Trevor J Pugh

List of Publications by Citations

149 papers	24,259 citations	57 h-index	155 g-index
168 ext. papers	29,921 ext. citations	17.2 avg, IF	7.18 L-index

#	Paper	IF	Citations
149	Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, **2013**, 499, 214-218	50.4	3616
148	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
147	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. *Cell*, **2012**, 150, 1107-20	50.4	1304
146	Initial genome sequencing and analysis of multiple myeloma. *Nature*, **2011**, 471, 467-72	50.4	1117
145	The genomic complexity of primary human prostate cancer. *Nature*, **2011**, 470, 214-20	50.4	984
144	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*, **2009**, 461, 809-13	50.4	879
143	Activation of the PD-1 pathway contributes to immune escape in EGFR-driven lung tumors. *Cancer Discovery*, **2013**, 3, 1355-63	24.4	831
142	The genetic landscape of high-risk neuroblastoma. *Nature Genetics*, **2013**, 45, 279-84	36.3	717
141	DNA-Demethylating Agents Target Colorectal Cancer Cells by Inducing Viral Mimicry by Endogenous Transcripts. *Cell*, **2015**, 162, 961-73	56.2	705
140	AACR Project GENIE: Powering Precision Medicine through an International Consortium. *Cancer Discovery*, **2017**, 7, 818-831	24.4	629
139	Dissecting the genomic complexity underlying medulloblastoma. *Nature*, **2012**, 488, 100-5	50.4	623
138	Melanoma genome sequencing reveals frequent PREX2 mutations. *Nature*, **2012**, 485, 502-6	50.4	555
137	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. *Nature*, **2012**, 488, 106-10	50.4	552
136	Landscape of genomic alterations in cervical carcinomas. *Nature*, **2014**, 506, 371-5	50.4	541
135	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothened inhibition. *Cancer Cell*, **2014**, 25, 393-405	24.3	469
134	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. *Nature*, **2014**, 506, 445-50	50.4	434
133	Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. *Clinical Cancer Research*, **2015**, 21, 632-41	12.9	398

132	Prediction of acute myeloid leukaemia risk in healthy individuals. *Nature*, **2018**, 559, 400-404	50.4	368
131	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. *Nature*, **2018**, 563, 579-583	50.4	344
130	Oncotator: cancer variant annotation tool. *Human Mutation*, **2015**, 36, E2423-9	4.7	332
129	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. *BioTechniques*, **2008**, 45, 81-94	2.5	322
128	Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations. *Nature Genetics*, **2015**, 47, 864-71	36.3	313
127	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	20.1	301
126	Subgroup-specific prognostic implications of TP53 mutation in medulloblastoma. *Journal of Clinical Oncology*, **2013**, 31, 2927-35	2.2	290
125	Oligonucleotide microarray analysis of genomic imbalance in children with mental retardation. *American Journal of Human Genetics*, **2006**, 79, 500-13	11	247
124	Institutional implementation of clinical tumor profiling on an unselected cancer population. *JCI Insight*, **2016**, 1, e87062	9.9	245
123	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. *Nature Genetics*, **2011**, 43, 964-968	36.3	242
122	Alternative expression analysis by RNA sequencing. *Nature Methods*, **2010**, 7, 843-7	21.6	227
121	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. *Nature Genetics*, **2013**, 45, 1483-6	36.3	219
120	The landscape of genetic variation in dilated cardiomyopathy as surveyed by clinical DNA sequencing. *Genetics in Medicine*, **2014**, 16, 601-8	8.1	215
119	Divergent clonal selection dominates medulloblastoma at recurrence. *Nature*, **2016**, 529, 351-7	50.4	206
118	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. *Nature*, **2017**, 549, 227-232	50.4	197
117	Recurrent and functional regulatory mutations in breast cancer. *Nature*, **2017**, 547, 55-60	50.4	192
116	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. *Nature Genetics*, **2016**, 48, 1142-50	36.3	158
115	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. *Nature*, **2019**, 572, 67-73	50.4	149

