Vincent A Miller

List of Publications by Year
in descending order

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		13087	7340
423	25,458	68	152
papers	citations	h-index	g-index

424	424	424	30590
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	EGF receptor gene mutations are common in lung cancers from "never smokers" and are associated with sensitivity of tumors to gefitinib and erlotinib. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13306-13311.	3.3	4,106
2	Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden. Genome Medicine, 2017, 9, 34.	3.6	2,480
3	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	9.4	1,785
4	Tumor Mutational Burden as an Independent Predictor of Response to Immunotherapy in Diverse Cancers. Molecular Cancer Therapeutics, 2017, 16, 2598-2608.	1.9	1,779
5	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.	7.7	696
6	Emergence of Constitutively Active Estrogen Receptor-Î± Mutations in Pretreated Advanced Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2014, 20, 1757-1767.	3.2	529
7	Kinase fusions are frequent in Spitz tumours and spitzoid melanomas. Nature Communications, 2014, 5, 3116.	5.8	521
8	Molecular profiling of cancer patients enables personalized combination therapy: the I-PREDICT study. Nature Medicine, 2019, 25, 744-750.	15.2	443
9	Targeted Next Generation Sequencing Identifies Markers of Response to PD-1 Blockade. Cancer Immunology Research, 2016, 4, 959-967.	1.6	428
10	RAS/MAPK Activation Is Associated with Reduced Tumor-Infiltrating Lymphocytes in Triple-Negative Breast Cancer: Therapeutic Cooperation Between MEK and PD-1/PD-L1 Immune Checkpoint Inhibitors. Clinical Cancer Research, 2016, 22, 1499-1509.	3.2	428
11	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. Cancer Discovery, 2016, 6, 154-165.	7.7	372
12	Inflammatory Myofibroblastic Tumors Harbor Multiple Potentially Actionable Kinase Fusions. Cancer Discovery, 2014, 4, 889-895.	7.7	334
13	Biliary cancer: Utility of nextâ€generation sequencing for clinical management. Cancer, 2016, 122, 3838-3847.	2.0	289
14	Characterization of 298 Patients with Lung Cancer Harboring MET Exon 14 Skipping Alterations. Journal of Thoracic Oncology, 2016, 11, 1493-1502.	0.5	288
15	The distribution of <scp>BRAF</scp> gene fusions in solid tumors and response to targeted therapy. International Journal of Cancer, 2016, 138, 881-890.	2.3	248
16	Impact of EML4-ALK Variant on Resistance Mechanisms and Clinical Outcomes in ALK-Positive Lung Cancer. Journal of Clinical Oncology, 2018, 36, 1199-1206.	0.8	246
17	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood, 2016, 127, 3004-3014.	0.6	244
18	Genomic and functional analysis of leukemic transformation of myeloproliferative neoplasms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5401-10.	3.3	238

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19	Broad, Hybrid Captureâ€“Based Next-Generation Sequencing Identifies Actionable Genomic Alterations in Lung Adenocarcinomas Otherwise Negative for Such Alterations by Other Genomic Testing Approaches. Clinical Cancer Research, 2015, 21, 3631-3639.	3.2	236
20	Real-Time Targeted Genome Profile Analysis of Pancreatic Ductal Adenocarcinomas Identifies Genetic Alterations That Might Be Targeted With Existing Drugs or Used as Biomarkers. Gastroenterology, 2019, 156, 2242-2253.e4.	0.6	224
21	Prevalence of PDL1 Amplification and Preliminary Response to Immune Checkpoint Blockade in Solid Tumors. JAMA Oncology, 2018, 4, 1237.	3.4	214
22	Lung Master Protocol (Lung-MAP)â€”A Biomarker-Driven Protocol for Accelerating Development of Therapies for Squamous Cell Lung Cancer: SWOG S1400. Clinical Cancer Research, 2015, 21, 1514-1524.	3.2	205
23	Cancer Therapy Directed by Comprehensive Genomic Profiling: A Single Center Study. Cancer Research, 2016, 76, 3690-3701.	0.4	203
24	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.	0.6	192
25	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.	1.5	191
26	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.	3.6	188
27	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.	1.9	176
28	BRAF Fusions Define a Distinct Molecular Subset of Melanomas with Potential Sensitivity to MEK Inhibition. Clinical Cancer Research, 2013, 19, 6696-6702.	3.2	160
29	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.	0.5	158
30	Genomic Profiling of Small-Bowel Adenocarcinoma. JAMA Oncology, 2017, 3, 1546.	3.4	154
31	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.	7.7	151
32	Fluorescence In Situ Hybridization, Immunohistochemistry, and Next-Generation Sequencing for Detection of EML4-ALK Rearrangement in Lung Cancer. Oncologist, 2015, 20, 316-322.	1.9	151
33	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.	1.2	149
34	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.	1.2	147
35	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.	7.7	145
36	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.	3.9	134

