Trevor J Pugh

List of Publications by Year
in descending order

156	33,496	15466 65	8835 145
papers	citations	h-index	g-index

168	168	168	50819
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
2	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	13.7	2,496
3	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
4	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	13.7	1,288
5	AACR Project GENIE: Powering Precision Medicine through an International Consortium. Cancer Discovery, 2017, 7, 818-831.	7.7	1,235
6	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
7	DNA-Demethylating Agents Target Colorectal Cancer Cells by Inducing Viral Mimicry by Endogenous Transcripts. Cell, 2015, 162, 961-973.	13.5	1,075
8	Activation of the PD-1 Pathway Contributes to Immune Escape in EGFR-Driven Lung Tumors. Cancer Discovery, 2013, 3, 1355-1363.	7.7	1,073
9	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	9.4	990
10	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	13.7	984
11	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	13.7	765
12	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
13	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110.	13.7	675
14	Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506.	13.7	671
15	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	7.7	627
16	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. Nature, 2018, 563, 579-583.	13.7	624
17	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	13.7	617
18	Integrative and Comparative Genomic Analysis of HPV-Positive and HPV-Negative Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2015, 21, 632-641.	3.2	525

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19	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	13.7	521
20	Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations. Nature Genetics, 2015, 47, 864-871.	9.4	451
21	Oncotator: Cancer Variant Annotation Tool. Human Mutation, 2015, 36, E2423-E2429.	1.1	448
22	Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. Nucleic Acids Research, 2013, 41, e67-e67.	6.5	407
23	Subgroup-Specific Prognostic Implications of TP53 Mutation in Medulloblastoma. Journal of Clinical Oncology, 2013, 31, 2927-2935.	0.8	381
24	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	0.8	355
25	Institutional implementation of clinical tumor profiling on an unselected cancer population. JCI Insight, 2016, 1, e87062.	2.3	340
26	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	13.7	321
27	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. Nature, 2019, 572, 67-73.	13.7	293
28	The landscape of genetic variation in dilated cardiomyopathy as surveyed by clinical DNA sequencing. Genetics in Medicine, 2014, 16, 601-608.	1.1	284
29	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	9.0	283
30	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. Nature Genetics, 2013, 45, 1483-1486.	9.4	275
31	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	9.4	270
32	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	13.7	269
33	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	13.7	266
34	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. American Journal of Human Genetics, 2006, 79, 500-513.	2.6	261
35	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. Cell, 2021, 184, 226-242.e21.	13.5	258
36	Personalized circulating tumor DNA analysis as a predictive biomarker in solid tumor patients treated with pembrolizumab. Nature Cancer, 2020, 1, 873-881.	5.7	253

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37	Molecular profiling of advanced solid tumors and patient outcomes with genotype-matched clinical trials: the Princess Margaret IMPACT/COMPACT trial. Genome Medicine, 2016, 8, 109.	3.6	211
38	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. Nature Genetics, 2016, 48, 1142-1150.	9.4	196
39	Rare driver mutations in head and neck squamous cell carcinomas converge on NOTCH signaling. Science, 2020, 367, 1264-1269.	6.0	190
40	Tryptophan-derived microbial metabolites activate the aryl hydrocarbon receptor in tumor-associated macrophages to suppress anti-tumor immunity. Immunity, 2022, 55, 324-340.e8.	6.6	179
41	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirusâ€“Unrelated Head and Neck Cancer: A Multicenter, Phase II Trial. Clinical Cancer Research, 2020, 26, 5140-5152.	3.2	163
42	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	13.9	159
43	Inhibitor-Sensitive FGFR2 and FGFR3 Mutations in Lung Squamous Cell Carcinoma. Cancer Research, 2013, 73, 5195-5205.	0.4	153
44	A systematic approach to assessing the clinical significance of genetic variants. Clinical Genetics, 2013, 84, 453-463.	1.0	153
45	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. Nature Cancer, 2021, 2, 157-173.	5.7	147
46	Exome sequencing of pleuropulmonary blastoma reveals frequent biallelic loss of TP53 and two hits in DICER1 resulting in retention of 5p-derived miRNA hairpin loop sequences. Oncogene, 2014, 33, 5295-5302.	2.6	132
47	A distinct innate lymphoid cell population regulates tumor-associated T cells. Nature Medicine, 2017, 23, 368-375.	15.2	131
48	DNA hypermethylation within TERT promoter upregulates TERT expression in cancer. Journal of Clinical Investigation, 2018, 129, 223-229.	3.9	130
49	Epidermal growth factor receptor (EGFR) is transcriptionally induced by the Y-box binding protein-1 (YB-1) and can be inhibited with Iressa in basal-like breast cancer, providing a potential target for therapy. Breast Cancer Research, 2007, 9, R61.	2.2	126
50	Adavosertib plus gemcitabine for platinum-resistant or platinum-refractory recurrent ovarian cancer: a double-blind, randomised, placebo-controlled, phase 2 trial. Lancet, The, 2021, 397, 281-292.	6.3	125
51	The genomic landscape of schwannoma. Nature Genetics, 2016, 48, 1339-1348.	9.4	124
52	A patient with vertebral, cognitive and behavioural abnormalities and a de novo deletion of NRXN1Â. Journal of Medical Genetics, 2007, 45, 239-243.	1.5	123
53	Circulating tumour DNA sequence analysis as an alternative to multiple myeloma bone marrow aspirates. Nature Communications, 2017, 8, 15086.	5.8	107
54	Human Papillomavirus Genotype Association With Survival in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2016, 2, 823.	3.4	98