114	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	14.4	149
113	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. *Genome Biology*, **2010**, 11, R82	18.3	144
112	Inhibitor-sensitive FGFR2 and FGFR3 mutations in lung squamous cell carcinoma. *Cancer Research*, **2013**, 73, 5195-205	10.1	136
111	A systematic approach to assessing the clinical significance of genetic variants. *Clinical Genetics*, **2013**, 84, 453-63	4	124
110	Rare driver mutations in head and neck squamous cell carcinomas converge on NOTCH signaling. *Science*, **2020**, 367, 1264-1269	33.3	112
109	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	8.3	112
108	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, 5295-302	9.2	105
107	A patient with vertebral, cognitive and behavioural abnormalities and a de novo deletion of NRXN1alpha. *Journal of Medical Genetics*, **2008**, 45, 239-43	5.8	104
106	A distinct innate lymphoid cell population regulates tumor-associated T cells. *Nature Medicine*, **2017**, 23, 368-375	50.5	97
105	Personalized circulating tumor DNA analysis as a predictive biomarker in solid tumor patients treated with pembrolizumab.. *Nature Cancer*, **2020**, 1, 873-881	15.4	89
104	IMMU-14. COMPUTATIONAL DECONVOLUTION OF TUMOR-INFILTRATING IMMUNE COMPONENTS IN PEDIATRIC NERVOUS SYSTEM TUMORS. *Neuro-Oncology*, **2021**, 23, i30-i30	1	78
103	Circulating tumour DNA sequence analysis as an alternative to multiple myeloma bone marrow aspirates. *Nature Communications*, **2017**, 8, 15086	17.4	77
102	The genomic landscape of schwannoma. *Nature Genetics*, **2016**, 48, 1339-1348	36.3	74
101	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirus-Unrelated Head and Neck Cancer: A Multicenter, Phase II Trial. *Clinical Cancer Research*, **2020**, 26, 5140-5152	12.9	71
100	Impact of whole genome amplification on analysis of copy number variants. *Nucleic Acids Research*, **2008**, 36, e80	20.1	70
99	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. *Cell*, **2021**, 184, 226-242.e21	38.6	68
98	Human Papillomavirus Genotype Association With Survival in Head and Neck Squamous Cell Carcinoma. *JAMA Oncology*, **2016**, 2, 823-6	13.4	66
97	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. *PLoS Genetics*, **2016**, 12, e1006242	6	62

96	DNA hypermethylation within TERT promoter upregulates TERT expression in cancer. *Journal of Clinical Investigation*, **2019**, 129, 223-229	15.9	62
95	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
94	Development and validation of a computational method for assessment of missense variants in hypertrophic cardiomyopathy. *American Journal of Human Genetics*, **2011**, 88, 183-92	11	60
93	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	2.2	59
92	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. *Nature Genetics*, **2016**, 48, 1260-6	36.3	53
91	Molecular characteristics and therapeutic vulnerabilities across paediatric solid tumours. *Nature Reviews Cancer*, **2019**, 19, 420-438	31.3	52
90	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	12.9	51
89	Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. *Human Mutation*, **2015**, 36, 1080-7	4.7	51
88	VisCap: inference and visualization of germ-line copy-number variants from targeted clinical sequencing data. *Genetics in Medicine*, **2016**, 18, 712-9	8.1	46
87	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	12.9	46
86	Landscape of genomic alterations in high-grade serous ovarian cancer from exceptional long- and short-term survivors. *Genome Medicine*, **2018**, 10, 81	14.4	46
85	Therapeutic radiation for childhood cancer drives structural aberrations of NF2 in meningiomas. *Nature Communications*, **2017**, 8, 186	17.4	45
84	Comprehensive diagnostic testing for stereocilin: an approach for analyzing medically important genes with high homology. *Journal of Molecular Diagnostics*, **2014**, 16, 639-47	5.1	41
83	Patient-Derived Xenografts for Prognostication and Personalized Treatment for Head and Neck Squamous Cell Carcinoma. *Cell Reports*, **2018**, 25, 1318-1331.e4	10.6	41
82	A comprehensive assay for CFTR mutational analysis using next-generation sequencing. *Clinical Chemistry*, **2013**, 59, 1481-8	5.5	40
81	A shower of second hit events as the cause of multifocal renal cell carcinoma in tuberous sclerosis complex. *Human Molecular Genetics*, **2015**, 24, 1836-42	5.6	39
80	Sequence variant discovery in DNA repair genes from radiosensitive and radiotolerant prostate brachytherapy patients. *Clinical Cancer Research*, **2009**, 15, 5008-16	12.9	39
79	Translational genomics of nasopharyngeal cancer. *Seminars in Cancer Biology*, **2020**, 61, 84-100	12.7	35

