Helen M Hansen

List of Publications by Year
in descending order

51 papers	1,926 citations	394286 19 h-index	276775 41 g-index
51 all docs	51 docs citations	51 times ranked	4551 citing authors

#	Article	IF	Citations
1	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.	9.4	259
2	Adult infiltrating gliomas with WHO 2016 integrated diagnosis: additional prognostic roles of ATRX and TERT. Acta Neuropathologica, 2017, 133, 1001-1016.	3.9	245
3	An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray. Genome Biology, 2018, 19, 64.	3.8	245
4	Variants near TERT and TERC influencing telomere length are associated with high-grade glioma risk. Nature Genetics, 2014, 46, 731-735.	9.4	161
5	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling. Nature Communications, 2022, 13, 761.	5.8	93
6	Longer genotypically-estimated leukocyte telomere length is associated with increased adult glioma risk. Oncotarget, 2015, 6, 42468-42477.	0.8	87
7	GWAS in childhood acute lymphoblastic leukemia reveals novel genetic associations at chromosomes 17q12 and 8q24.21. Nature Communications, 2018, 9, 286.	5.8	75
8	Genetic Variation Associated with Longer Telomere Length Increases Risk of Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1043-1049.	1.1	61
9	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. Clinical Epigenetics, 2017, 9, 10.	1.8	60
10	Sex-specific gene and pathway modeling of inherited glioma risk. Neuro-Oncology, 2019, 21, 71-82.	0.6	52
11	Genome-wide association study confirms lung cancer susceptibility loci on chromosomes 5p15 and 15q25 in an African-American population. Lung Cancer, 2016, 98, 33-42.	0.9	49
12	Genetic Risk Can Be Decreased: Quitting Smoking Decreases and Delays Lung Cancer for Smokers With High and Low CHRNA5 Risk Genotypes â€" A Meta-Analysis. EBioMedicine, 2016, 11, 219-226.	2.7	40
13	Fine mapping of chromosome 15q25.1 lung cancer susceptibility in African-Americans. Human Molecular Genetics, 2010, 19, 3652-3661.	1.4	38
14	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.	0.4	38
15	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	0.6	37
16	The genome-wide impact of trisomy 21 on DNA methylation and its implications for hematopoiesis. Nature Communications, 2021, 12, 821.	5.8	32
17	Correlates of Prenatal and Early-Life Tobacco Smoke Exposure and Frequency of Common Gene Deletions in Childhood Acute Lymphoblastic Leukemia. Cancer Research, 2017, 77, 1674-1683.	0.4	28
18	DNA Quantification of Whole Genome Amplified Samples for Genotyping on a Multiplexed Bead Array Platform. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1686-1690.	1.1	27

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19	Germline cancer predisposition variants and pediatric glioma: a population-based study in California. Neuro-Oncology, 2020, 22, 864-874.	0.6	24
20	BMI1 enhancer polymorphism underlies chromosome 10p12.31 association with childhood acute lymphoblastic leukemia. International Journal of Cancer, 2018, 143, 2647-2658.	2.3	23
21	Using germline variants to estimate glioma and subtype risks. Neuro-Oncology, 2019, 21, 451-461.	0.6	23
22	Common genetic variation and risk of osteosarcoma in a multi-ethnic pediatric and adolescent population. Bone, 2020, 130, 115070.	1.4	22
23	Mendelian randomization provides support for obesity as a risk factor for meningioma. Scientific Reports, 2019, 9, 309.	1.6	21
24	Genetic determinants of childhood and adult height associated with osteosarcoma risk. Cancer, 2018, 124, 3742-3752.	2.0	20
25	Adult diffuse glioma GWAS by molecular subtype identifies variants inD2HGDHandFAM20C. Neuro-Oncology, 2020, 22, 1602-1613.	0.6	19
26	Heritable variation at the chromosome 21 gene ERG is associated with acute lymphoblastic leukemia risk in children with and without Down syndrome. Leukemia, 2019, 33, 2746-2751.	3.3	18
27	Predisposing germline mutations in high hyperdiploid acute lymphoblastic leukemia in children. Genes Chromosomes and Cancer, 2019, 58, 723-730.	1.5	17
28	Accelerated epigenetic aging in newborns with Down syndrome. Aging Cell, 2022, 21, .	3.0	17
29	European genetic ancestry associated with risk of childhood ependymoma. Neuro-Oncology, 2020, 22, 1637-1646.	0.6	16
30	Genetic predisposition to longer telomere length and risk of childhood, adolescent and adult-onset ependymoma. Acta Neuropathologica Communications, 2020, 8, 173.	2.4	15
31	Clonal and microclonal mutational heterogeneity in high hyperdiploid acute lymphoblastic leukemia. Oncotarget, 2016, 7, 72733-72745.	0.8	12
32	Longer genotypically-estimated leukocyte telomere length is associated with increased meningioma risk. Journal of Neuro-Oncology, 2019, 142, 479-487.	1.4	11
33	Interactions of Age and Blood Immune Factors and Noninvasive Prediction of Glioma Survival. Journal of the National Cancer Institute, 2022, 114, 446-457.	3.0	11
34	The immunogenetics of viral antigen response is associated with subtype-specific glioma risk and survival. American Journal of Human Genetics, 2022, 109, 1105-1116.	2.6	7
35	Somatic Mutation Allelic Ratio Test Using ddPCR (SMART-ddPCR): An Accurate Method for Assessment of Preferential Allelic Imbalance in Tumor DNA. PLoS ONE, 2015, 10, e0143343.	1.1	4
36	Germline polymorphisms in myeloid-associated genes are not associated with survival in glioma patients. Journal of Neuro-Oncology, 2018, 136, 33-39.	1.4	4

