Vincent A Miller

List of Publications by Citations

423 papers	18,210 citations	60 h-index	132 g-index
424 ext. papers	22,410 ext. citations	4.7 avg, IF	6.17 L-index

#	Paper	IF	Citations
423	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, 13306-11	11.5	3659
422	Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden. *Genome Medicine*, **2017**, 9, 34	14.4	1509
421	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. *Nature Biotechnology*, **2013**, 31, 1023-31	44.5	1353
420	Tumor Mutational Burden as an Independent Predictor of Response to Immunotherapy in Diverse Cancers. *Molecular Cancer Therapeutics*, **2017**, 16, 2598-2608	6.1	1183
419	Co-occurring genomic alterations define major subsets of KRAS-mutant lung adenocarcinoma with distinct biology, immune profiles, and therapeutic vulnerabilities. *Cancer Discovery*, **2015**, 5, 860-77	24.4	476
418	Emergence of constitutively active estrogen receptor-□ mutations in pretreated advanced estrogen receptor-positive breast cancer. *Clinical Cancer Research*, **2014**, 20, 1757-1767	12.9	415
417	Kinase fusions are frequent in Spitz tumours and spitzoid melanomas. *Nature Communications*, **2014**, 5, 3116	17.4	394
416	Targeted Next Generation Sequencing Identifies Markers of Response to PD-1 Blockade. *Cancer Immunology Research*, **2016**, 4, 959-967	12.5	318
415	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, 1499-509	12.9	311
414	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. *Cancer Discovery*, **2016**, 6, 154-65	24.4	269
413	Inflammatory myofibroblastic tumors harbor multiple potentially actionable kinase fusions. *Cancer Discovery*, **2014**, 4, 889-95	24.4	250
412	Molecular profiling of cancer patients enables personalized combination therapy: the I-PREDICT study. *Nature Medicine*, **2019**, 25, 744-750	50.5	240
411	Biliary cancer: Utility of next-generation sequencing for clinical management. *Cancer*, **2016**, 122, 3838-3847	6.4	185
410	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. *Blood*, **2016**, 127, 3004-14	2.2	185
409	Broad, Hybrid Capture-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, 3631-9	12.9	183
408	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	11.5	183
407	Characterization of 298 Patients with Lung Cancer Harboring MET Exon 14 Skipping Alterations. *Journal of Thoracic Oncology*, **2016**, 11, 1493-502	8.9	177

406	The distribution of BRAF gene fusions in solid tumors and response to targeted therapy. *International Journal of Cancer*, **2016**, 138, 881-90	7.5	168
405	Lung Master Protocol (Lung-MAP)-A Biomarker-Driven Protocol for Accelerating Development of Therapies for Squamous Cell Lung Cancer: SWOG S1400. *Clinical Cancer Research*, **2015**, 21, 1514-24	12.9	165
404	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	14.4	158
403	Impact of EML4-ALK Variant on Resistance Mechanisms and Clinical Outcomes in ALK-Positive Lung Cancer. *Journal of Clinical Oncology*, **2018**, 36, 1199-1206	2.2	155
402	Cancer Therapy Directed by Comprehensive Genomic Profiling: A Single Center Study. *Cancer Research*, **2016**, 76, 3690-701	10.1	154
401	Prevalence of PDL1 Amplification and Preliminary Response to Immune Checkpoint Blockade in Solid Tumors. *JAMA Oncology*, **2018**, 4, 1237-1244	13.4	149
400	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	2.8	131
399	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	5.7	126
398	Fluorescence in situ hybridization, immunohistochemistry, and next-generation sequencing for detection of EML4-ALK rearrangement in lung cancer. *Oncologist*, **2015**, 20, 316-22	5.7	125
397	BRAF fusions define a distinct molecular subset of melanomas with potential sensitivity to MEK inhibition. *Clinical Cancer Research*, **2013**, 19, 6696-702	12.9	122
396	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	13.3	117
395	Comprehensive genomic profiling of pancreatic acinar cell carcinomas identifies recurrent RAF fusions and frequent inactivation of DNA repair genes. *Cancer Discovery*, **2014**, 4, 1398-405	24.4	112
394	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	5	109
393	Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy. *Modern Pathology*, **2014**, 27, 271-80	9.8	108
392	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	2.2	108
391	Analytical Validation of a Hybrid Capture-Based Next-Generation Sequencing Clinical Assay for Genomic Profiling of Cell-Free Circulating Tumor DNA. *Journal of Molecular Diagnostics*, **2018**, 20, 686-702	5.1	103
390	Genomic Profiling of Small-Bowel Adenocarcinoma. *JAMA Oncology*, **2017**, 3, 1546-1553	13.4	101
389	Inactivation of Capicua drives cancer metastasis. *Nature Genetics*, **2017**, 49, 87-96	36.3	92