78	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. *Science Immunology*, **2019**, 4,	28	34
77	WNT activation by lithium abrogates TP53 mutation associated radiation resistance in medulloblastoma. *Acta Neuropathologica Communications*, **2014**, 2, 174	7.3	32
76	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	4.8	32
75	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	40	32
74	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. *Genome Research*, **2019**, 29, 1211-1222	9.7	31
73	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. *Nature Cancer*, **2021**, 2, 157-173	15.4	31
72	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	12.9	30
71	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. *F1000Research*, **2019**, 8,	3.6	28
70	Next generation sequencing-based copy number analysis reveals low prevalence of deletions and duplications in 46 genes associated with genetic cardiomyopathies. *Molecular Genetics & Genomic Medicine*, **2016**, 4, 143-51	2.3	27
69	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. *F1000Research*, **2019**, 8, 296	3.6	23
68	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. *Nature Communications*, **2021**, 12, 979	17.4	23
67	Circulating Tumour DNA for Detecting Minimal Residual Disease in Multiple Myeloma. *Seminars in Hematology*, **2018**, 55, 38-40	4	22
66	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	5	21
65	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. *Nature Communications*, **2020**, 11, 441	17.4	21
64	Data resources for the identification and interpretation of actionable mutations by clinicians. *Annals of Oncology*, **2017**, 28, 946-957	10.3	18
63	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	8.7	18
62	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. *Pharmacogenomics Journal*, **2013**, 13, 148-58	3.5	18
61	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE) **2019**, 7, 72		16

60	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. *Cancer Research*, **2019**, 79, 2111-2123	10.1	14
59	Clinical impact of combined epigenetic and molecular analysis of pediatric low-grade gliomas. *Neuro-Oncology*, **2020**, 22, 1474-1483	1	14
58	Tryptophan-derived microbial metabolites activate the aryl hydrocarbon receptor in tumor-associated macrophages to suppress anti-tumor immunity.. *Immunity*, **2022**, 55, 324-340.e8	32.3	14
57	Phase I/II Trial of the Combination of Lutetium Prostate specific Membrane Antigen 617 and Idronoxil (NOX66) in Men with End-stage Metastatic Castration-resistant Prostate Cancer (LuPIN). *European Urology Oncology*, **2020**, 4, 963-963	6.7	14
56	Wnt activation as a therapeutic strategy in medulloblastoma. *Nature Communications*, **2020**, 11, 4323	17.4	13
55	High efficiency error suppression for accurate detection of low-frequency variants. *Nucleic Acids Research*, **2019**, 47, e87	20.1	12
54	An open-label, phase II multicohort study of an oral hypomethylating agent CC-486 and durvalumab in advanced solid tumors **2020**, 8,		12
53	Transplant Oncology in Primary and Metastatic Liver Tumors: Principles, Evidence, and Opportunities. *Annals of Surgery*, **2021**, 273, 483-493	7.8	11
52	Epigenomic, genomic, and transcriptomic landscape of schwannomatosis. *Acta Neuropathologica*, **2021**, 141, 101-116	14.3	11
51	IL6 Induces an IL22 CD8 T-cell Subset with Potent Antitumor Function. *Cancer Immunology Research* , **2020**, 8, 321-333	12.5	10
50	A BAC clone fingerprinting approach to the detection of human genome rearrangements. *Genome Biology*, **2007**, 8, R224	18.3	10
49	Whole-genome profiling of nasopharyngeal carcinoma reveals viral-host co-operation in inflammatory NF-B activation and immune escape. *Nature Communications*, **2021**, 12, 4193	17.4	10
48	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	3.7	9
47	CapTCR-seq: hybrid capture for T-cell receptor repertoire profiling. *Blood Advances*, **2018**, 2, 3506-3514	7.8	9
46	Pugh et al. reply. *Nature*, **2015**, 520, E12-4	50.4	8
45	Minimalist approaches to cancer tissue-of-origin classification by DNA methylation. *Modern Pathology*, **2020**, 33, 1874-1888	9.8	8
44	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	2.3	8
43	Landscape mapping of shared antigenic epitopes and their cognate TCRs of tumor-infiltrating T lymphocytes in melanoma. *ELife*, **2020**, 9,	8.9	6

