutic Blockade of HER2. Clinical Cancer Research, 2017, 23, 4323-4334.	7.0	64
76	Prospective Comprehensive Genomic Profiling of Primary and Metastatic Prostate Tumors. JCO Precision Oncology, 2019, 3, 1-23.	3.0	63
77	Loss of function of NF1 is a mechanism of acquired resistance to endocrine therapy in lobular breast cancer. Annals of Oncology, 2019, 30, 115-123.	1.2	63
78	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. OncoImmunology, 2019, 8, 1550341.	4.6	60
79	First-in-Human Phase I Study of the Tamoxifen Metabolite Z-Endoxifen in Women With Endocrine-Refractory Metastatic Breast Cancer. Journal of Clinical Oncology, 2017, 35, 3391-3400.	1.6	58
80	Patient-derived xenotransplants can recapitulate the genetic driver landscape of acute leukemias. Leukemia, 2017, 31, 151-158.	7.2	57
81	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. Blood, 2018, 131, 2501-2505.	1.4	57
82	Clinical genomic profiling in the management of patients with soft tissue and bone sarcoma. Nature Communications, 2022, 13, .	12.8	51
83	High Tumor Mutational Burden Correlates with Longer Survival in Immunotherapy-NaÃ¯ve Patients with Diverse Cancers. Molecular Cancer Therapeutics, 2020, 19, 2139-2145.	4.1	50
84	Reliability and Reproducibility of Gene Expression Measurements Using Amplified RNA from Laser-Microdissected Primary Breast Tissue with Oligonucleotide Arrays. Journal of Molecular Diagnostics, 2005, 7, 57-64.	2.8	47
85	Clinical Benefit in Response to Palbociclib Treatment in Refractory Uterine Leiomyosarcomas with a Common CDKN2A Alteration. Oncologist, 2017, 22, 416-421.	3.7	46
86	MET 14 Deletion in Sarcomatoid Non-Small-Cell Lung Cancer Detected by Next-Generation Sequencing and Successfully Treated with a MET Inhibitor. Journal of Thoracic Oncology, 2015, 10, e113-e114.	1.1	42
87	Profiling of 3,634 cholangiocarcinomas (CCA) to identify genomic alterations (GA), tumor mutational burden (TMB), and genomic loss of heterozygosity (gLOH).. Journal of Clinical Oncology, 2019, 37, 4087-4087.	1.6	42
88	Genomic landscape of advanced basal cell carcinoma: Implications for precision treatment with targeted and immune therapies. OncoImmunology, 2018, 7, e1404217.	4.6	41
89	Correlation Between Molecular Subclassifications of Clear Cell Renal Cell Carcinoma and Targeted Therapy Response. European Urology Focus, 2016, 2, 204-209.	3.1	40
90	Mutation load and an effector T-cell gene signature may distinguish immunologically distinct and clinically relevant lymphoma subsets. Blood Advances, 2017, 1, 1884-1890.	5.2	40

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91	Pan-Cancer Analysis of CDK12 Loss-of-Function Alterations and Their Association with the Focal Tandem-Duplicator Phenotype. Oncologist, 2019, 24, 1526-1533.	3.7	39
92	Comprehensive genomic profiling identifies novel NTRK fusions in neuroendocrine tumors. Oncotarget, 2018, 9, 35809-35812.	1.8	39
93	Pharmacogenomic Identification of Targets for Adjuvant Therapy with the Topoisomerase Poison Camptothecin. Cancer Research, 2004, 64, 2096-2104.	0.9	38
94	The genomic landscape of metastatic breast cancer: Insights from 11,000 tumors. PLoS ONE, 2020, 15, e0231999.	2.5	36
95	CpG island structure and trithorax/polycomb chromatin domains in human cells. Genomics, 2012, 100, 320-326.	2.9	35
96	GNAS, GNAQ, and GNA11 alterations in patients with diverse cancers. Cancer, 2018, 124, 4080-4089.	4.1	34
97	Comprehensive Genomic Profiling Identifies Frequent Drug-Sensitive EGFR Exon 19 Deletions in NSCLC not Identified by Prior Molecular Testing. Clinical Cancer Research, 2016, 22, 3281-3285.	7.0	33
98	Severe nivolumab-induced pneumonitis preceding durable clinical remission in a patient with refractory, metastatic lung squamous cell cancer: a case report. Journal of Hematology and Oncology, 2017, 10, 64.	17.0	30