388	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	8.9	85
387	Genomic Characterization of Renal Cell Carcinoma with Sarcomatoid Dedifferentiation Pinpoints Recurrent Genomic Alterations. *European Urology*, **2016**, 70, 348-57	10.2	82
386	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	12.9	81
385	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	8.9	75
384	Metastatic basal cell carcinoma with amplification of PD-L1: exceptional response to anti-PD1 therapy. *Npj Genomic Medicine*, **2016**, 1,	6.2	74
383	Triple-negative breast cancers with amplification of JAK2 at the 9p24 locus demonstrate JAK2-specific dependence. *Science Translational Medicine*, **2016**, 8, 334ra53	17.5	73
382	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. *Journal of Molecular Diagnostics*, **2019**, 21, 1053-1066	5.1	72
381	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	8.9	72
380	Identification of NTRK fusions in pediatric mesenchymal tumors. *Pediatric Blood and Cancer*, **2017**, 64, e26433	3	71
379	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. *Cancer Research*, **2017**, 77, 2464-2475	10.1	71
378	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	24.3	69
377	RICTOR Amplification Defines a Novel Subset of Patients with Lung Cancer Who May Benefit from Treatment with mTORC1/2 Inhibitors. *Cancer Discovery*, **2015**, 5, 1262-70	24.4	69
376	Comprehensive Genomic Profiling of Advanced Esophageal Squamous Cell Carcinomas and Esophageal Adenocarcinomas Reveals Similarities and Differences. *Oncologist*, **2015**, 20, 1132-9	5.7	69
375	Identification of recurrent FGFR3-TACC3 fusion oncogenes from lung adenocarcinoma. *Clinical Cancer Research*, **2014**, 20, 6551-8	12.9	67
374	An Acquired Gatekeeper Mutation Induces Resistance to Neratinib in a Patient with HER2 Mutant-Driven Breast Cancer. *Cancer Discovery*, **2017**, 7, 575-585	24.4	66
373	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	8.9	65
372	EGFR Fusions as Novel Therapeutic Targets in Lung Cancer. *Cancer Discovery*, **2016**, 6, 601-11	24.4	65
371	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, 791-9	7.5	64

370	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. *Journal of Clinical Investigation* , **2019**, 129, 4276-4289	15.9	64
369	Enrichment of Targetable Mutations in the Relapsed Neuroblastoma Genome. *PLoS Genetics*, **2016**, 12, e1006501	6	64
368	ROS1 Fusions Rarely Overlap with Other Oncogenic Drivers in Non-Small Cell Lung Cancer. *Journal of Thoracic Oncology*, **2017**, 12, 872-877	8.9	63
367	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, 357-9	5.9	63
366	Characterization of Clinical Cases of Collecting Duct Carcinoma of the Kidney Assessed by Comprehensive Genomic Profiling. *European Urology*, **2016**, 70, 516-21	10.2	61
365	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, 684-91	5.7	61
364	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. *Cancer Research*, **2017**, 77, 509-519	10.1	60
363	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	8.9	59
362	The Genomic Landscape of Merkel Cell Carcinoma and Clinicogenomic Biomarkers of Response to Immune Checkpoint Inhibitor Therapy. *Clinical Cancer Research*, **2019**, 25, 5961-5971	12.9	58
361	Comprehensive genomic profiling of inflammatory breast cancer cases reveals a high frequency of clinically relevant genomic alterations. *Breast Cancer Research and Treatment*, **2015**, 154, 155-62	4.4	57
360	STUMP un"stumped": 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	22.4	56
359	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. *Oncologist*, **2016**, 21, 33-9	5.7	55
358	Effect of the RET Inhibitor Vandetanib in a Patient With RET Fusion-Positive Metastatic Non-Small-Cell Lung Cancer. *Journal of Clinical Oncology*, **2016**, 34, e141-4	2.2	55
357	Oncogenic alterations in ERBB2/HER2 represent potential therapeutic targets across tumors from diverse anatomic sites of origin. *Oncologist*, **2015**, 20, 7-12	5.7	54
356	Characterization of Clinical Cases of Advanced Papillary Renal Cell Carcinoma via Comprehensive Genomic Profiling. *European Urology*, **2018**, 73, 71-78	10.2	54
355	BRAFV600E Mutations in High-Grade Colorectal Neuroendocrine Tumors May Predict Responsiveness to BRAF-MEK Combination Therapy. *Cancer Discovery*, **2016**, 6, 594-600	24.4	52
354	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	12.9	51
353	TP53 Alterations Correlate with Response to VEGF/VEGFR Inhibitors: Implications for Targeted Therapeutics. *Molecular Cancer Therapeutics*, **2016**, 15, 2475-2485	6.1	49