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37	Inactivation of Capicua drives cancer metastasis. Nature Genetics, 2017, 49, 87-96.	9.4	130
38	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.	0.5	129
39	Total mutation burden (TMB) in lung cancer (LC) and relationship with response to PD-1/PD-L1 targeted therapies.. Journal of Clinical Oncology, 2016, 34, 9017-9017.	0.8	129
40	Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy. Modern Pathology, 2014, 27, 271-280.	2.9	122
41	The Genomic Landscape of Merkel Cell Carcinoma and Clinicogenomic Biomarkers of Response to Immune Checkpoint Inhibitor Therapy. Clinical Cancer Research, 2019, 25, 5961-5971.	3.2	118
42	Genomic Characterization of Renal Cell Carcinoma with Sarcomatoid Dedifferentiation Pinpoints Recurrent Genomic Alterations. European Urology, 2016, 70, 348-357.	0.9	111
43	Triple-negative breast cancers with amplification of JAK2 at the 9p24 locus demonstrate JAK2-specific dependence. Science Translational Medicine, 2016, 8, 334ra53.	5.8	105
44	Metastatic basal cell carcinoma with amplification of PD-L1: exceptional response to anti-PD1 therapy. Npj Genomic Medicine, 2016, 1, .	1.7	103
45	Receptor Tyrosine Kinase Fusions and BRAF Kinase Fusions are Rare but Actionable Resistance Mechanisms to EGFR Tyrosine Kinase Inhibitors. Journal of Thoracic Oncology, 2018, 13, 1312-1323.	0.5	103
46	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.	1.5	103
47	Emergence of Preexisting MET Y1230C Mutation as a Resistance Mechanism to Crizotinib in NSCLC with MET Exon 14 Skipping. Journal of Thoracic Oncology, 2017, 12, 137-140.	0.5	102
48	Profiling of 149 Salivary Duct Carcinomas, Carcinoma Ex Pleomorphic Adenomas, and Adenocarcinomas, Not Otherwise Specified Reveals Actionable Genomic Alterations. Clinical Cancer Research, 2016, 22, 6061-6068.	3.2	99
49	Enrichment of Targetable Mutations in the Relapsed Neuroblastoma Genome. PLoS Genetics, 2016, 12, e1006501.	1.5	98
50	EGFR Fusions as Novel Therapeutic Targets in Lung Cancer. Cancer Discovery, 2016, 6, 601-611.	7.7	97
51	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. Cancer Research, 2017, 77, 2464-2475.	0.4	93
52	Identification of NTRK fusions in pediatric mesenchymal tumors. Pediatric Blood and Cancer, 2017, 64, e26433.	0.8	92
53	Characterization of Clinical Cases of Collecting Duct Carcinoma of the Kidney Assessed by Comprehensive Genomic Profiling. European Urology, 2016, 70, 516-521.	0.9	90
54	ROS1 Fusions Rarely Overlap with Other Oncogenic Drivers in Nonâ€“Small Cell Lung Cancer. Journal of Thoracic Oncology, 2017, 12, 872-877.	0.5	87

