

# Garrett M Frampton

## List of Publications by Year in descending order

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163  
papers

31,062  
citations

15880

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8627

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164  
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164  
docs citations

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times ranked

48213  
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational and Functional Analyses of HER2 Mutations Reveal Allosteric Activation Mechanisms and Altered Pharmacologic Effects. <i>Cancer Research</i> , 2023, 83, 1531-1542.	0.4	2
2	ERBB2 Copy Number as a Quantitative Biomarker for Real-World Outcomes to Anti-HER2 Human Epidermal Growth Factor Receptor 2 Therapy in Advanced Gastroesophageal Adenocarcinoma. <i>JCO Precision Oncology</i> , 2022, 6, e2100330.	1.5	3
3	Clinical and analytical validation of FoundationOne®CDx, a comprehensive genomic profiling assay for solid tumors. <i>PLoS ONE</i> , 2022, 17, e0264138.	1.1	100
4	Comprehensive characterization of PTEN mutational profile in a series of 34,129 colorectal cancers. <i>Nature Communications</i> , 2022, 13, 1618.	5.8	23
5	The Genomics of Colorectal Cancer in Populations with African and European Ancestry. <i>Cancer Discovery</i> , 2022, 12, 1282-1293.	7.7	28
6	Association of CD274 (PD-L1) Copy Number Changes with Immune Checkpoint Inhibitor Clinical Benefit in Non-Squamous Non-Small Cell Lung Cancer. <i>Oncologist</i> , 2022, 27, 732-739.	1.9	5
7	Clustered 8-Oxo-Guanine Mutations and Oncogenic Gene Fusions in Microsatellite-Unstable Colorectal Cancer. <i>JCO Precision Oncology</i> , 2022, 6, e2100477.	1.5	2
8	Real-world (rw) analysis of quantitative MET copy number (CN) as a biomarker in NSCLC. <i>Journal of Clinical Oncology</i> , 2022, 40, 9123-9123.	0.8	3
9	Clinical genomic profiling in the management of patients with soft tissue and bone sarcoma. <i>Nature Communications</i> , 2022, 13, .	5.8	51
10	PARP Inhibitor Insensitivity to BRCA1/2 Monoallelic Mutations in Microsatellite Instability-High Cancers. <i>JCO Precision Oncology</i> , 2022, .	1.5	15
11	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. <i>Cancer Discovery</i> , 2021, 11, 282-292.	7.7	132
12	Early-onset metastatic and clinically advanced prostate cancer is a distinct clinical and molecular entity characterized by increased TMPRSS2-ERG fusions. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 558-566.	2.0	9
13	FoundationOne CDx testing accurately determines whole arm 1p19q codeletion status in gliomas. <i>Neuro-Oncology Advances</i> , 2021, 3, vdab017.	0.4	6
14	Landscape of Biomarkers in Non-small Cell Lung Cancer Using Comprehensive Genomic Profiling and PD-L1 Immunohistochemistry. <i>Pathology and Oncology Research</i> , 2021, 27, 592997.	0.9	11
15	Frequency of longitudinal changes in TP53 mutation status from gene sequencing of serial tumor biopsies from a large cohort of cancer patients. <i>Journal of Clinical Oncology</i> , 2021, 39, 3124-3124.	0.8	0
16	ERBB2 copy number (CN) as a quantitative biomarker for real-world (RW) outcomes to anti-HER2 therapy in advanced gastroesophageal adenocarcinoma (adv GEA). <i>Journal of Clinical Oncology</i> , 2021, 39, 4045-4045.	0.8	2
17	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
18	Prevalence of inferred clonal hematopoiesis (CH) detected on comprehensive genomic profiling (CGP) of solid tumor tissue or circulating tumor DNA (ctDNA). <i>Journal of Clinical Oncology</i> , 2021, 39, 3009-3009.	0.8	6

