

Brennan Decker

List of Publications by Year in descending order

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45
papers

3,042
citations

471509

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docs citations

45
times ranked

5903
citing authors

#	ARTICLE	IF	CITATIONS
1	The Pan-Tumor Landscape of Targetable Kinase Fusions in Circulating Tumor DNA. <i>Clinical Cancer Research</i> , 2022, 28, 728-737.	7.0	20
2	Expanding the use of targeted therapy for urothelial bladder cancer (UBC): Non-FGFR3 receptor tyrosine kinase (RTK) gene rearrangements (ReAr) and fusions (fus).. <i>Journal of Clinical Oncology</i> , 2022, 40, 550-550.	1.6	0
3	Association of RB1 mutational status with overall genomic landscape in neuroendocrine prostate cancer (NEPC).. <i>Journal of Clinical Oncology</i> , 2022, 40, 156-156.	1.6	0
4	Abstract P5-13-02: Serially biopsied BRCA1/2 mutant breast tumors frequently acquire alterations in BRCA1, BRCA2, and CREBBP. <i>Cancer Research</i> , 2022, 82, P5-13-02-P5-13-02.	0.9	0
5	Impact of PD-L1 expression on conventional urothelial bladder carcinoma (UBC) genomic alteration (GA) profile.. <i>Journal of Clinical Oncology</i> , 2022, 40, 563-563.	1.6	0
6	Genomic classification of clinically advanced major genito-urinary cancers (GUca) based on methylthioadenosine phosphorylase (MTAP) genomic loss.. <i>Journal of Clinical Oncology</i> , 2022, 40, 164-164.	1.6	0
7	Comprehensive genomic profiling (CGP) of chromophobe renal cell carcinoma (chrRCC) compared with clear cell RCC (ccRCC): Impact of FLCN genomic alteration (GA) status.. <i>Journal of Clinical Oncology</i> , 2022, 40, 292-292.	1.6	0
8	Prevalence of UV Mutational Signatures Among Cutaneous Primary Tumors. <i>JAMA Network Open</i> , 2022, 5, e223833.	5.9	11
9	OUP accepted manuscript. <i>Oncologist</i> , 2022, , .	3.7	1
10	Clinicopathologic and Genomic Landscape of Non-Small Cell Lung Cancer Brain Metastases. <i>Oncologist</i> , 2022, 27, 839-848.	3.7	18
11	Homologous Recombination Repair in Biliary Tract Cancers: A Prime Target for PARP Inhibition?. <i>Cancers</i> , 2022, 14, 2561.	3.7	4
12	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	27.0	532
13	Genomic landscape of MSH6-mutated clinically advanced castrate-resistant prostate cancer (mCRPC).. <i>Journal of Clinical Oncology</i> , 2021, 39, 5062-5062.	1.6	1
14	Pan-cancer landscape of CD274 (PD-L1) copy number changes in 244 584 patient samples and the correlation with PD-L1 protein expression. , 2021, 9, e002680.		13
15	Genomic landscape of non-small cell lung cancer (NSCLC) with methylthioadenosine phosphorylase (MTAP) deletion.. <i>Journal of Clinical Oncology</i> , 2021, 39, 9116-9116.	1.6	0
16	Clinically advanced pelvic squamous cell carcinomas (pSCC) in men and women: A comprehensive genomic profiling (CGP) study.. <i>Journal of Clinical Oncology</i> , 2021, 39, 3130-3130.	1.6	1
17	Comprehensive molecular profiling of pleural mesothelioma according to histologic subtype.. <i>Journal of Clinical Oncology</i> , 2021, 39, 8555-8555.	1.6	0
18	Pan-cancer analysis of CD274 (PD-L1) mutations in 314,631 patient samples and subset correlation with PD-L1 protein expression.. <i>Journal of Clinical Oncology</i> , 2021, 39, 2605-2605.	1.6	0