99	PARP-1 activity (PAR) determines the sensitivity of cervical cancer to olaparib. Gynecologic Oncology, 2019, 155, 144-150.	1.4	28
100	The Genomics of Colorectal Cancer in Populations with African and European Ancestry. Cancer Discovery, 2022, 12, 1282-1293.	9.4	28
101	Clinical utility of tumor genomic profiling in patients with high plasma circulating tumor DNA burden or metabolically active tumors. Journal of Hematology and Oncology, 2018, 11, 129.	17.0	27
102	Clinical and Immunological Implications of Frameshift Mutations in Lung Cancer. Journal of Thoracic Oncology, 2019, 14, 1807-1817.	1.1	27
103	Characterization of Clinical Cases of Malignant PEComa via Comprehensive Genomic Profiling of DNA and RNA. Oncology, 2020, 98, 905-912.	1.9	27
104	Comprehensive genomic profiling in FIGHT-202 reveals the landscape of actionable alterations in advanced cholangiocarcinoma.. Journal of Clinical Oncology, 2019, 37, 4080-4080.	1.6	25
105	BRAF in Lung Cancers: Analysis of Patient Cases Reveals Recurrent BRAF Mutations, Fusions, Kinase Duplications, and Concurrent Alterations. JCO Precision Oncology, 2018, 2, 1-15.	3.0	24
106	Phenotypic and Genomic Determinants of Immunotherapy Response Associated with Squamousness. Cancer Immunology Research, 2019, 7, 866-873.	3.4	23
107	Comprehensive characterization of PTEN mutational profile in a series of 34,129 colorectal cancers. Nature Communications, 2022, 13, 1618.	12.8	23
108	Characterization of 1,387 NSCLCs with MET exon 14 (METex14) skipping alterations (SA) and potential acquired resistance (AR) mechanisms.. Journal of Clinical Oncology, 2020, 38, 9511-9511.	1.6	22

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109	General paucity of genomic alteration and low tumor mutation burden in refractory and metastatic hepatoblastoma: comprehensive genomic profiling study. Human Pathology, 2017, 70, 84-91.	2.0	20
110	Biomarkers in Breast Cancer: An Integrated Analysis of Comprehensive Genomic Profiling and PD-L1 Immunohistochemistry Biomarkers in 312 Patients with Breast Cancer. Oncologist, 2020, 25, 943-953.	3.7	19
111	Next-Generation Sequencing Reveals Potentially Actionable Alterations in the Majority of Patients With Lymphoid Malignancies. JCO Precision Oncology, 2017, 1, 1-13.	3.0	18
112	Unusually long-term responses to vemurafenib in BRAF V600E mutated colon and thyroid cancers followed by the development of rare RAS activating mutations. Cancer Biology and Therapy, 2018, 19, 871-874.	3.4	18
113	Multiple configurations of EGFR exon 20 resistance mutations after first- and third-generation EGFR TKI treatment affect treatment options in NSCLC. PLoS ONE, 2018, 13, e0208097.	2.5	17
114	Clinical and Genomic Characteristics of Small Cell Lung Cancer in Never Smokers. Chest, 2020, 158, 1723-1733.	0.8	16
115	Patient-matched tissue and liquid biopsies identify shared and acquired genomic alterations in breast cancer.. Journal of Clinical Oncology, 2020, 38, 1050-1050.	1.6	15
116	PARP Inhibitor Insensitivity to BRCA1/2 Monoallelic Mutations in Microsatellite Instability-High Cancers. JCO Precision Oncology, 2022, , .	3.0	15
117	Abstract 1599: Determining patient ancestry based on targeted tumor comprehensive genomic profiling. Cancer Research, 2019, 79, 1599-1599.	0.9	14
118	The Panâ€Cancer Landscape of Coamplification of the Tyrosine Kinases KIT, KDR, and PDGFRA. Oncologist, 2020, 25, e39-e47.	3.7	13
119	Pan-cancer landscape of CD274 (PD-L1) copy number changes in 244 584 patient samples and the correlation with PD-L1 protein expression. , 2021, 9, e002680.		13
120	Genomic profiling of solid tumors harboring BRD4-NUT and response to immune checkpoint inhibitors. Translational Oncology, 2021, 14, 101184.	3.7	13
121	Characterization of Nonâ€“Small-Cell Lung Cancers With MET Exon 14 Skipping Alterations Detected in Tissue or Liquid: Clinicogenomics and Real-World Treatment Patterns. JCO Precision Oncology, 2021, 5, 1354-1376.	3.0	12