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55	Molecular characteristics and therapeutic vulnerabilities across paediatric solid tumours. Nature Reviews Cancer, 2019, 19, 420-438.	12.8	98
56	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. PLoS Genetics, 2016, 12, e1006242.	1.5	93
57	Translational genomics of nasopharyngeal cancer. Seminars in Cancer Biology, 2020, 61, 84-100.	4.3	90
58	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. Science Immunology, 2019, 4, .	5.6	85
59	EVOLVE: A Multicenter Open-Label Single-Arm Clinical and Translational Phase II Trial of Cediranib Plus Olaparib for Ovarian Cancer after PARP Inhibition Progression. Clinical Cancer Research, 2020, 26, 4206-4215.	3.2	84
60	Somatic BRCA1/2 Recovery as a Resistance Mechanism After Exceptional Response to Poly (ADP-ribose) Polymerase Inhibition. Journal of Clinical Oncology, 2017, 35, 1240-1249.	0.8	79
61	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. Nature Communications, 2021, 12, 979.	5.8	77
62	Therapeutic radiation for childhood cancer drives structural aberrations of NF2 in meningiomas. Nature Communications, 2017, 8, 186.	5.8	76
63	Regulatory T Cells in Ovarian Cancer Are Characterized by a Highly Activated Phenotype Distinct from that in Melanoma. Clinical Cancer Research, 2018, 24, 5685-5696.	3.2	76
64	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. Nature Genetics, 2016, 48, 1260-1266.	9.4	75
65	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
66	Impact of whole genome amplification on analysis of copy number variants. Nucleic Acids Research, 2008, 36, e80-e80.	6.5	74
67	Development and Validation of a Computational Method for Assessment of Missense Variants in Hypertrophic Cardiomyopathy. American Journal of Human Genetics, 2011, 88, 183-192.	2.6	73
68	Landscape of genomic alterations in high-grade serous ovarian cancer from exceptional long- and short-term survivors. Genome Medicine, 2018, 10, 81.	3.6	72
69	The Role of Minimal Residual Disease Testing in Myeloma Treatment Selection and Drug Development: Current Value and Future Applications. Clinical Cancer Research, 2017, 23, 3980-3993.	3.2	71
70	Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. Human Mutation, 2015, 36, 1080-1087.	1.1	67
71	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. Nature Communications, 2021, 12, 5137.	5.8	63
72	VisCap: inference and visualization of germ-line copy-number variants from targeted clinical sequencing data. Genetics in Medicine, 2016, 18, 712-719.	1.1	61

