Jeanette E Eckel-Passow

List of Publications by Year
in descending order

77 papers	4,875 citations	147801 31 h-index	98798 67 g-index
78 all docs	78 docs citations	78 times ranked	10433 citing authors

#	Article	IF	Citations
1	Preclinical modeling in glioblastoma patient-derived xenograft (GBM PDX) xenografts to guide clinical development of lisavanbulinâ€"a novel tumor checkpoint controller targeting microtubules. Neuro-Oncology, 2022, 24, 384-395.	1.2	7
2	Pediatric brain tumor cell lines exhibit miRNA-depleted, Y RNA-enriched extracellular vesicles. Journal of Neuro-Oncology, 2022, 156, 269-279.	2.9	7
3	RBBP4-p300 axis modulates expression of genes essential for cell survival and is a potential target for therapy in glioblastoma. Neuro-Oncology, 2022, 24, 1261-1272.	1.2	6
4	Inherited genetics of adult diffuse glioma and polygenic risk scoresâ€"a review. Neuro-Oncology Practice, 2022, 9, 259-270.	1.6	3
5	The immunogenetics of viral antigen response is associated with subtype-specific glioma risk and survival. American Journal of Human Genetics, 2022, 109, 1105-1116.	6.2	7
6	Effects of Heterozygous Variants in the Leptin-Melanocortin Pathway on Roux-en-Y Gastric Bypass Outcomes: a 15-Year Caseâ€"Control Study. Obesity Surgery, 2022, 32, 2632-2640.	2.1	15
7	CpGtools: a python package for DNA methylation analysis. Bioinformatics, 2021, 37, 1598-1599.	4.1	19
8	Functional analysis of low-grade glioma genetic variants predicts key target genes and transcription factors. Neuro-Oncology, 2021, 23, 638-649.	1.2	9
9	Identification of DNA methylation signatures associated with poor outcome in lower-risk Stage, Size, Grade and Necrosis (SSIGN) score clear cell renal cell cancer. Clinical Epigenetics, 2021, 13, 12.	4.1	8
10	Statistical analysis of comparative tumor growth repeated measures experiments in the ovarian cancer patient derived xenograft (PDX) setting. Scientific Reports, 2021, 11, 8076.	3.3	9
11	Heterogeneous delivery across the blood-brain barrier limits the efficacy of an EGFR-targeting antibody drug conjugate in glioblastoma. Neuro-Oncology, 2021, 23, 2042-2053.	1.2	37
12	Generative Adversarial Networks to Synthesize Missing T1 and FLAIR MRI Sequences for Use in a Multisequence Brain Tumor Segmentation Model. Radiology, 2021, 299, 313-323.	7.3	46
13	Precision Medicine for Obesity. Digestive Disease Interventions, 2021, 05, 239-248.	0.2	9
14	Experimental Design of Preclinical Experiments: Number of PDX Lines versus Subsampling within PDX Lines. Neuro-Oncology, 2021, 23, 2066-2075.	1.2	1
15	Association of gastric emptying with postprandial appetite and satiety sensations in obesity. Obesity, 2021, 29, 1497-1507.	3.0	13
16	Glioma: interaction of acquired and germline genetics. Aging, 2021, 13, 19085-19087.	3.1	1
17	Glioma risk associated with extent of estimated European genetic ancestry in African Americans and Hispanics. International Journal of Cancer, 2020, 146, 739-748.	5.1	23
18	Concordance of PDâ€1 and PDâ€L1 (B7â€H1) in paired primary and metastatic clear cell renal cell carcinoma. Cancer Medicine, 2020, 9, 1152-1160.	2.8	17