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19	Clinicopathologic and Genomic Landscape of Breast Carcinoma Brain Metastases. <i>Oncologist</i> , 2021, 26, 835-844.	3.7	16
20	Abstract 2231: Utility of plasma tumor fraction (TF) to inform sensitivity of FoundationOne Liquid CDx (F1LCDx). <i>Cancer Research</i> , 2021, 81, 2231-2231.	0.9	6
21	Contrasting genomic profiles from metastatic sites, primary tumors, and liquid biopsies of advanced prostate cancer. <i>Cancer</i> , 2021, 127, 4557-4564.	4.1	5
22	Identification of KMT2A-ARHGEF12 fusion in a child with a high-grade B-cell lymphoma. <i>Cancer Genetics</i> , 2021, 258-259, 23-26.	0.4	4
23	Germline Sequencing Improves Tumor-Only Sequencing Interpretation in a Precision Genomic Study of Patients With Pediatric Solid Tumor. <i>JCO Precision Oncology</i> , 2021, 5, 1840-1852.	3.0	8
24	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	1.6	270
25	Peptide- α -TLR-7/8a conjugate vaccines chemically programmed for nanoparticle self-assembly enhance CD8 T-cell immunity to tumor antigens. <i>Nature Biotechnology</i> , 2020, 38, 320-332.	17.5	210
26	Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. <i>Nature Communications</i> , 2019, 10, 1489.	12.8	220
27	Prevalence of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants in a large, unselected breast cancer cohort. <i>International Journal of Cancer</i> , 2019, 144, 1195-1204.	5.1	31
28	Targeted Resequencing of the Coding Sequence of 38 Genes Near Breast Cancer GWAS Loci in a Large Case-Control Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 822-825.	2.5	7
29	Inherited mutations in <i>BRCA1</i> and <i>BRCA2</i> in an unselected multiethnic cohort of Asian patients with breast cancer and healthy controls from Malaysia. <i>Journal of Medical Genetics</i> , 2018, 55, 97-103.	3.2	34
30	Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. <i>Cancer Research</i> , 2018, 78, 6329-6338.	0.9	19
31	Prediction of DNA Repair Inhibitor Response in Short-Term Patient-Derived Ovarian Cancer Organoids. <i>Cancer Discovery</i> , 2018, 8, 1404-1421.	9.4	311
32	Topology of Interactions between Titin Molecules and Myosin Thick Filaments. <i>Biophysical Journal</i> , 2018, 114, 646a.	0.5	1
33	Topology of interaction between titin and myosin thick filaments. <i>Journal of Structural Biology</i> , 2018, 203, 46-53.	2.8	5
34	Rare, protein-truncating variants in <i>ATM</i> , <i>CHEK2</i> and <i>PALB2</i> , but not <i>XRCC2</i> , are associated with increased breast cancer risks. <i>Journal of Medical Genetics</i> , 2017, 54, 732-741.	3.2	68
35	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies <i>TANGO2</i> , <i>OR5H14</i> , and <i>CHAD</i> as new prostate cancer susceptibility genes. <i>Oncotarget</i> , 2017, 8, 1495-1507.	1.8	11
36	Biallelic BRCA2 Mutations Shape the Somatic Mutational Landscape of Aggressive Prostate Tumors. <i>American Journal of Human Genetics</i> , 2016, 98, 818-829.	6.2	34

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37	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
38	Homologous Mutation to Human BRAF V600E Is Common in Naturally Occurring Canine Bladder Cancer—Evidence for a Relevant Model System and Urine-Based Diagnostic Test. <i>Molecular Cancer Research</i> , 2015, 13, 993-1002.	3.4	117
39	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. <i>Genome Research</i> , 2015, 25, 1646-1655.	5.5	63
40	Dysregulation of the homeobox transcription factor gene <i>HOXB13</i> : role in prostate cancer. <i>Pharmacogenomics and Personalized Medicine</i> , 2014, 7, 193.	0.7	25
41	A Copy Number Variant at the <i>KITLG</i> Locus Likely Confers Risk for Canine Squamous Cell Carcinoma of the Digit. <i>PLoS Genetics</i> , 2013, 9, e1003409.	3.5	60
42	Structure of Synthetic Vertebrate Myosin Thick Filaments Explored with High-Resolution AFM. <i>Biophysical Journal</i> , 2013, 104, 308a-309a.	0.5	0
43	Variation of <i>BMP3</i> Contributes to Dog Breed Skull Diversity. <i>PLoS Genetics</i> , 2012, 8, e1002849.	3.5	159
44	Making a definitive diagnosis: Successful clinical application of whole exome sequencing in a child with intractable inflammatory bowel disease. <i>Genetics in Medicine</i> , 2011, 13, 255-262.	2.4	651
45	Periodically Arranged Interactions within the Myosin Filament Backbone Revealed by Mechanical Unzipping. <i>Journal of Molecular Biology</i> , 2008, 377, 307-310.	4.2	12