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73	Patient-Derived Xenografts for Prognostication and Personalized Treatment for Head and Neck Squamous Cell Carcinoma. Cell Reports, 2018, 25, 1318-1331.e4.	2.9	56
74	Whole-genome profiling of nasopharyngeal carcinoma reveals viral-host co-operation in inflammatory NF-Î²B activation and immune escape. Nature Communications, 2021, 12, 4193.	5.8	56
75	Comprehensive Diagnostic Testing for Stereocilin. Journal of Molecular Diagnostics, 2014, 16, 639-647.	1.2	53
76	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency. Nature Medicine, 2022, 28, 125-135.	15.2	53
77	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. Genome Research, 2019, 29, 1211-1222.	2.4	52
78	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. Nature Communications, 2020, 11, 441.	5.8	51
79	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	49
80	A shower of second hit events as the cause of multifocal renal cell carcinoma in tuberous sclerosis complex. Human Molecular Genetics, 2015, 24, 1836-1842.	1.4	45
81	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	45
82	A Comprehensive Assay for CFTR Mutational Analysis Using Next-Generation Sequencing. Clinical Chemistry, 2013, 59, 1481-1488.	1.5	44
83	Sequence Variant Discovery in DNA Repair Genes from Radiosensitive and Radiotolerant Prostate Brachytherapy Patients. Clinical Cancer Research, 2009, 15, 5008-5016.	3.2	42
84	Clinical impact of combined epigenetic and molecular analysis of pediatric low-grade gliomas. Neuro-Oncology, 2020, 22, 1474-1483.	0.6	39
85	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE). , 2019, 7, 72.		38
86	HPV Sequencing Facilitates Ultrasensitive Detection of HPV Circulating Tumor DNA. Clinical Cancer Research, 2021, 27, 5857-5868.	3.2	38
87	WNT activation by lithium abrogates TP53 mutation associated radiation resistance in medulloblastoma. Acta Neuropathologica Communications, 2014, 2, 174.	2.4	37
88	Correlations of EGFR mutations and increases in EGFR and HER2 copy number to gefitinib response in a retrospective analysis of lung cancer patients. BMC Cancer, 2007, 7, 128.	1.1	36
89	High efficiency error suppression for accurate detection of low-frequency variants. Nucleic Acids Research, 2019, 47, e87-e87.	6.5	36
90	An open-label, phase II multicohort study of an oral hypomethylating agent CC-486 and durvalumab in advanced solid tumors. , 2020, 8, e000883.		36

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91	Safety and tolerability of CFI-400945, a first-in-class, selective PLK4 inhibitor in advanced solid tumours: a phase 1 dose-escalation trial. British Journal of Cancer, 2019, 121, 318-324.	2.9	35
92	Circulating Tumour DNA for Detecting Minimal Residual Disease in Multiple Myeloma. Seminars in Hematology, 2018, 55, 38-40.	1.8	34
93	Wnt activation as a therapeutic strategy in medulloblastoma. Nature Communications, 2020, 11, 4323.	5.8	34
94	Transplant Oncology in Primary and Metastatic Liver Tumors. Annals of Surgery, 2021, 273, 483-493.	2.1	33
95	Coenzyme A fuels TÂcell anti-tumor immunity. Cell Metabolism, 2021, 33, 2415-2427.e6.	7.2	31
96	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. Pharmacogenomics Journal, 2013, 13, 148-158.	0.9	29
97	Next generation sequencingâ€based copy number analysis reveals low prevalence of deletions and duplications in 46 genes associated with genetic cardiomyopathies. Molecular Genetics & Genomic Medicine, 2016, 4, 143-151.	0.6	29
98	Integration of Technical, Bioinformatic, and Variant Assessment Approaches in the Validation of a Targeted Next-Generation Sequencing Panel for Myeloid Malignancies. Archives of Pathology and Laboratory Medicine, 2017, 141, 759-775.	1.2	29
99	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. Cancer Research, 2019, 79, 2111-2123.	0.4	28
100	Phase I/II Trial of the Combination of 177Lutetium Prostate specific Membrane Antigen 617 and Idronoxil (NOX66) in Men with End-stage Metastatic Castration-resistant Prostate Cancer (LuPIN). European Urology Oncology, 2021, 4, 963-970.	2.6	27
101	AACR Project GENIE: 100,000 Cases and Beyond. Cancer Discovery, 2022, 12, 2044-2057.	7.7	27
102	IL6 Induces an IL22+ CD8+ T-cell Subset with Potent Antitumor Function. Cancer Immunology Research, 2020, 8, 321-333.	1.6	26
103	Epigenomic, genomic, and transcriptomic landscape of schwannomatosis. Acta Neuropathologica, 2021, 141, 101-116.	3.9	26
104	Minimal Residual Disease in Myeloma: Application for Clinical Care and New Drug Registration. Clinical Cancer Research, 2021, 27, 5195-5212.	3.2	26
105	Data resources for the identification and interpretation of actionable mutations by clinicians. Annals of Oncology, 2017, 28, 946-957.	0.6	20
106	Antitumor immune effects of preoperative sitravatinib and nivolumab in oral cavity cancer: SNOW window-of-opportunity study. , 2021, 9, e003476.		20
107	Unsupervised Resolution of Histomorphologic Heterogeneity in Renal Cell Carcinoma Using a Brain Tumorâ€“Educated Neural Network. JCO Clinical Cancer Informatics, 2020, 4, 811-821.	1.0	19
108	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. Leukemia, 2021, 35, 796-808.	3.3	19