122	An ErbB2 splice variant lacking exon 16 drives lung carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20139-20148.	7.1	11
123	Landscape of Biomarkers in Non-small Cell Lung Cancer Using Comprehensive Genomic Profiling and PD-L1 Immunohistochemistry. Pathology and Oncology Research, 2021, 27, 592997.	1.9	11
124	Pan-cancer analysis of FGFR1-3 genomic alterations to reveal a complex molecular landscape.. Journal of Clinical Oncology, 2020, 38, 3620-3620.	1.6	10
125	Early-onset metastatic and clinically advanced prostate cancer is a distinct clinical and molecular entity characterized by increased TMPRSS2â€“ERG fusions. Prostate Cancer and Prostatic Diseases, 2021, 24, 558-566.	3.9	9
126	Concomitant targeting of the mTOR/MAPK pathways: novel therapeutic strategy in subsets of RICTOR/KRAS-altered non-small cell lung cancer. Oncotarget, 2018, 9, 33995-34008.	1.8	9

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127	Tumor mutational burden is not predictive of cytotoxic chemotherapy response. OncoImmunology, 2020, 9, 1781997.	4.6	8
128	Genomic Profiling of Combined Hepatocellular Cholangiocarcinoma Reveals Genomics Similar to Either Hepatocellular Carcinoma or Cholangiocarcinoma. JCO Precision Oncology, 2021, 5, 1285-1296.	3.0	8
129	Clinical Activity of Crizotinib in Lung Adenocarcinoma Harboring a Rare ZCCHC8-ROS1 Fusion. Journal of Thoracic Oncology, 2018, 13, e148-e150.	1.1	7
130	FoundationOne CDx testing accurately determines whole arm 1p19q codeletion status in gliomas. Neuro-Oncology Advances, 2021, 3, vdab017.	0.7	6
131	Prevalence of inferred clonal hematopoiesis (CH) detected on comprehensive genomic profiling (CGP) of solid tumor tissue or circulating tumor DNA (ctDNA).. Journal of Clinical Oncology, 2021, 39, 3009-3009.	1.6	6
132	Intra-patient stability of tumor mutational burden from tissue biopsies at different time points in advanced cancers. Genome Medicine, 2021, 13, 159.	8.2	5
133	Association of CD274 (PD-L1) Copy Number Changes with Immune Checkpoint Inhibitor Clinical Benefit in Non-Squamous Non-Small Cell Lung Cancer. Oncologist, 2022, 27, 732-739.	3.7	5
134	Patient Derived Xenograft (PDX) Models Recapitulate the Genomic-Driver Composition of Acute Leukemia Samples. Blood, 2014, 124, 286-286.	1.4	4
135	Prediction and characterization of diffuse large B-cell lymphoma cell-of-origin subtypes using targeted sequencing. Future Oncology, 2021, 17, 4171-4183.	2.4	3
136	Cancer gene profile of metastatic breast cancer.. Journal of Clinical Oncology, 2012, 30, 1015-1015.	1.6	3
137	Next-generation sequencing of FFPE solid tumor specimens for clinical use.. Journal of Clinical Oncology, 2012, 30, 10524-10524.	1.6	3
138	Tumor mutational burden (TMB) and response rates to immune checkpoint inhibitors (ICIs) targeting PD-1, CTLA-4, and combination.. Journal of Clinical Oncology, 2019, 37, 2578-2578.	1.6	3
139	Tumor mutational burden (TMB) and PD-L1 expression as predictors of response to immunotherapy (IO) in NSCLC.. Journal of Clinical Oncology, 2019, 37, 2630-2630.	1.6	3
140	ERBB2 Copy Number as a Quantitative Biomarker for Real-World Outcomes to Antiâ€“Human Epidermal Growth Factor Receptor 2 Therapy in Advanced Gastroesophageal Adenocarcinoma. JCO Precision Oncology, 2022, 6, e2100330.	3.0	3
141	Real-world (rw) analysis of quantitative MET copy number (CN) as a biomarker in NSCLC.. Journal of Clinical Oncology, 2022, 40, 9123-9123.	1.6	3
142	Primary Intraosseous Smooth Muscle Tumor of Uncertain Malignant Potential: Original Report and Molecular Characterization. Rare Tumors, 2016, 8, 155-158.	0.6	2
143	Comprehensive Genomic Profiling of Renal Cell Carcinoma at Initial Diagnosis and Putative Local Recurrence. European Urology Focus, 2018, 4, 267-269.	3.1	2
144	ERBB2 copy number (CN) as a quantitative biomarker for real-world (RW) outcomes to anti-HER2 therapy in advanced gastroesophageal adenocarcinoma (adv GEA).. Journal of Clinical Oncology, 2021, 39, 4045-4045.	1.6	2