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19	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.	0.8	1
20	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.	0.8	0
21	Analysis of real-world (RW) data for metastatic breast cancer (mBC) patients (pts) with somatic <i>BRCA1/2</i> (<i>sBRCA</i>) or other homologous recombination (HR)-pathway gene mutations (mut) treated with PARP inhibitors (PARPi).. Journal of Clinical Oncology, 2021, 39, 10512-10512.	0.8	1
22	Prediction and characterization of diffuse large B-cell lymphoma cell-of-origin subtypes using targeted sequencing. Future Oncology, 2021, 17, 4171-4183.	1.1	3
23	Abstract 2233: Landscape of driver mutations in MAPK/PI3K/AKT signaling pathways reveals insights into therapeutic targeting strategies. , 2021, , .		0
24	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.	1.5	12
25	Genomic Profiling of Combined Hepatocellular Cholangiocarcinoma Reveals Genomics Similar to Either Hepatocellular Carcinoma or Cholangiocarcinoma. JCO Precision Oncology, 2021, 5, 1285-1296.	1.5	8
26	Genomic profiling of solid tumors harboring BRD4-NUT and response to immune checkpoint inhibitors. Translational Oncology, 2021, 14, 101184.	1.7	13
27	Intra-patient stability of tumor mutational burden from tissue biopsies at different time points in advanced cancers. Genome Medicine, 2021, 13, 159.	3.6	5
28	Tumor Mutational Burden as a Predictive Biomarker for Response to Immune Checkpoint Inhibitors: A Review of Current Evidence. Oncologist, 2020, 25, e147-e159.	1.9	220
29	The Panâ€“Cancer Landscape of Coamplification of the Tyrosine Kinases KIT, KDR, and PDGFRA. Oncologist, 2020, 25, e39-e47.	1.9	13
30	Characterization of Clinical Cases of Malignant PEComa via Comprehensive Genomic Profiling of DNA and RNA. Oncology, 2020, 98, 905-912.	0.9	27
31	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.	1.9	19
32	Tumor mutational burden is not predictive of cytotoxic chemotherapy response. OncoImmunology, 2020, 9, 1781997.	2.1	8
33	Genomic Profiling of Prostate Cancers from Men with African and European Ancestry. Clinical Cancer Research, 2020, 26, 4651-4660.	3.2	68
34	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.	3.3	11
35	High Tumor Mutational Burden Correlates with Longer Survival in Immunotherapy-Naïve Patients with Diverse Cancers. Molecular Cancer Therapeutics, 2020, 19, 2139-2145.	1.9	50
36	Prevalence of High Tumor Mutational Burden and Association With Survival in Patients With Less Common Solid Tumors. JAMA Network Open, 2020, 3, e2025109.	2.8	92