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109	Mutations in the RAS/MAPK Pathway Drive Replication Repairâ€“Deficient Hypermutated Tumors and Confer Sensitivity to MEK Inhibition. Cancer Discovery, 2021, 11, 1454-1467.	7.7	19
110	CapTCR-seq: hybrid capture for T-cell receptor repertoire profiling. Blood Advances, 2018, 2, 3506-3514.	2.5	18
111	CReSCENT: CanceR Single Cell ExpressioN Toolkit. Nucleic Acids Research, 2020, 48, W372-W379.	6.5	18
112	Minimalist approaches to cancer tissue-of-origin classification by DNA methylation. Modern Pathology, 2020, 33, 1874-1888.	2.9	18
113	Pre-encoded responsiveness to type I interferon in the peripheral immune system defines outcome of PD1 blockade therapy. Nature Immunology, 2022, 23, 1273-1283.	7.0	17
114	Performance characteristics of screening strategies to identify Lynch syndrome in women with ovarian cancer. Cancer, 2020, 126, 4886-4894.	2.0	15
115	Assessing genome-wide copy number aberrations and copy-neutral loss-of-heterozygosity as best practice: An evidence-based review from the Cancer Genomics Consortium working group for plasma cell disorders. Cancer Genetics, 2018, 228-229, 184-196.	0.2	14
116	Assessment of Genetic Drift in Large Pharmacogenomic Studies. Cell Systems, 2020, 11, 393-401.e2.	2.9	14
117	Brain Tumor Stem Cell Dependence on Glutaminase Reveals a Metabolic Vulnerability through the Amino Acid Deprivation Response Pathway. Cancer Research, 2020, 80, 5478-5490.	0.4	14
118	Predicting Toxicity and Response to Pembrolizumab Through Germline Genomic HLA Class 1 Analysis. JNCI Cancer Spectrum, 2021, 5, pkaa115.	1.4	14
119	Landscape mapping of shared antigenic epitopes and their cognate TCRs of tumor-infiltrating T lymphocytes in melanoma. ELife, 2020, 9, .	2.8	13
120	An Integrative DNA Sequencing and Methylation Panel to Assess Mismatch Repair Deficiency. Journal of Molecular Diagnostics, 2021, 23, 242-252.	1.2	12
121	Applications of Circulating Tumor DNA in a Cohort of Phase I Solid Tumor Patients Treated With Immunotherapy. JNCI Cancer Spectrum, 2021, 5, pkaa122.	1.4	12
122	Prospective observational study and serosurvey of SARS-CoV-2 infection in asymptomatic healthcare workers at a Canadian tertiary care center. PLoS ONE, 2021, 16, e0247258.	1.1	12
123	Longitudinal single-cell analysis of a myeloma mouse model identifies subclonal molecular programs associated with progression. Nature Communications, 2021, 12, 6322.	5.8	12
124	All is not lost: learning from 9p21 loss in cancer. Trends in Immunology, 2022, 43, 379-390.	2.9	12
125	Tumor genomic, transcriptomic, and immune profiling characterizes differential response to firstâ€line platinum chemotherapy in high grade serous ovarian cancer. Cancer Medicine, 2021, 10, 3045-3058.	1.3	11
126	Dual role of allele-specific DNA hypermethylation within the TERT promoter in cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	11