42	Tumor genomic, transcriptomic, and immune profiling characterizes differential response to first-line platinum chemotherapy in high grade serous ovarian cancer. *Cancer Medicine*, **2021**, 10, 3045-3058	4.8	6
41	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. *Leukemia*, **2021**, 35, 796-808	10.7	6
40	Mutations in the RAS/MAPK Pathway Drive Replication Repair-Deficient Hypermutated Tumors and Confer Sensitivity to MEK Inhibition. *Cancer Discovery*, **2021**, 11, 1454-1467	24.4	6
39	HPV Sequencing Facilitates Ultrasensitive Detection of HPV Circulating Tumor DNA. *Clinical Cancer Research*, **2021**, 27, 5857-5868	12.9	6
38	CReSCENT: CanceR Single Cell ExpressioN Toolkit. *Nucleic Acids Research*, **2020**, 48, W372-W379	20.1	5
37	Childhood Cerebellar Tumors Mirror Conserved Fetal Transcriptional Programs		5
36	Unsupervised Resolution of Histomorphologic Heterogeneity in Renal Cell Carcinoma Using a Brain Tumor-Educated Neural Network. *JCO Clinical Cancer Informatics*, **2020**, 4, 811-821	5.2	5
35	Brain Tumor Stem Cell Dependence on Glutaminase Reveals a Metabolic Vulnerability through the Amino Acid Deprivation Response Pathway. *Cancer Research*, **2020**, 80, 5478-5490	10.1	5
34	Performance characteristics of screening strategies to identify Lynch syndrome in women with ovarian cancer. *Cancer*, **2020**, 126, 4886-4894	6.4	5
33	An Integrative DNA Sequencing and Methylation Panel to Assess Mismatch Repair Deficiency. *Journal of Molecular Diagnostics*, **2021**, 23, 242-252	5.1	5
32	Applications of Circulating Tumor DNA in a Cohort of Phase I Solid Tumor Patients Treated With Immunotherapy. *JNCI Cancer Spectrum*, **2021**, 5, pkaa122	4.6	5
31	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. *Nature Communications*, **2021**, 12, 5137	17.4	5
30	Coenzyme A fuels T□cell anti-tumor immunity. *Cell Metabolism*, **2021**, 33, 2415-2427.e6	24.6	4
29	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNAsequencing data		4
28	Heterogeneous alteration of the ERBB3-MYC axis associated with MEK inhibitor resistance in a -mutated low-grade serous ovarian cancer patient. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	4
27	Minimal Residual Disease in Myeloma: Application for Clinical Care and New Drug Registration. *Clinical Cancer Research*, **2021**,	12.9	4
26	Antitumor immune effects of preoperative sitravatinib and nivolumab in oral cavity cancer: SNOW window-of-opportunity study **2021**, 9,		4
25	Bamgineer: Introduction of simulated allele-specific copy number variants into exome and targeted sequence data sets. *PLoS Computational Biology*, **2018**, 14, e1006080	5	3