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37	MHC-I genotype and tumor mutational burden predict response to immunotherapy. <i>Genome Medicine</i> , 2020, 12, 45.	3.6	70
38	Pan-Cancer Analysis of <i>BRCA1</i> and <i>BRCA2</i> Genomic Alterations and Their Association With Genomic Instability as Measured by Genome-Wide Loss of Heterozygosity. <i>JCO Precision Oncology</i> , 2020, 4, 442-465.	1.5	103
39	The genomic landscape of metastatic breast cancer: Insights from 11,000 tumors. <i>PLoS ONE</i> , 2020, 15, e0231999.	1.1	36
40	Clinical and Genomic Characteristics of Small Cell Lung Cancer in Never Smokers. <i>Chest</i> , 2020, 158, 1723-1733.	0.4	16
41	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020, 580, 517-523.	13.7	374
42	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	7.7	151
43	Pan-cancer analysis of <i>FGFR1-3</i> genomic alterations to reveal a complex molecular landscape.. <i>Journal of Clinical Oncology</i> , 2020, 38, 3620-3620.	0.8	10
44	Characterization of 1,387 NSCLCs with <i>MET</i> exon 14 ( <i>METex14</i> ) skipping alterations (SA) and potential acquired resistance (AR) mechanisms.. <i>Journal of Clinical Oncology</i> , 2020, 38, 9511-9511.	0.8	22
45	<i>RICTOR</i> amplification as a novel therapeutic target for lung cancer brain metastases.. <i>Journal of Clinical Oncology</i> , 2020, 38, 3597-3597.	0.8	0
46	Patient-matched tissue and liquid biopsies identify shared and acquired genomic alterations in breast cancer.. <i>Journal of Clinical Oncology</i> , 2020, 38, 1050-1050.	0.8	15
47	Exploring impact of mutations in non- <i>BRCA</i> DNA damage response (DDR) and non-DDR genes on efficacy in phase III <i>EMBRACA</i> study of talazoparib (TALA) in patients (pts) with germline <i>BRCA1/2</i> mutated (gBRCAm) <i>HER2</i> -negative ( <i>HER2</i> -) advanced breast cancer (ABC).. <i>Journal of Clinical Oncology</i> , 2020, 38, 1018-1018.	0.8	1
48	<i>PD-L1</i> expression, tumor mutational burden, and microsatellite instability status in 746 pancreas ductal adenocarcinomas.. <i>Journal of Clinical Oncology</i> , 2020, 38, 757-757.	0.8	2
49	<i>PATH-16</i> . COMPREHENSIVE GENOMIC PROFILING ACCURATELY DETERMINES 1p19q CODELETION STATUS IN GLIOMAS. <i>Neuro-Oncology</i> , 2020, 22, ii167-ii167.	0.6	0
50	Comprehensive characterization of <i>RAS</i> mutations in colon and rectal cancers in old and young patients. <i>Nature Communications</i> , 2019, 10, 3722.	5.8	131
51	Microsatellite-Stable Tumors with High Mutational Burden Benefit from Immunotherapy. <i>Cancer Immunology Research</i> , 2019, 7, 1570-1573.	1.6	190
52	Comprehensive Genomic Landscapes in Early and Later Onset Colorectal Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 5852-5858.	3.2	116
53	<i>PARP-1</i> activity (PAR) determines the sensitivity of cervical cancer to olaparib. <i>Gynecologic Oncology</i> , 2019, 155, 144-150.	0.6	28
54	A Novel Next-Generation Sequencing Approach to Detecting Microsatellite Instability and Pan-Tumor Characterization of 1000 Microsatellite Instability-High Cases in 67,000 Patient Samples. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 1053-1066.	1.2	147