352	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or Refractory Cancers. *Oncologist*, **2016**, 21, 1315-1325	5.7	49
351	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, 76-9	5.9	48
350	Real-time genomic profiling of histiocytoses identifies early-kinase domain BRAF alterations while improving treatment outcomes. *JCI Insight*, **2017**, 2, e89473	9.9	48
349	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	5.7	43
348	Pediatric, Adolescent, and Young Adult Thyroid Carcinoma Harbors Frequent and Diverse Targetable Genomic Alterations, Including Kinase Fusions. *Oncologist*, **2017**, 22, 255-263	5.7	42
347	Checkpoint inhibitor is active against large cell neuroendocrine carcinoma with high tumor mutation burden **2017**, 5, 75		42
346	Comprehensive genomic profiling of extrahepatic cholangiocarcinoma reveals a long tail of therapeutic targets. *Journal of Clinical Pathology*, **2016**, 69, 403-8	3.9	40
345	Pan-Cancer Analysis of and Genomic Alterations and Their Association With Genomic Instability as Measured by Genome-Wide Loss of Heterozygosity. *JCO Precision Oncology*, **2020**, 4, 442-465	3.6	38
344	Response of an ERBB2-mutated inflammatory breast carcinoma to human epidermal growth factor receptor 2-targeted therapy. *Journal of Clinical Oncology*, **2014**, 32, e88-91	2.2	38
343	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	12.9	37
342	Hybrid Capture-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	12.9	36
341	Combined Blockade of Activating Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. *Clinical Cancer Research*, **2019**, 25, 277-289	12.9	35
340	Clinical Benefit in Response to Palbociclib Treatment in Refractory Uterine Leiomyosarcomas with a Common Alteration. *Oncologist*, **2017**, 22, 416-421	5.7	33
339	Detection of Known and Novel FGFR Fusions in Non-Small Cell Lung Cancer by Comprehensive Genomic Profiling. *Journal of Thoracic Oncology*, **2019**, 14, 54-62	8.9	33
338	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. *Blood*, **2018**, 131, 2501-2505	2.2	32
337	Comprehensive genomic profiling of malignant phyllodes tumors of the breast. *Breast Cancer Research and Treatment*, **2017**, 162, 597-602	4.4	31
336	Comprehensive genomic profiling of different subtypes of nasopharyngeal carcinoma reveals similarities and differences to guide targeted therapy. *Cancer*, **2017**, 123, 3628-3637	6.4	30
335	Identification of a novel TMEM106B-ROS1 fusion variant in lung adenocarcinoma by comprehensive genomic profiling. *Lung Cancer*, **2015**, 88, 352-4	5.9	30

334	Correlation Between Molecular Subclassifications of Clear Cell Renal Cell Carcinoma and Targeted Therapy Response. *European Urology Focus*, **2016**, 2, 204-209	5.1	30
333	Clonal diversity predicts adverse outcome in chronic lymphocytic leukemia. *Leukemia*, **2019**, 33, 390-402	10.7	30
332	Genomic landscape of advanced basal cell carcinoma: Implications for precision treatment with targeted and immune therapies. *OncoImmunology*, **2018**, 7, e1404217	7.2	30
331	Prospective Comprehensive Genomic Profiling of Primary and Metastatic Prostate Tumors. *JCO Precision Oncology*, **2019**, 3,	3.6	29
330	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	5.9	29
329	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, 164-72	0.8	29
328	Hybrid Capture-Based Genomic Profiling of Circulating Tumor DNA from Patients with Advanced Non-Small Cell Lung Cancer. *Journal of Thoracic Oncology*, **2019**, 14, 255-264	8.9	28
327	Phosphatidylinositol 3-kinase pathway genomic alterations in 60,991 diverse solid tumors informs targeted therapy opportunities. *Cancer*, **2019**, 125, 1185-1199	6.4	27
326	Use of comprehensive genomic profiling to direct point-of-care management of patients with gynecologic cancers. *Gynecologic Oncology*, **2016**, 141, 2-9	4.9	26
325	Comprehensive Genomic Profiling of Esthesioneuroblastoma Reveals Additional Treatment Options. *Oncologist*, **2017**, 22, 834-842	5.7	26
324	Biomarker-driven therapies for previously treated squamous non-small-cell lung cancer (Lung-MAP SWOG S1400): a biomarker-driven master protocol. *Lancet Oncology, The*, **2020**, 21, 1589-1601	21.7	26
323	A Case of Metastatic Atypical Neuroendocrine Tumor with Translocation and Diffuse Brain Metastases. *Oncologist*, **2017**, 22, 768-773	5.7	25
322	Targeted genomic landscape of metastases compared to primary tumours in clear cell metastatic renal cell carcinoma. *British Journal of Cancer*, **2018**, 118, 1238-1242	8.7	25
321	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	3	25
320	Durable Response to Crizotinib in a MET-Amplified, KRAS-Mutated Carcinoma of Unknown Primary. *Case Reports in Oncology*, **2014**, 7, 503-8	1	25
319	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	8.9	25
318	Tumor mutational burden as a potential biomarker for PD1/PD-L1 therapy in colorectal cancer.. *Journal of Clinical Oncology*, **2016**, 34, 3587-3587	2.2	24
317	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	2.2	24