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55	Acquired FGFR and FGF Alterations Confer Resistance to Estrogen Receptor (ER) Targeted Therapy in ER+ Metastatic Breast Cancer. Clinical Cancer Research, 2020, 26, 5974-5989.	3.2	87
56	Characterization of Clinical Cases of Advanced Papillary Renal Cell Carcinoma via Comprehensive Genomic Profiling. European Urology, 2018, 73, 71-78.	0.9	87
57	Identification of Recurrent FGFR3â€“TACC3 Fusion Oncogenes from Lung Adenocarcinoma. Clinical Cancer Research, 2014, 20, 6551-6558.	3.2	85
58	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.	1.9	85
59	An Acquired HER2â€T798I Gatekeeper Mutation Induces Resistance to Neratinib in a Patient with HER2 Mutantâ€“Driven Breast Cancer. Cancer Discovery, 2017, 7, 575-585.	7.7	85
60	Comprehensive Genomic Profiling of Advanced Esophageal Squamous Cell Carcinomas and Esophageal Adenocarcinomas Reveals Similarities and Differences. Oncologist, 2015, 20, 1132-1139.	1.9	84
61	RICTOR Amplification Defines a Novel Subset of Patients with Lung Cancer Who May Benefit from Treatment with mTORC1/2 Inhibitors. Cancer Discovery, 2015, 5, 1262-1270.	7.7	84
62	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.	1.3	83
63	Emergence of RET rearrangement co-existing with activated EGFR mutation in EGFR -mutated NSCLC patients who had progressed on first- or second-generation EGFR TKI. Lung Cancer, 2015, 89, 357-359.	0.9	82
64	On-target Resistance to the Mutant-Selective EGFR Inhibitor Osimertinib Can Develop in an Allele-Specific Manner Dependent on the Original EGFR-Activating Mutation. Clinical Cancer Research, 2019, 25, 3341-3351.	3.2	80
65	STUMP unâ€œstumpedâ€• anti-tumor response to anaplastic lymphoma kinase (ALK) inhibitor based targeted therapy in uterine inflammatory myofibroblastic tumor with myxoid features harboring DCTN1-ALK fusion. Journal of Hematology and Oncology, 2015, 8, 66.	6.9	75
66	BRAF V600E Mutations in High-Grade Colorectal Neuroendocrine Tumors May Predict Responsiveness to BRAFâ€“MEK Combination Therapy. Cancer Discovery, 2016, 6, 594-600.	7.7	75
67	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. Cancer Research, 2017, 77, 509-519.	0.4	75
68	HER2 Transmembrane Domain (TMD) Mutations (V659/G660) That Stabilize Homo- and Heterodimerization Are Rare Oncogenic Drivers in Lung Adenocarcinoma That Respond to Afatinib. Journal of Thoracic Oncology, 2017, 12, 446-457.	0.5	75
69	Combined Blockade of Activating ERBB2 Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. Clinical Cancer Research, 2019, 25, 277-289.	3.2	74
70	TP53 Alterations Correlate with Response to VEGF/VEGFR Inhibitors: Implications for Targeted Therapeutics. Molecular Cancer Therapeutics, 2016, 15, 2475-2485.	1.9	73
71	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.	1.9	73
72	Comprehensive genomic profiling of inflammatory breast cancer cases reveals a high frequency of clinically relevant genomic alterations. Breast Cancer Research and Treatment, 2015, 154, 155-162.	1.1	72

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73	Oncogenic Alterations in ERBB2/HER2 Represent Potential Therapeutic Targets Across Tumors From Diverse Anatomic Sites of Origin. Oncologist, 2015, 20, 7-12.	1.9	69
74	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	1.9	69
75	Biomarker-driven therapies for previously treated squamous non-small-cell lung cancer (Lung-MAP) Tj ETQq1 1 0.784314 rgBT /Overlo	5.1	68
76	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or Refractory Cancers. Oncologist, 2016, 21, 1315-1325.	1.9	64
77	Detection of Known and Novel FGFR Fusions in Nonâ€“Small Cell Lung Cancer by Comprehensive Genomic Profiling. Journal of Thoracic Oncology, 2019, 14, 54-62.	0.5	64
78	Prospective Comprehensive Genomic Profiling of Primary and Metastatic Prostate Tumors. JCO Precision Oncology, 2019, 3, 1-23.	1.5	63
79	Real-time genomic profiling of histiocytoses identifies early-kinase domain BRAF alterations while improving treatment outcomes. JCI Insight, 2017, 2, e89473.	2.3	63
80	Effect of the RET Inhibitor Vandetanib in a Patient With RET Fusionâ€“Positive Metastatic Nonâ€“Small-Cell Lung Cancer. Journal of Clinical Oncology, 2016, 34, e141-e144.	0.8	60
81	Pediatric, Adolescent, and Young Adult Thyroid Carcinoma Harbors Frequent and Diverse Targetable Genomic Alterations, Including Kinase Fusions. Oncologist, 2017, 22, 255-263.	1.9	60
82	Hybrid Captureâ€“Based Genomic Profiling of Circulating Tumor DNA from Patients with Advanced Cancers of the Gastrointestinal Tract or Anus. Clinical Cancer Research, 2018, 24, 1881-1890.	3.2	59
83	Systemic and CNS activity of the RET inhibitor vandetanib combined with the mTOR inhibitor everolimus in KIF5B-RET re-arranged non-small cell lung cancer with brain metastases. Lung Cancer, 2015, 89, 76-79.	0.9	58
84	Comprehensive Genomic Profiling of Upper-tract and Bladder Urothelial Carcinoma. European Urology Focus, 2021, 7, 1339-1346.	1.6	58
85	Comprehensive genomic profiling of different subtypes of nasopharyngeal carcinoma reveals similarities and differences to guide targeted therapy. Cancer, 2017, 123, 3628-3637.	2.0	57
86	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. Blood, 2018, 131, 2501-2505.	0.6	57
87	Comprehensive genomic profiling of extrahepatic cholangiocarcinoma reveals a long tail of therapeutic targets. Journal of Clinical Pathology, 2016, 69, 403-408.	1.0	56
88	Hybrid Captureâ€“Based Genomic Profiling of Circulating Tumor DNA from Patients with Advanced Nonâ€“Small Cell Lung Cancer. Journal of Thoracic Oncology, 2019, 14, 255-264.	0.5	53
89	Checkpoint inhibitor is active against large cell neuroendocrine carcinoma with high tumor mutation burden. , 2017, 5, 75.		52
90	Clinical Benefit in Response to Palbociclib Treatment in Refractory Uterine Leiomyosarcomas with a Common CDKN2A Alteration. Oncologist, 2017, 22, 416-421.	1.9	46