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55	Clinical and Immunological Implications of Frameshift Mutations in Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1807-1817.	0.5	27
56	Pan-Cancer Landscape and Analysis of ERBB2 Mutations Identifies Poziotinib as a Clinically Active Inhibitor and Enhancer of T-DM1 Activity. <i>Cancer Cell</i> , 2019, 36, 444-457.e7.	7.7	145
57	Prospective Comprehensive Genomic Profiling of Primary and Metastatic Prostate Tumors. <i>JCO Precision Oncology</i> , 2019, 3, 1-23.	1.5	63
58	Phenotypic and Genomic Determinants of Immunotherapy Response Associated with Squamousness. <i>Cancer Immunology Research</i> , 2019, 7, 866-873.	1.6	23
59	Association of Patient Characteristics and Tumor Genomics With Clinical Outcomes Among Patients With Non-Small Cell Lung Cancer Using a Clinicogenomic Database. <i>JAMA - Journal of the American Medical Association</i> , 2019, 321, 1391.	3.8	370
60	Analysis of DNA Damage Response Gene Alterations and Tumor Mutational Burden Across 17,486 Tubular Gastrointestinal Carcinomas: Implications for Therapy. <i>Oncologist</i> , 2019, 24, 1340-1347.	1.9	73
61	Pan-Cancer Analysis of CDK12 Loss-of-Function Alterations and Their Association with the Focal Tandem-Duplicator Phenotype. <i>Oncologist</i> , 2019, 24, 1526-1533.	1.9	39
62	The Genomic Landscape of Merkel Cell Carcinoma and Clinicogenomic Biomarkers of Response to Immune Checkpoint Inhibitor Therapy. <i>Clinical Cancer Research</i> , 2019, 25, 5961-5971.	3.2	118
63	Loss of function of NF1 is a mechanism of acquired resistance to endocrine therapy in lobular breast cancer. <i>Annals of Oncology</i> , 2019, 30, 115-123.	0.6	63
64	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. <i>Oncoimmunology</i> , 2019, 8, 1550341.	2.1	60
65	Abstract 1599: Determining patient ancestry based on targeted tumor comprehensive genomic profiling. <i>Cancer Research</i> , 2019, 79, 1599-1599.	0.4	14
66	PD-L1 expression and tumor mutational burden are independent biomarkers in most cancers. <i>JCI Insight</i> , 2019, 4, .	2.3	345
67	Immunotherapy predictive biomarkers in metastatic breast cancer (MBC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 1023-1023.	0.8	2
68	Tumor mutational burden (TMB) and response rates to immune checkpoint inhibitors (ICIs) targeting PD-1, CTLA-4, and combination.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2578-2578.	0.8	3
69	Tumor mutational burden (TMB) and PD-L1 expression as predictors of response to immunotherapy (IO) in NSCLC.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2630-2630.	0.8	3
70	Comprehensive genomic profiling in FIGHT-202 reveals the landscape of actionable alterations in advanced cholangiocarcinoma.. <i>Journal of Clinical Oncology</i> , 2019, 37, 4080-4080.	0.8	25
71	Profiling of 3,634 cholangiocarcinomas (CCA) to identify genomic alterations (GA), tumor mutational burden (TMB), and genomic loss of heterozygosity (gLOH).. <i>Journal of Clinical Oncology</i> , 2019, 37, 4087-4087.	0.8	42
72	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. <i>Blood</i> , 2018, 131, 2501-2505.	0.6	57

