Heather L Mulder

List of Publications by Year
in descending order

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47 papers	5,052 citations	257450 24 h-index	265206 42 g-index
47 all docs	47 docs citations	47 times ranked	9849 citing authors

#	Article	IF	Citations
1	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	2.7	5
2	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. Genome Medicine, 2022, 14, 32.	8.2	12
3	Somatic LINE-1 promoter acquisition drives oncogenic FOXR2 activation in pediatric brain tumor. Acta Neuropathologica, 2022, 143, 605-607.	7.7	4
4	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 597-605.	6.3	37
5	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	8.8	15
6	Persistent variations of blood DNA methylation associated with treatment exposures and risk for cardiometabolic outcomes in long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Genome Medicine, 2021, 13, 53.	8.2	16
7	The Association of Mitochondrial Copy Number With Sarcopenia in Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 1570-1580.	6.3	7
8	Abstract 685: A social epigenomic investigation of racial disparity in pulmonary impairment among aging survivors of childhood cancer. , 2021, , .		0
9	Abstract 904: Epigenome-wide association study of dyslipidemia in survivors of childhood cancer: A report from the St. Jude lifetime cohort. , 2021, , .		0
10	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2096-2104.	2.5	11
11	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. Blood Cancer Discovery, 2021, 2, 586-599.	5.0	21
12	In a multi-institutional cohort of myeloid sarcomas, NFE2 mutation prevalence is lower than previously reported. Blood Advances, 2021, 5, 5057-5059.	5.2	2
13	Estimated number of adult survivors of childhood cancer in United States with cancerâ€predisposing germline variants. Pediatric Blood and Cancer, 2020, 67, e28047.	1.5	13
14	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	12.8	87
15	Pathogenic Germline Mutations in DNA Repair Genes in Combination With Cancer Treatment Exposures and Risk of Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2020, 38, 2728-2740.	1.6	34
16	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66
17	Shortened Leukocyte Telomere Length Associates with an Increased Prevalence of Chronic Health Conditions among Survivors of Childhood Cancer: A Report from the St. Jude Lifetime Cohort. Clinical Cancer Research, 2020, 26, 2362-2371.	7.0	34
18	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171

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19	Latent cellular analysis robustly reveals subtle diversity in large-scale single-cell RNA-seq data. Nucleic Acids Research, 2019, 47, e143-e143.	14.5	26
20	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
21	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. Nature Medicine, 2019, 25, 597-602.	30.7	61
22	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	8.8	196
23	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
24	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	7.7	63
25	Polygenic risk of subsequent thyroid cancer after childhood cancer: A report from St. Jude lifetime cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2019, 37, 10060-10060.	1.6	0
26	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
27	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). Clinical Cancer Research, 2018, 24, 6230-6235.	7.0	18
28	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
29	Data Access and Interactive Visualization of Whole Genome Sequence of Sickle Cell Patients within the St. Jude Cloud. Blood, 2018, 132, 723-723.	1.4	2
30	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	1.4	3
31	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. Blood, 2018, 132, 917-917.	1.4	0
32	Pediatric nonâ€“Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. Nature Genetics, 2017, 49, 451-456.	21.4	152
33	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
34	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
35	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathologica, 2016, 131, 833-845.	7.7	288
36	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148

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37	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
38	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
39	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	1.4	1
40	Next Generation Sequencing Identifies a Novel Subset of Non-Down Syndrome Acute Megakaryoblastic Leukemia Characterized By Chimeric Transcripts Involving HOX Cluster Genes. Blood, 2015, 126, 171-171.	1.4	0
41	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	1.2	1
42	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
43	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
44	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
45	Analysis of TERT promoter mutations in pediatric melanoma.. Journal of Clinical Oncology, 2014, 32, 9023-9023.	1.6	2
46	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252
47	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. Cancer Cell, 2012, 22, 683-697.	16.8	213