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127	A BAC clone fingerprinting approach to the detection of human genome rearrangements. Genome Biology, 2007, 8, R224.	13.9	10
128	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. Cell Genomics, 2021, 1, 100033.	3.0	10
129	OCTANE (Ontario-Wide Cancer Targeted Nucleic Acid Evaluation): A Platform for Intraprovincial, National, and International Clinical Data-Sharing. Current Oncology, 2019, 26, 618-623.	0.9	9
130	Centromeric cohesion failure invokes a conserved choreography of chromosomal mis-segregations in pancreatic neuroendocrine tumor. Genome Medicine, 2020, 12, 38.	3.6	9
131	The DEAD-box helicase DDX56 is a conserved stemness regulator in normal and cancer stem cells. Cell Reports, 2021, 34, 108903.	2.9	9
132	Understanding the clinical implication of mismatch repair deficiency in endometrioid endometrial cancer through a prospective study. Gynecologic Oncology, 2021, 161, 221-227.	0.6	9
133	Pugh et al. reply. Nature, 2015, 520, E12-E14.	13.7	8
134	Heterogeneous alteration of the ERBB3â€“MYC axis associated with MEK inhibitor resistance in a KRAS-mutated low-grade serous ovarian cancer patient. Journal of Physical Education and Sports Management, 2019, 5, a004341.	0.5	8
135	Considerations for the use of circulating tumor DNA sequencing as a screening tool in cancer predisposition syndromes. Pediatric Blood and Cancer, 2020, 67, e28758.	0.8	6
136	Integration of intra-sample contextual error modeling for improved detection of somatic mutations from deep sequencing. Science Advances, 2020, 6, .	4.7	6
137	Elevation in viral entry genes and innate immunity compromise underlying increased infectivity and severity of COVID-19 in cancer patients. Scientific Reports, 2021, 11, 4533.	1.6	6
138	Maximizing cancer prevention through genetic navigation for Lynch syndrome detection in women with newly diagnosed endometrial and nonserous/nonmucinous epithelial ovarian cancer. Cancer, 2021, 127, 3082-3091.	2.0	6
139	Implementation of serological and molecular tools to inform COVID-19 patient management: protocol for the GENCOV prospective cohort study. BMJ Open, 2021, 11, e052842.	0.8	6
140	Bamgineer: Introduction of simulated allele-specific copy number variants into exome and targeted sequence data sets. PLoS Computational Biology, 2018, 14, e1006080.	1.5	6
141	Early Detection of Multiple Resistance Mechanisms by ctDNA Profiling in a Patient With EGFR-mutant Lung Adenocarcinoma Treated With Osimertinib. Clinical Lung Cancer, 2020, 21, e488-e492.	1.1	5
142	Tumor site discordance in mismatch repair deficiency in synchronous endometrial and ovarian cancers. International Journal of Gynecological Cancer, 2020, 30, 1951-1958.	1.2	5
143	â€œGame Changerâ€• Health Professionalsâ€™ Views on the Clinical Utility of Circulating Tumor DNA Testing in Hereditary Cancer Syndrome Management. Oncologist, 2022, 27, e393-e401.	1.9	5
144	An Anaplastic Lymphoma Kinase Immunohistochemistryâ€“Negative but Fluorescence InÂSitu Hybridizationâ€“Positive Lung Adenocarcinoma IsÂResistant to Crizotinib. Journal of Thoracic Oncology, 2016, 11, 2248-2252.	0.5	3

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145	Mutations in Noncoding Cis-Regulatory Elements Reveal Cancer Driver Cistromes in Luminal Breast Cancer. Molecular Cancer Research, 2022, 20, 102-113.	1.5	3
146	DNA Methylation-Based Classification of Small B-Cell Lymphomas. Journal of Molecular Diagnostics, 2021, 23, 1774-1786.	1.2	2
147	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.8	1
148	Genomic Landscape of Malignant Peripheral Nerve Sheath Tumorâ€'Like Melanoma. Journal of Investigative Dermatology, 2021, 141, 2470-2479.	0.3	1
149	Double trouble: whole genome doubling distinguishes early from late ovarian cancer. Clinical Cancer Research, 2022, , .	3.2	1
150	REFLECTions on Combination Therapies Empowered by Data Sharing. Cancer Discovery, 2022, 12, 1416-1418.	7.7	1
151	Facilitated Loading of Horizontal Gels Using a Capillary Comb Loader. BioTechniques, 2003, 34, 814-818.	0.8	0
152	Townes-Brocks Syndrome. , 2009, , 2092-2094.		0
153	IMMU-14. COMPUTATIONAL DECONVOLUTION OF TUMOR-INFILTRATING IMMUNE COMPONENTS IN PEDIATRIC NERVOUS SYSTEM TUMORS. Neuro-Oncology, 2021, 23, i30-i30.	0.6	0
154	Identification of Acquired Notch3 Dependency in Metastatic Head and Neck Cancer. SSRN Electronic Journal, 0, , .	0.4	0
155	Selective Cell State in the Clonally Expanded T-Cell Compartment of Vβ*MYC Mice Responding to Treatment with Checkpoint Inhibitors. Blood, 2021, 138, 1581-1581.	0.6	0
156	Brief family history questionnaire to screen for Lynch syndrome in women with newly diagnosed non-serous, non-mucinous ovarian cancers. International Journal of Gynecological Cancer, 2022, , ijgc-2021-003082.	1.2	0