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37	Two HLA Class II Gene Variants Are Independently Associated with Pediatric Osteosarcoma Risk. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1151-1158.	1.1	4
38	Tobacco Smoke and Ras Mutations Among Latino and Non-Latino Children with Acute Lymphoblastic Leukemia. Archives of Medical Research, 2016, 47, 677-683.	1.5	3
39	Interaction between maternal killer immunoglobulin-like receptors and offspring HLAs and susceptibility of childhood ALL. Blood Advances, 2022, 6, 3756-3766.	2.5	3
40	COMP-05. EVALUATION OF A DEEP LEARNING ARCHITECTURE FOR MRI PREDICTION OF IDH, 1p19q AND TERT IN GLIOMA PATIENTS. Neuro-Oncology, 2018, 20, vi64-vi64.	0.6	2
41	Immune factors preceding diagnosis of glioma: a Prostate Lung Colorectal Ovarian Cancer Screening Trial nested caseâ€“control study. Neuro-Oncology Advances, 2019, 1, vdz031.	0.4	2
42	Epigenome-wide association study of acute lymphoblastic leukemia in children with Down syndrome. Blood Advances, 2022, 6, 4132-4136.	2.5	1
43	GENE-55. CONSTITUTIONAL MUTATIONS IN TERT AND MENINGIOMA RISK. Neuro-Oncology, 2017, 19, vi104-vi105.	0.6	0
44	EPID-12. USING GERMLINE VARIANTS TO PREDICT GLIOMA RISK AND IDENTIFY GLIOMA SUBTYPE PRE-OPERATIVELY. Neuro-Oncology, 2018, 20, vi82-vi82.	0.6	0
45	IMMU-07. IMMUNE PROFILES IN THE SAN FRANCISCO ADULT GLIOMA STUDY (AGS) USING IMMUNOMETHYLOMICS. Neuro-Oncology, 2018, 20, vi122-vi122.	0.6	0
46	EPID-04. LEVERAGING GENOMIC DATA TO IDENTIFY RISK FACTORS FOR CHILDHOOD EPENDYMOMA. Neuro-Oncology, 2018, 20, vi80-vi80.	0.6	0
47	Epigenome-Wide Association Study of Acute Lymphoblastic Leukemia in Children with Down Syndrome. Blood, 2021, 138, 214-214.	0.6	0
48	BIOM-13. DNA METHYLATION MARKS GLUCOCORTICOID PATHWAY RESPONSE IN DEXAMETHASONE-TREATED BRAIN TUMOR PATIENTS. Neuro-Oncology, 2020, 22, ii4-ii4.	0.6	0
49	EPID-08. PRE-SURGERY IMMUNE PROFILES OF ADULT GLIOMA PATIENTS. Neuro-Oncology, 2020, 22, ii79-ii80.	0.6	0
50	EPCO-25. AN IMMUNOMETHYLOMIC PLATFORM INTEGRATING SYSTEMIC IMMUNE PROFILES AND EPIGENETIC AGE IN NEURO-ONCOLOGY. Neuro-Oncology, 2020, 22, ii74-ii74.	0.6	0
51	BIOM-50. GENETIC PREDISPOSITION TO LONGER TELOMERE LENGTH AND RISK OF CHILDHOOD, ADOLESCENT AND ADULT-ONSET EPENDYMOMA. Neuro-Oncology, 2020, 22, ii12-ii12.	0.6	0