316	Antitumor Response of VEGFR2- and VEGFR3-Amplified Angiosarcoma to Pazopanib. *Journal of the National Comprehensive Cancer Network: JNCCN*, **2016**, 14, 499-502	7.3	23
315	Pan-Cancer Analysis of Loss-of-Function Alterations and Their Association with the Focal Tandem-Duplicator Phenotype. *Oncologist*, **2019**, 24, 1526-1533	5.7	23
314	Comprehensive Genomic Profiling Identifies Frequent Drug-Sensitive EGFR Exon 19 Deletions in NSCLC not Identified by Prior Molecular Testing. *Clinical Cancer Research*, **2016**, 22, 3281-5	12.9	22
313	Comprehensive genomic profiling identifies novel NTRK fusions in neuroendocrine tumors. *Oncotarget*, **2018**, 9, 35809-35812	3.3	22
312	RET Fusion Lung Carcinoma: Response to Therapy and Clinical Features in a Case Series of 14 Patients. *Clinical Lung Cancer*, **2017**, 18, e223-e232	4.9	21
311	Acquired ALK L1152R Mutation Confers Resistance to Ceritinib and Predicts Response to Alectinib. *Journal of Thoracic Oncology*, **2016**, 11, e87-8	8.9	21
310	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	12.1	20
309	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	2.2	20
308	Comprehensive Genomic Profiling of Upper-tract and Bladder Urothelial Carcinoma. *European Urology Focus*, **2021**, 7, 1339-1346	5.1	20
307	Exceptional Response on Addition of Everolimus to Taxane in Urothelial Carcinoma Bearing an NF2 Mutation. *European Urology*, **2015**, 67, 1195-1196	10.2	19
306	Comprehensive Assessment of Immuno-oncology Biomarkers in Adenocarcinoma, Urothelial Carcinoma, and Squamous-cell Carcinoma of the Bladder. *European Urology*, **2020**, 77, 548-556	10.2	19
305	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	2.8	18
304	Antitumor response of an ERBB2 amplified inflammatory breast carcinoma with EGFR mutation to the EGFR-TKI erlotinib. *Clinical Breast Cancer*, **2014**, 14, e14-6	3	18
303	Personalized Treatment for a Patient With a BRAF V600E 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	7.3	18
302	Exceptional durable response to everolimus in a patient with biphenotypic breast cancer harboring an variant. *Journal of Physical Education and Sports Management*, **2017**, 3,	2.8	17
301	C2 Domain Deletions Hyperactivate Phosphoinositide 3-kinase (PI3K), Generate Oncogene Dependence, and Are Exquisitely Sensitive to PI3K Inhibitors. *Clinical Cancer Research*, **2018**, 24, 1426-1435	12.9	17
300	Comprehensive Genomic Profiling of Hodgkin Lymphoma Reveals Recurrently Mutated Genes and Increased Mutation Burden. *Oncologist*, **2019**, 24, 219-228	5.7	17
299	Comprehensive genetic alteration profiling in primary and recurrent glioblastoma. *Journal of Neuro-Oncology*, **2019**, 142, 111-118	4.8	17