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19	8q24 clear cell renal cell carcinoma germline variant is associated with VHL mutation status and clinical aggressiveness. BMC Urology, 2020, 20, 173.	1.4	1
20	Adult diffuse glioma GWAS by molecular subtype identifies variants inD2HGDHandFAM20C. Neuro-Oncology, 2020, 22, 1602-1613.	1.2	19
21	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. Clinical Cancer Research, 2020, 26, 1094-1104.	7.0	124
22	Sex-specific gene and pathway modeling of inherited glioma risk. Neuro-Oncology, 2019, 21, 71-82.	1.2	52
23	Molecular profiling of long-term IDH-wildtype glioblastoma survivors. Neuro-Oncology, 2019, 21, 1458-1469.	1.2	47
24	Using germline variants to estimate glioma and subtype risks. Neuro-Oncology, 2019, 21, 451-461.	1.2	23
25	Identification of factors associated with duplicate rate in ChIP-seq data. PLoS ONE, 2019, 14, e0214723.	2.5	6
26	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€”A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	8.4	59
27	Transcriptome-Wide Association Study Identifies New Candidate Susceptibility Genes for Glioma. Cancer Research, 2019, 79, 2065-2071.	0.9	26
28	Prevalent Homozygous Deletions of Type I Interferon and Defensin Genes in Human Cancers Associate with Immunotherapy Resistance. Clinical Cancer Research, 2018, 24, 3299-3308.	7.0	37
29	Mendelian randomisation study of the relationship between vitamin D and risk of glioma. Scientific Reports, 2018, 8, 2339.	3.3	23
30	Impact of atopy on risk of glioma: a Mendelian randomisation study. BMC Medicine, 2018, 16, 42.	5.5	38
31	Influence of obesity-related risk factors in the aetiology of glioma. British Journal of Cancer, 2018, 118, 1020-1027.	6.4	32
32	Molecular subtyping of tumors from patients with familial glioma. Neuro-Oncology, 2018, 20, 810-817.	1.2	8
33	TMOD-18. THE PATIENT DERIVED XENOGRAFT NATIONAL RESOURCE: A COMPREHENSIVE COLLECTION OF HIGH-GRADE GLIOMA MODELS FOR PRE-CLINICAL AND TRANSLATIONAL STUDIES. Neuro-Oncology, 2018, 20, vi272-vi272.	1.2	0
34	Ageâ€specific genomeâ€wide association study in glioblastoma identifies increased proportion of â€˜lower grade gliomaâ€™â€like features associated with younger age. International Journal of Cancer, 2018, 143, 2359-2366.	5.1	21
35	Sex-specific glioma genome-wide association study identifies new risk locus at 3p21.31 in females, and finds sex-differences in risk at 8q24.21. Scientific Reports, 2018, 8, 7352.	3.3	56
36	Adult infiltrating gliomas with WHO 2016 integrated diagnosis: additional prognostic roles of ATRX and TERT. Acta Neuropathologica, 2017, 133, 1001-1016.	7.7	245

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37	Management of diffuse low-grade gliomas in adults â€" use of molecular diagnostics. Nature Reviews Neurology, 2017, 13, 340-351.	10.1	95
38	Clear Cell Type A and B Molecular Subtypes in Metastatic Clear Cell Renal Cell Carcinoma: Tumor Heterogeneity and Aggressiveness. European Urology, 2017, 71, 979-985.	1.9	52
39	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	12.8	106
40	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	21.4	259
41	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
42	Coffee consumption and risk of renal cell carcinoma. Cancer Causes and Control, 2017, 28, 857-866.	1.8	16
43	BAP1 and PBRM1 in metastatic clear cell renal cell carcinoma: tumor heterogeneity and concordance with paired primary tumor. BMC Urology, 2017, 17, 19.	1.4	26
44	Multicenter Validation of Enhancer of Zeste Homolog 2 Expression as an Independent Prognostic Marker in Localized Clear Cell Renal Cell Carcinoma. Journal of Clinical Oncology, 2017, 35, 3706-3713.	1.6	34
45	Determining the frequency of pathogenic germline variants from exome sequencing in patients with castrate-resistant prostate cancer. BMJ Open, 2016, 6, e010332.	1.9	32
46	Validation of Gene Expression Signatures to Identify Low-risk Clear-cell Renal Cell Carcinoma Patients at Higher Risk for Disease-related Death. European Urology Focus, 2016, 2, 608-615.	3.1	7
47	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
48	Multiplex matrix network analysis of protein complexes in the human TCR signalosome. Science Signaling, 2016, 9, rs7.	3.6	30
49	Measure transcript integrity using RNA-seq data. BMC Bioinformatics, 2016, 17, 58.	2.6	187
50	Statistical considerations on prognostic models for glioma. Neuro-Oncology, 2016, 18, 609-623.	1.2	20
51	Understanding inherited genetic risk of adult glioma â€" a review. Neuro-Oncology Practice, 2016, 3, 10-16.	1.6	62
52	Loss of histone H3 lysine 36 trimethylation is associated with an increased risk of renal cell carcinoma-specific death. Modern Pathology, 2016, 29, 34-42.	5.5	55
53	A microRNA biomarker panel for the non-invasive detection of bladder cancer. Oncotarget, 2016, 7, 86290-86299.	1.8	58
54	Urinary mRNA biomarker panel for the detection of urothelial carcinoma. Oncotarget, 2016, 7, 38731-38740.	1.8	30