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91	Response of an ERBB2-Mutated Inflammatory Breast Carcinoma to Human Epidermal Growth Factor Receptor 2â€“Targeted Therapy. Journal of Clinical Oncology, 2014, 32, e88-e91.	0.8	44
92	Emergence of FGFR3-TACC3 fusions as a potential by-pass resistance mechanism to EGFR tyrosine kinase inhibitors in EGFR mutated NSCLC patients. Lung Cancer, 2017, 111, 61-64.	0.9	44
93	Clonal diversity predicts adverse outcome in chronic lymphocytic leukemia. Leukemia, 2019, 33, 390-402.	3.3	44
94	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.	0.8	42
95	Genomic landscape of advanced basal cell carcinoma: Implications for precision treatment with targeted and immune therapies. OncoImmunology, 2018, 7, e1404217.	2.1	41
96	Comprehensive Assessment of Immuno-oncology Biomarkers in Adenocarcinoma, Urothelial Carcinoma, and Squamous-cell Carcinoma of the Bladder. European Urology, 2020, 77, 548-556.	0.9	41
97	Correlation Between Molecular Subclassifications of Clear Cell Renal Cell Carcinoma and Targeted Therapy Response. European Urology Focus, 2016, 2, 204-209.	1.6	40
98	Use of comprehensive genomic profiling to direct point-of-care management of patients with gynecologic cancers. Gynecologic Oncology, 2016, 141, 2-9.	0.6	40
99	Pan-Cancer Analysis of CDK12 Loss-of-Function Alterations and Their Association with the Focal Tandem-Duplicator Phenotype. Oncologist, 2019, 24, 1526-1533.	1.9	39
100	Comprehensive genomic profiling identifies novel NTRK fusions in neuroendocrine tumors. Oncotarget, 2018, 9, 35809-35812.	0.8	39
101	Comprehensive genomic profiling of malignant phyllodes tumors of the breast. Breast Cancer Research and Treatment, 2017, 162, 597-602.	1.1	38
102	Comprehensive Genomic Profiling of Esthesioneuroblastoma Reveals Additional Treatment Options. Oncologist, 2017, 22, 834-842.	1.9	37
103	Identification of a novel TMEM106B-ROS1 fusion variant in lung adenocarcinoma by comprehensive genomic profiling. Lung Cancer, 2015, 88, 352-354.	0.9	36
104	Phosphatidylinositol 3â€kinase pathway genomic alterations in 60,991 diverse solid tumors informs targeted therapy opportunities. Cancer, 2019, 125, 1185-1199.	2.0	36
105	Presence of both alterations in FGFR/FGF and PI3K/AKT/mTOR confer improved outcomes for patients with metastatic breast cancer treated with PI3K/AKT/mTOR inhibitors. Oncoscience, 2016, 3, 164-172.	0.9	34
106	Mutation of MET Y1230 as an Acquired Mechanism of Crizotinib Resistance in NSCLC with MET Exon 14 Skipping. Journal of Thoracic Oncology, 2017, 12, e89-e90.	0.5	34
107	BRCA2 Reversion Mutation Associated With Acquired Resistance to Olaparib in Estrogen Receptor-positive Breast Cancer Detected by Genomic Profiling of Tissue and Liquid Biopsy. Clinical Breast Cancer, 2018, 18, 184-188.	1.1	34
108	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.	3.2	33