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73	Targeting HER2 in colorectal cancer: The landscape of amplification and short variant mutations in <i>ERBB2</i> and <i>ERBB3</i> . <i>Cancer</i> , 2018, 124, 1358-1373.	2.0	151
74	Recurrent hyperactive ESR1 fusion proteins in endocrine therapy-resistant breast cancer. <i>Annals of Oncology</i> , 2018, 29, 872-880.	0.6	73
75	RET fusions in a small subset of advanced colorectal cancers at risk of being neglected. <i>Annals of Oncology</i> , 2018, 29, 1394-1401.	0.6	72
76	Comprehensive Genomic Profiling of Renal Cell Carcinoma at Initial Diagnosis and Putative Local Recurrence. <i>European Urology Focus</i> , 2018, 4, 267-269.	1.6	2
77	Genomic landscape of advanced basal cell carcinoma: Implications for precision treatment with targeted and immune therapies. <i>Oncotarget</i> , 2018, 7, e1404217.	2.1	41
78	<i>BRAF</i> in Lung Cancers: Analysis of Patient Cases Reveals Recurrent <i>BRAF</i> Mutations, Fusions, Kinase Duplications, and Concurrent Alterations. <i>JCO Precision Oncology</i> , 2018, 2, 1-15.	1.5	24
79	Beyond microsatellite testing: assessment of tumor mutational burden identifies subsets of colorectal cancer who may respond to immune checkpoint inhibition. <i>Journal of Gastrointestinal Oncology</i> , 2018, 9, 610-617.	0.6	192
80	Clinical utility of tumor genomic profiling in patients with high plasma circulating tumor DNA burden or metabolically active tumors. <i>Journal of Hematology and Oncology</i> , 2018, 11, 129.	6.9	27
81	Multiple configurations of EGFR exon 20 resistance mutations after first- and third-generation EGFR TKI treatment affect treatment options in NSCLC. <i>PLoS ONE</i> , 2018, 13, e0208097.	1.1	17
82	Successful Treatment of HIV-Associated Kaposi Sarcoma with Immune Checkpoint Blockade. <i>Cancer Immunology Research</i> , 2018, 6, 1129-1135.	1.6	81
83	<i>GNAS</i> , <i>GNAQ</i> and <i>GNA11</i> alterations in patients with diverse cancers. <i>Cancer</i> , 2018, 124, 4080-4089.	2.0	34
84	Diverse EGFR Exon 20 Insertions and Co-Occurring Molecular Alterations Identified by Comprehensive Genomic Profiling of NSCLC. <i>Journal of Thoracic Oncology</i> , 2018, 13, 1560-1568.	0.5	158
85	<i>STK11/LKB1</i> Mutations and PD-1 Inhibitor Resistance in <i>KRAS</i> -Mutant Lung Adenocarcinoma. <i>Cancer Discovery</i> , 2018, 8, 822-835.	7.7	1,108
86	Analytical Validation of a Hybrid Capture-Based Next-Generation Sequencing Clinical Assay for Genomic Profiling of Cell-Free Circulating Tumor DNA. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 686-702.	1.2	149
87	Clinical Activity of Crizotinib in Lung Adenocarcinoma Harboring a Rare ZCCHC8-ROS1 Fusion. <i>Journal of Thoracic Oncology</i> , 2018, 13, e148-e150.	0.5	7
88	Unusually long-term responses to vemurafenib in BRAF V600E mutated colon and thyroid cancers followed by the development of rare RAS activating mutations. <i>Cancer Biology and Therapy</i> , 2018, 19, 871-874.	1.5	18
89	Prevalence of <i>PDL1</i> Amplification and Preliminary Response to Immune Checkpoint Blockade in Solid Tumors. <i>JAMA Oncology</i> , 2018, 4, 1237.	3.4	214
90	A computational approach to distinguish somatic vs. germline origin of genomic alterations from deep sequencing of cancer specimens without a matched normal. <i>PLoS Computational Biology</i> , 2018, 14, e1005965.	1.5	191