298	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	22.4	17
297	Detection of an Fusion in Colorectal Carcinoma by Hybrid Capture-Based Assay of Circulating Tumor DNA. *Oncologist*, **2017**, 22, 774-779	5.7	14
296	Next Generation Sequencing Reveals Potentially Actionable Alterations in the Majority of Patients with Lymphoid Malignancies. *JCO Precision Oncology*, **2017**, 1,	3.6	14
295	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	5.9	14
294	Genomic Profiling of T-Cell Neoplasms Reveals Frequent and Mutations With Clonal Evasion From Targeted Therapies. *JCO Precision Oncology*, **2018**, 2018,	3.6	14
293	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	3.7	13
292	Phenotypic and Genomic Determinants of Immunotherapy Response Associated with Squamousness. *Cancer Immunology Research*, **2019**, 7, 866-873	12.5	13
291	Clinically advanced and metastatic pure mucinous carcinoma of the breast: a comprehensive genomic profiling study. *Breast Cancer Research and Treatment*, **2016**, 155, 405-13	4.4	13
290	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	2.2	13
289	MDM2 amplification (Amp) to mediate cabozantinib resistance in patients (Pts) with advanced RET-rearranged lung cancers.. *Journal of Clinical Oncology*, **2016**, 34, 9068-9068	2.2	13
288	Landscape of genomic alterations (GA) and tumor mutational burden (TMB) in different metastatic melanoma (MM) subtypes.. *Journal of Clinical Oncology*, **2017**, 35, 9536-9536	2.2	13
287	Approach to evaluating tumor mutational burden in routine clinical practice. *Translational Lung Cancer Research*, **2018**, 7, 678-681	4.4	13
286	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	5.9	12
285	Core Clinical Data Elements for Cancer Genomic Repositories: A Multi-stakeholder Consensus. *Cell*, **2017**, 171, 982-986	56.2	12
284	Identification of a novel fusion TBL1XR1-PDGFRB in a patient with acute myeloid leukemia harboring the DEK-NUP214 fusion and clinical response to dasatinib. *Leukemia and Lymphoma*, **2017**, 58, 2969-2972	1.9	11
283	Genomic Features of Metastatic Testicular Sex Cord Stromal Tumors. *European Urology Focus*, **2019**, 5, 748-755	5.1	11
282	Extended Antitumor Response of a BRAF V600E Papillary Thyroid Carcinoma to Vemurafenib. *Case Reports in Oncology*, **2014**, 7, 343-8	1	11
281	Association of ALK resistance mutations by EML4-ALK variant (v3 vs. non-v3) in ALK+ non-small cell lung cancer (NSCLC).. *Journal of Clinical Oncology*, **2017**, 35, 9010-9010	2.2	11

280	Unique metastases of ALK mutated lung cancer activated to the adnexa of the uterus. *Case Reports in Clinical Pathology*, **2014**, 1, 151-154	0.1	10
279	A phase II study of HSP90 inhibitor AUY922 and erlotinib (E) for patients (pts) with EGFR-mutant lung cancer and acquired resistance (AR) to EGFR tyrosine kinase inhibitors (EGFR TKIs).. *Journal of Clinical Oncology*, **2013**, 31, 8036-8036	2.2	10
278	Comprehensive genomic profiling of biliary tract cancers to reveal tumor-specific differences and genomic alterations.. *Journal of Clinical Oncology*, **2015**, 33, 231-231	2.2	10
277	Evaluation of microsatellite instability (MSI) status in 11,573 diverse solid tumors using comprehensive genomic profiling (CGP).. *Journal of Clinical Oncology*, **2016**, 34, 1523-1523	2.2	10
276	Genomic alterations (GA) and tumor mutational burden (TMB) in large cell neuroendocrine carcinoma of lung (L-LCNEC) as compared to small cell lung carcinoma (SCLC) as assessed via comprehensive genomic profiling (CGP).. *Journal of Clinical Oncology*, **2017**, 35, 8517-8517	2.2	10
275	Distinct age-associated molecular profiles in acute myeloid leukemia defined by comprehensive clinical genomic profiling. *Oncotarget*, **2018**, 9, 26417-26430	3.3	10
274	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	4.9	9
273	Detection of Crizotinib-Sensitive Lung Adenocarcinomas With MET, ALK, and ROS1 Genomic Alterations via Comprehensive Genomic Profiling. *Clinical Lung Cancer*, **2015**, 16, e105-9	4.9	9
272	Epidermal Growth Factor Receptor P753S Mutation in Cutaneous Squamous Cell Carcinoma Responsive to Cetuximab-Based Therapy. *Journal of Clinical Oncology*, **2016**, 34, e34-7	2.2	9
271	Response to rapamycin analogs but not PD-1 inhibitors in PTEN-mutated metastatic non-small-cell lung cancer with high tumor mutational burden. *Lung Cancer: Targets and Therapy*, **2018**, 9, 45-47	2.9	9
270	Genomic alterations in human epidermal growth factor receptor 2 (HER2/ERBB2) in head and neck squamous cell carcinoma. *Head and Neck*, **2017**, 39, E15-E19	4.2	9
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