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109	A Case of Metastatic Atypical Neuroendocrine Tumor with ALK Translocation and Diffuse Brain Metastases. Oncologist, 2017, 22, 768-773.	1.9	33
110	Targeted genomic landscape of metastases compared to primary tumours in clear cell metastatic renal cell carcinoma. British Journal of Cancer, 2018, 118, 1238-1242.	2.9	33
111	Durable Response to Crizotinib in a MET-Amplified, KRAS-Mutated Carcinoma of Unknown Primary. Case Reports in Oncology, 2014, 7, 503-508.	0.3	32
112	Antitumor Response of VEGFR2- and VEGFR3-Amplified Angiosarcoma to Pazopanib. Journal of the National Comprehensive Cancer Network: JNCCN, 2016, 14, 499-502.	2.3	32
113	Mutational Landscapes of Smoking-Related Cancers in Caucasians and African Americans: Precision Oncology Perspectives at Wake Forest Baptist Comprehensive Cancer Center. Theranostics, 2017, 7, 2914-2923.	4.6	31
114	Genomic profiling of cell-free circulating tumor DNA in patients with colorectal cancer and its fidelity to the genomics of the tumor biopsy. Journal of Gastrointestinal Oncology, 2019, 10, 831-840.	0.6	31
115	Comprehensive Genomic Profiling of Hodgkin Lymphoma Reveals Recurrently Mutated Genes and Increased Mutation Burden. Oncologist, 2019, 24, 219-228.	1.9	30
116	Genomic Features of Metastatic Testicular Sex Cord Stromal Tumors. European Urology Focus, 2019, 5, 748-755.	1.6	29
117	PIK3CA C2 Domain Deletions Hyperactivate Phosphoinositide 3-kinase (PI3K), Generate Oncogene Dependence, and Are Exquisitely Sensitive to PI3KÎ± Inhibitors. Clinical Cancer Research, 2018, 24, 1426-1435.	3.2	27
118	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.	6.9	27
119	Characterization of Clinical Cases of Malignant PEComa via Comprehensive Genomic Profiling of DNA and RNA. Oncology, 2020, 98, 905-912.	0.9	27
120	Comprehensive genetic alteration profiling in primary and recurrent glioblastoma. Journal of Neuro-Oncology, 2019, 142, 111-118.	1.4	26
121	Tumor mutational burden as a potential biomarker for PD1/PD-L1 therapy in colorectal cancer.. Journal of Clinical Oncology, 2016, 34, 3587-3587.	0.8	26
122	Impact of next-generation sequencing (NGS) on diagnostic and therapeutic options in soft-tissue and bone sarcoma.. Journal of Clinical Oncology, 2017, 35, 11001-11001.	0.8	26
123	Retrospective analysis of real-world data to determine clinical outcomes of patients with advanced non-small cell lung cancer following cell-free circulating tumor DNA genomic profiling. Lung Cancer, 2020, 148, 69-78.	0.9	25
124	Distinct age-associated molecular profiles in acute myeloid leukemia defined by comprehensive clinical genomic profiling. Oncotarget, 2018, 9, 26417-26430.	0.8	25
125	Acquired ALK L1152R Mutation Confers Resistance to Ceritinib and Predicts Response to Alectinib. Journal of Thoracic Oncology, 2016, 11, e87-e88.	0.5	24
126	RET Fusion Lung Carcinoma: Response to Therapy and Clinical Features in a Case Series of 14 Patients. Clinical Lung Cancer, 2017, 18, e223-e232.	1.1	24