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91	Characterization of Clinical Cases of Advanced Papillary Renal Cell Carcinoma via Comprehensive Genomic Profiling. <i>European Urology</i> , 2018, 73, 71-78.	0.9	87
92	Concomitant targeting of the mTOR/MAPK pathways: novel therapeutic strategy in subsets of <i>RICTOR/KRAS</i> -altered non-small cell lung cancer. <i>Oncotarget</i> , 2018, 9, 33995-34008.	0.8	9
93	Comprehensive genomic profiling identifies novel NTRK fusions in neuroendocrine tumors. <i>Oncotarget</i> , 2018, 9, 35809-35812.	0.8	39
94	Patient-derived xenotransplants can recapitulate the genetic driver landscape of acute leukemias. <i>Leukemia</i> , 2017, 31, 151-158.	3.3	57
95	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. <i>Cancer Research</i> , 2017, 77, 509-519.	0.4	75
96	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. <i>Cancer Research</i> , 2017, 77, 2464-2475.	0.4	93
97	Severe nivolumab-induced pneumonitis preceding durable clinical remission in a patient with refractory, metastatic lung squamous cell cancer: a case report. <i>Journal of Hematology and Oncology</i> , 2017, 10, 64.	6.9	30
98	Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden. <i>Genome Medicine</i> , 2017, 9, 34.	3.6	2,480
99	OA20.01 Tumor Mutation Burden (TMB) is Associated with Improved Efficacy of Atezolizumab in 1L and 2L+ NSCLC Patients. <i>Journal of Thoracic Oncology</i> , 2017, 12, S321-S322.	0.5	80
100	HER2-Overexpressing Breast Cancers Amplify FGFR Signaling upon Acquisition of Resistance to Dual Therapeutic Blockade of HER2. <i>Clinical Cancer Research</i> , 2017, 23, 4323-4334.	3.2	64
101	Clinical Benefit in Response to Palbociclib Treatment in Refractory Uterine Leiomyosarcomas with a Common <i>CDKN2A</i> Alteration. <i>Oncologist</i> , 2017, 22, 416-421.	1.9	46
102	Pulmonary Sarcomatoid Carcinomas Commonly Harbor Either Potentially Targetable Genomic Alterations or High Tumor Mutational Burden as Observed by Comprehensive Genomic Profiling. <i>Journal of Thoracic Oncology</i> , 2017, 12, 932-942.	0.5	129
103	Hybrid capture-based genomic profiling of circulating tumor DNA from patients with estrogen receptor-positive metastatic breast cancer. <i>Annals of Oncology</i> , 2017, 28, 2866-2873.	0.6	67
104	<i>ALK</i> Fusions in a Wide Variety of Tumor Types Respond to Anti-ALK Targeted Therapy. <i>Oncologist</i> , 2017, 22, 1444-1450.	1.9	81
105	General paucity of genomic alteration and low tumor mutation burden in refractory and metastatic hepatoblastoma: comprehensive genomic profiling study. <i>Human Pathology</i> , 2017, 70, 84-91.	1.1	20
106	Tumor Mutational Burden as an Independent Predictor of Response to Immunotherapy in Diverse Cancers. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2598-2608.	1.9	1,779
107	Comprehensive Genomic Profiling of 282 Pediatric Low- and High-Grade Gliomas Reveals Genomic Drivers, Tumor Mutational Burden, and Hypermutation Signatures. <i>Oncologist</i> , 2017, 22, 1478-1490.	1.9	176
108	Comprehensive genomic profiles of metastatic and relapsed salivary gland carcinomas are associated with tumor type and reveal new routes to targeted therapies. <i>Annals of Oncology</i> , 2017, 28, 2539-2546.	0.6	84

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109	Mutation load and an effector T-cell gene signature may distinguish immunologically distinct and clinically relevant lymphoma subsets. <i>Blood Advances</i> , 2017, 1, 1884-1890.	2.5	40
110	Response of a Metastatic Breast Carcinoma With a Previously Uncharacterized ERBB2 G776V Mutation to Human Epidermal Growth Factor Receptor 2-Targeted Therapy. <i>JCO Precision Oncology</i> , 2017, 1, 1-9.	1.5	0
111	First-in-Human Phase I Study of the Tamoxifen Metabolite Z-Endoxifen in Women With Endocrine-Refractory Metastatic Breast Cancer. <i>Journal of Clinical Oncology</i> , 2017, 35, 3391-3400.	0.8	58
112	Next-Generation Sequencing Reveals Potentially Actionable Alterations in the Majority of Patients With Lymphoid Malignancies. <i>JCO Precision Oncology</i> , 2017, 1, 1-13.	1.5	18
113	Primary Intraosseous Smooth Muscle Tumor of Uncertain Malignant Potential: Original Report and Molecular Characterization. <i>Rare Tumors</i> , 2016, 8, 155-158.	0.3	2
114	Metastatic basal cell carcinoma with amplification of PD-L1: exceptional response to anti-PD1 therapy. <i>Npj Genomic Medicine</i> , 2016, 1, .	1.7	103
115	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. <i>Oncologist</i> , 2016, 21, 684-691.	1.9	85
116	Comprehensive genomic profiling of anal squamous cell carcinoma reveals distinct genomically defined classes. <i>Annals of Oncology</i> , 2016, 27, 1336-1341.	0.6	78
117	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. <i>Blood</i> , 2016, 127, 3004-3014.	0.6	244
118	Targeted Next Generation Sequencing Identifies Markers of Response to PD-1 Blockade. <i>Cancer Immunology Research</i> , 2016, 4, 959-967.	1.6	428
119	Characterization of 298 Patients with Lung Cancer Harboring MET Exon 14 Skipping Alterations. <i>Journal of Thoracic Oncology</i> , 2016, 11, 1493-1502.	0.5	288
120	Comprehensive Genomic Profiling Identifies a Subset of Crizotinib-Responsive <i>ALK</i> -Rearranged Non-Small Cell Lung Cancer Not Detected by Fluorescence In Situ Hybridization. <i>Oncologist</i> , 2016, 21, 762-770.	1.9	119
121	Correlation Between Molecular Subclassifications of Clear Cell Renal Cell Carcinoma and Targeted Therapy Response. <i>European Urology Focus</i> , 2016, 2, 204-209.	1.6	40
122	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. <i>Oncologist</i> , 2016, 21, 33-39.	1.9	69
123	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. <i>Lancet, The</i> , 2016, 387, 1909-1920.	6.3	3,077
124	Comprehensive Genomic Profiling Identifies Frequent Drug-Sensitive EGFR Exon 19 Deletions in NSCLC not Identified by Prior Molecular Testing. <i>Clinical Cancer Research</i> , 2016, 22, 3281-3285.	3.2	33
125	Mutation Load and a Functional T Effector Signature May Distinguish Immunologically Distinct and Clinically Relevant Lymphoma Subsets. <i>Blood</i> , 2016, 128, 913-913.	0.6	1
126	MET 14 Deletion in Sarcomatoid Non-Small-Cell Lung Cancer Detected by Next-Generation Sequencing and Successfully Treated with a MET Inhibitor. <i>Journal of Thoracic Oncology</i> , 2015, 10, e113-e114.	0.5	42