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145	Patient Derived Xenograft (PDX) Models Faithfully Recapitulate The Genetic Composition Of Primary AML. Blood, 2013, 122, 1328-1328.	1.4	2
146	Identification Of Actionable Genomic Alterations In Hematologic Malignancies By a Clinical Next Generation Sequencing-Based Assay. Blood, 2013, 122, 230-230.	1.4	2
147	Immunotherapy predictive biomarkers in metastatic breast cancer (MBC).. Journal of Clinical Oncology, 2019, 37, 1023-1023.	1.6	2
148	PD-L1 expression, tumor mutational burden, and microsatellite instability status in 746 pancreas ductal adenocarcinomas.. Journal of Clinical Oncology, 2020, 38, 757-757.	1.6	2
149	Computational and Functional Analyses of HER2 Mutations Reveal Allosteric Activation Mechanisms and Altered Pharmacologic Effects. Cancer Research, 2023, 83, 1531-1542.	0.9	2
150	Clustered 8-Oxo-Guanine Mutations and Oncogenic Gene Fusions in Microsatellite-Unstable Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100477.	3.0	2
151	Identification of potential germline (GL) variants by routine clinical comprehensive genomic profiling (CGP) and confirmatory GL testing in 24 tumor types.. Journal of Clinical Oncology, 2021, 39, 10596-10596.	1.6	1
152	Analysis of real-world (RW) data for metastatic breast cancer (mBC) patients (pts) with somatic BRCA1/2 (sBRCA) or other homologous recombination (HR)-pathway gene mutations (muts) treated with PARP inhibitors (PARPi).. Journal of Clinical Oncology, 2021, 39, 10512-10512.	1.6	1
153	Mutation Load and a Functional T Effector Signature May Distinguish Immunologically Distinct and Clinically Relevant Lymphoma Subsets. Blood, 2016, 128, 913-913.	1.4	1
154	Exploring impact of mutations in non-BRCA DNA damage response (DDR) and non-DDR genes on efficacy in phase III EMBRACA study of talazoparib (TALA) in patients (pts) with germline BRCA1/2 mutated (gBRCAm) HER2-negative (HER2-) advanced breast cancer (ABC).. Journal of Clinical Oncology, 2020, 38, 1018-1018.	1.6	1
155	Response of a Metastatic Breast Carcinoma With a Previously Uncharacterized ERBB2 G776V Mutation to Human Epidermal Growth Factor Receptor 2â€“Targeted Therapy. JCO Precision Oncology, 2017, 1, 1-9.	3.0	0
156	Frequency of longitudinal changes in TP53 mutation status from gene sequencing of serial tumor biopsies from a large cohort of cancer patients.. Journal of Clinical Oncology, 2021, 39, 3124-3124.	1.6	0
157	Real-world pan-cancer landscape of frameshift mutations (FSM) and their role in predicting responses to immune checkpoint inhibitors (ICI) in patients (pts) with tumors with low tumor mutational burden (TMB).. Journal of Clinical Oncology, 2021, 39, 2599-2599.	1.6	0
158	Abstract 2233: Landscape of driver mutations in MAPK/PI3K/AKT signaling pathways reveals insights into therapeutic targeting strategies. , 2021, , .		0
159	Identifying cancer mutations in neuroendocrine prostate cancer (NEPC) through massively parallel DNA sequencing of formalin-fixed paraffin-embedded (FFPE) tissue.. Journal of Clinical Oncology, 2012, 30, 110-110.	1.6	0
160	Targeted next-generation sequencing (NGS) of advanced prostate cancer (PCA) using formalin-fixed tissue.. Journal of Clinical Oncology, 2012, 30, 4649-4649.	1.6	0
161	Concordance of driver mutations in primary and matched metastasis from patients with non-small cell lung cancer (NSCLC) using next-generation sequencing (NGS).. Journal of Clinical Oncology, 2012, 30, 7529-7529.	1.6	0
162	RICTOR amplification as a novel therapeutic target for lung cancer brain metastases.. Journal of Clinical Oncology, 2020, 38, 3597-3597.	1.6	0

#	Article	IF	Citations
163	PATH-16. COMPREHENSIVE GENOMIC PROFILING ACCURATELY DETERMINES 1p19q CODELETION STATUS IN GLIOMAS. Neuro-Oncology, 2020, 22, ii167-ii167.	1.2	0