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127	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.	1.5	24
128	Personalized Treatment for a Patient With aBRAFV600E Mutation Using Dabrafenib and a Tumor Treatment Fields Device in a High-Grade Glioma Arising From Ganglioglioma. Journal of the National Comprehensive Cancer Network: JNCCN, 2016, 14, 1345-1350.	2.3	23
129	Genomic Landscape of Appendiceal Neoplasms. JCO Precision Oncology, 2018, 2, 1-18.	1.5	23
130	Genomic Profiling of T-Cell Neoplasms Reveals Frequent JAK1 and JAK3 Mutations With Clonal Evasion From Targeted Therapies. JCO Precision Oncology, 2018, 2018, 1-16.	1.5	23
131	Approach to evaluating tumor mutational burden in routine clinical practice. Translational Lung Cancer Research, 2018, 7, 678-681.	1.3	23
132	Phenotypic and Genomic Determinants of Immunotherapy Response Associated with Squamousness. Cancer Immunology Research, 2019, 7, 866-873.	1.6	23
133	Antitumor Response of an ERBB2 Amplified Inflammatory Breast Carcinoma With EGFR Mutation to the EGFR-TKI Erlotinib. Clinical Breast Cancer, 2014, 14, e14-e16.	1.1	22
134	Exceptional Response on Addition of Everolimus to Taxane in Urothelial Carcinoma Bearing an NF2 Mutation. European Urology, 2015, 67, 1195-1196.	0.9	20
135	Exceptional durable response to everolimus in a patient with biphenotypic breast cancer harboring an STK11 variant. Journal of Physical Education and Sports Management, 2017, 3, a000778.	0.5	20
136	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.	1.1	20
137	MSI-H testing via hybrid capture based NGS sequencing of liquid biopsy samples.. Journal of Clinical Oncology, 2019, 37, 504-504.	0.8	19
138	Next-Generation Sequencing Reveals Potentially Actionable Alterations in the Majority of Patients With Lymphoid Malignancies. JCO Precision Oncology, 2017, 1, 1-13.	1.5	18
139	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and frequency of clinically relevant genomic alterations.. Journal of Clinical Oncology, 2015, 33, 4009-4009.	0.8	18
140	Landscape of genomic alterations (GA) and tumor mutational burden (TMB) in different metastatic melanoma (MM) subtypes.. Journal of Clinical Oncology, 2017, 35, 9536-9536.	0.8	18
141	Clinically advanced and metastatic pure mucinous carcinoma of the breast: a comprehensive genomic profiling study. Breast Cancer Research and Treatment, 2016, 155, 405-413.	1.1	17
142	Identification of a novel fusion TBL1XR1â€“PDGFRB in a patient with acute myeloid leukemia harboring the DEKâ€“NUP214 fusion and clinical response to dasatinib. Leukemia and Lymphoma, 2017, 58, 2969-2972.	0.6	17
143	Estimated Cost of Anticancer Therapy Directed by Comprehensive Genomic Profiling in a Single-Center Study. JCO Precision Oncology, 2018, 2, 1-11.	1.5	17
144	Detection of an ALK Fusion in Colorectal Carcinoma by Hybrid Capture-Based Assay of Circulating Tumor DNA. Oncologist, 2017, 22, 774-779.	1.9	16

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145	Continued use of afatinib with the addition of cetuximab after progression on afatinib in patients with EGFR mutation-positive non-small-cell lung cancer and acquired resistance to gefitinib or erlotinib. Lung Cancer, 2017, 113, 51-58.	0.9	16
146	FGFR2-Altered Gastroesophageal Adenocarcinomas Are an Uncommon Clinicopathologic Entity with a Distinct Genomic Landscape. Oncologist, 2019, 24, 1462-1468.	1.9	16
147	Unique Genomic Landscape of High-Grade Neuroendocrine Cervical Carcinoma: Implications for Rethinking Current Treatment Paradigms. JCO Precision Oncology, 2020, 4, 972-987.	1.5	16
148	Hybrid capture-based next-generation sequencing (HC NGS) in melanoma to identify markers of response to anti-PD-1/PD-L1.. Journal of Clinical Oncology, 2016, 34, 105-105.	0.8	16
149	Genomic Profiling of Circulating Tumor DNA in Relapsed EGFR -mutated Lung Adenocarcinoma Reveals an Acquired FGFR3 - TACC3 Fusion. Clinical Lung Cancer, 2017, 18, e219-e222.	1.1	15
150	MDM2 amplification (Amp) to mediate cabozantinib resistance in patients (Pts) with advanced RET-rearranged lung cancers.. Journal of Clinical Oncology, 2016, 34, 9068-9068.	0.8	15
151	Urothelial cancer harbours EGFR and HER2 amplifications and exon 20 insertions. BJU International, 2020, 125, 739-746.	1.3	14
152	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and genomic alterations.. Journal of Clinical Oncology, 2015, 33, 231-231.	0.8	14
153	Extended Antitumor Responseof a BRAF V600E Papillary Thyroid Carcinoma to Vemurafenib. Case Reports in Oncology, 2014, 7, 343-348.	0.3	13
154	Core Clinical Data Elements for Cancer Genomic Repositories: A Multi-stakeholder Consensus. Cell, 2017, 171, 982-986.	13.5	13
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