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55	Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. PLoS ONE, 2015, 10, e0145176.	2.5	26
56	Glioma Groups Based on 1p/19q,IDH, andTERTPromoter Mutations in Tumors. New England Journal of Medicine, 2015, 372, 2499-2508.	27.0	1,632
57	Genomic Analysis Reveals That Immune Function Genes Are Strongly Linked to Clinical Outcome in the North Central Cancer Treatment Group N9831 Adjuvant Trastuzumab Trial. Journal of Clinical Oncology, 2015, 33, 701-708.	1.6	171
58	Telomere maintenance and the etiology of adult glioma. Neuro-Oncology, 2015, 17, 1445-1452.	1.2	70
59	The Efficacy of the Wee1 Inhibitor MK-1775 Combined with Temozolomide Is Limited by Heterogeneous Distribution across the Bloodâ€“Brain Barrier in Glioblastoma. Clinical Cancer Research, 2015, 21, 1916-1924.	7.0	86
60	A Heritable Missense Polymorphism in CDKN2A Confers Strong Risk of Childhood Acute Lymphoblastic Leukemia and Is Preferentially Selected during Clonal Evolution. Cancer Research, 2015, 75, 4884-4894.	0.9	38
61	The association of copy number variation and percent mammographic density. BMC Research Notes, 2015, 8, 297.	1.4	2
62	Delineation ofMGMTHypermethylation as a Biomarker for Veliparib-Mediated Temozolomide-Sensitizing Therapy of Glioblastoma. Journal of the National Cancer Institute, 2015, 108, djv369.	6.3	102
63	Loss of PBRM1 and BAP1 expression is less common in nonâ€“clear cell renal cell carcinoma than in clear cell renal cell carcinoma. Urologic Oncology: Seminars and Original Investigations, 2015, 33, 23.e9-23.e14.	1.6	40
64	Assessing the clinical use of clear cell renal cell carcinoma molecular subtypes identified by RNA expression analysis1These authors contributed equally to the writing of this article.. Urologic Oncology: Seminars and Original Investigations, 2015, 33, 68.e17-68.e23.	1.6	10
65	Somatic expression of ENRAGE is associated with obesity status among patients with clear cell renal cell carcinoma. Carcinogenesis, 2014, 35, 822-827.	2.8	18
66	Higher Expression of Topoisomerase II Alpha Is an Independent Marker of Increased Risk of Cancer-specific Death in Patients with Clear Cell Renal Cell Carcinoma. European Urology, 2014, 66, 929-935.	1.9	29
67	Variants near TERT and TERC influencing telomere length are associated with high-grade glioma risk. Nature Genetics, 2014, 46, 731-735.	21.4	161
68	Re: Samira A. Brooks, A. Rose Brannon, Joel S. Parker, et al. ClearCode34: A Prognostic Risk Predictor for Localized Clear Cell Renal Cell Carcinoma. Eur Urol 2014;66:77â€“84. European Urology, 2014, 66, e90-e91.	1.9	2
69	A new statistic for identifying batch effects in high-throughput genomic data that uses guided principal component analysis. Bioinformatics, 2013, 29, 2877-2883.	4.1	118
70	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	2.9	31
71	Software comparison for evaluating genomic copy number variation for Affymetrix 6.0 SNP array platform. BMC Bioinformatics, 2011, 12, 220.	2.6	51
72	Tissue microarrays: one size does not fit all. Diagnostic Pathology, 2010, 5, 48.	2.0	42

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73	Whole Genome Copy Number Variation Analysis of Chronic Lymphocytic Leukemia (CLL) Cells From Early-Intermediate Stage, High Risk CLL Patients Prior to First Treatment Reveals New Loss of Heterozygosity and Duplication Events in the CLL Genome.. Blood, 2009, 114, 1265-1265.	1.4	0
74	Aberrant Regulation of the LEF-1 Locus in Monoclonal B Cell Lymphocytosis (MBL) and Chronic Lymphocytic Leukemia (CLL): A Possible Role for Epigenetic Regulation.. Blood, 2009, 114, 669-669.	1.4	2
75	Complex Interstitial Deletions of 11q and Copy-Neutral Loss of Heterozygosity of 11q Are Detected by Whole Genome Copy Number Variation Analysis of Early-Intermediate Stage, High Risk Chronic Lymphocytic Leukemia Patients.. Blood, 2009, 114, 1245-1245.	1.4	0
76	Overexpression of the LEF-1 and TCF4 Transcription Factors in B-CLL: Further Evidence for a Role of the Wnt Signaling Pathway in B-CLL Biology and Leukemogenesis. Blood, 2008, 112, 544-544.	1.4	1
77	Experimental Design and Analysis of Antibody Microarrays: Applying Methods from cDNA Arrays. Cancer Research, 2005, 65, 2985-2989.	0.9	41