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127	Activation of MET via Diverse Exon 14 Splicing Alterations Occurs in Multiple Tumor Types and Confers Clinical Sensitivity to MET Inhibitors. <i>Cancer Discovery</i> , 2015, 5, 850-859.	7.7	632
128	Genomic alterations in head and neck squamous cell carcinoma determined by cancer gene-targeted sequencing. <i>Annals of Oncology</i> , 2015, 26, 1216-1223.	0.6	163
129	Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i> -Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. <i>Cancer Discovery</i> , 2015, 5, 860-877.	7.7	696
130	Comparative analysis of primary tumour and matched metastases in colorectal cancer patients: Evaluation of concordance between genomic and transcriptional profiles. <i>European Journal of Cancer</i> , 2015, 51, 791-799.	1.3	83
131	Oncogenic Alterations in <i>ERBB2/HER2</i> Represent Potential Therapeutic Targets Across Tumors From Diverse Anatomic Sites of Origin. <i>Oncologist</i> , 2015, 20, 7-12.	1.9	69
132	A High Frequency of Activating Extracellular Domain <i>ERBB2</i> ( <i>HER2</i> ) Mutation in Micropapillary Urothelial Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 68-75.	3.2	120
133	Comprehensive Genomic Profiling of Pancreatic Acinar Cell Carcinomas Identifies Recurrent <i>RAF</i> Fusions and Frequent Inactivation of DNA Repair Genes. <i>Cancer Discovery</i> , 2014, 4, 1398-1405.	7.7	151
134	Emergence of Constitutively Active Estrogen Receptor Mutations in Pretreated Advanced Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 1757-1767.	3.2	529
135	Concordance of Genomic Alterations between Primary and Recurrent Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 1382-1389.	1.9	104
136	Patient Derived Xenograft (PDX) Models Recapitulate the Genomic-Driver Composition of Acute Leukemia Samples. <i>Blood</i> , 2014, 124, 286-286.	0.6	4
137	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. <i>Nature Biotechnology</i> , 2013, 31, 1023-1031.	9.4	1,785
138	Next-Generation Sequencing Reveals High Concordance of Recurrent Somatic Alterations Between Primary Tumor and Metastases From Patients With Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 2167-2172.	0.8	170
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