Heather L Mulder

List of Publications by Year
in descending order

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	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
2	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
3	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
4	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
5	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
6	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252
7	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
8	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
9	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
10	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	8.8	196
11	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
12	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
13	Pediatric non–Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. Nature Genetics, 2017, 49, 451-456.	21.4	152
14	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
15	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
16	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
17	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	12.8	87
18	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66

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19	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	7.7	63
20	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
21	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
22	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
23	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
24	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
25	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
26	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
27	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
28	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
29	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
30	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	8.8	15
31	Estimated number of adult survivors of childhood cancer in United States with cancer€predisposing germline variants. Pediatric Blood and Cancer, 2020, 67, e28047.	1.5	13
32	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
33	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
34	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
35	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	2.7	5
36	Somatic LINE-1 promoter acquisition drives oncogenic FOXR2 activation in pediatric brain tumor. Acta Neuropathologica, 2022, 143, 605-607.	7.7	4

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37	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	1.4	3
38	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
39	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
40	Analysis of TERT promoter mutations in pediatric melanoma.. Journal of Clinical Oncology, 2014, 32, 9023-9023.	1.6	2
41	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	1.2	1
42	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	1.4	1
43	Abstract 685: A social epigenomic investigation of racial disparity in pulmonary impairment among aging survivors of childhood cancer. , 2021, , .		0
44	Abstract 904: Epigenome-wide association study of dyslipidemia in survivors of childhood cancer: A report from the St. Jude lifetime cohort. , 2021, , .		0
45	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
46	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. Blood, 2018, 132, 917-917.	1.4	0
47	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