24	Predicting Toxicity and Response to Pembrolizumab Through Germline Genomic HLA Class 1 Analysis. *JNCI Cancer Spectrum*, **2021**, 5, pkaa115	4.6	3
23	Assessment of Genetic Drift in Large Pharmacogenomic Studies. *Cell Systems*, **2020**, 11, 393-401.e2	10.6	3
22	Integration of intra-sample contextual error modeling for improved detection of somatic mutations from deep sequencing. *Science Advances*, **2020**, 6,	14.3	2
21	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	4.9	2
20	Tumor site discordance in mismatch repair deficiency in synchronous endometrial and ovarian cancers. *International Journal of Gynecological Cancer*, **2020**, 30, 1951-1958	3.5	2
19	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. *Cell Genomics*, **2021**, 1, 100033		2
18	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency.. *Nature Medicine*, **2022**,	50.5	2
17	The DEAD-box helicase DDX56 is a conserved stemness regulator in normal and cancer stem cells. *Cell Reports*, **2021**, 34, 108903	10.6	2
16	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	6.4	2
15	An Anaplastic Lymphoma Kinase Immunohistochemistry-Negative but Fluorescence In Situ Hybridization-Positive Lung Adenocarcinoma Is Resistant to Crizotinib. *Journal of Thoracic Oncology*, **2016**, 11, 2248-2252	8.9	2
14	Centromeric cohesion failure invokes a conserved choreography of chromosomal mis-segregations in pancreatic neuroendocrine tumor. *Genome Medicine*, **2020**, 12, 38	14.4	1
13	OCTANE (Ontario-wide Cancer Targeted Nucleic Acid Evaluation): a platform for intraprovincial, national, and international clinical data-sharing. *Current Oncology*, **2019**, 26, e618-e623	2.8	1
12	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. *BMC Proceedings*, **2012**, 6,	2.3	1
11	CReSCENT: CanceR Single Cell ExpressioN Toolkit		1
10	Longitudinal single-cell analysis of a myeloma mouse model identifies subclonal molecular programs associated with progression. *Nature Communications*, **2021**, 12, 6322	17.4	1
9	Considerations for the use of circulating tumor DNA sequencing as a screening tool in cancer predisposition syndromes. *Pediatric Blood and Cancer*, **2020**, 67, e28758	3	1
8	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	4.9	1
7	Genomic Landscape of Malignant Peripheral Nerve Sheath Tumor-Like Melanoma. *Journal of Investigative Dermatology*, **2021**, 141, 2470-2479	4.3	1

6	Understanding the clinical implication of mismatch repair deficiency in endometrioid endometrial cancer through a prospective study. *Gynecologic Oncology*, **2021**, 161, 221-227	4.9	0
5	Implementation of serological and molecular tools to inform COVID-19 patient management: protocol for the GENCOV prospective cohort study. *BMJ Open*, **2021**, 11, e052842	3	0
4	REFLECTions on Combination Therapies Empowered by Data Sharing. *Cancer Discovery*, **2022**, 12, 1416-1418	41.4	0
3	Facilitated loading of horizontal gels using a capillary comb loader. *BioTechniques*, **2003**, 34, 814-8	2.5	
2	Selective Cell State in the Clonally Expanded T-Cell Compartment of V□MYC Mice Responding to Treatment with Checkpoint Inhibitors. *Blood*, **2021**, 138, 1581-1581	2.2	
1	DNA Methylation-Based Classification of Small B-Cell Lymphomas: A Proof-of-Principle Study. *Journal of Molecular Diagnostics*, **2021**, 23, 1774-1786	5.1	