Adam J De Smith

List of Publications by Year
in descending order

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74 papers	2,966 citations	218381 26 h-index	174990 52 g-index
77 all docs	77 docs citations	77 times ranked	5975 citing authors

#	Article	IF	Citations
1	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. Leukemia, 2022, 36, 865-868.	3.3	9
2	Mitochondrial 1555 G>A variant as a potential risk factor for childhood glioblastoma. Neuro-Oncology Advances, 2022, 4, vdac045.	0.4	1
3	Interaction between maternal killer immunoglobulin-like receptors and offspring HLAs and susceptibility of childhood ALL. Blood Advances, 2022, 6, 3756-3766.	2.5	3
4	Epigenome-wide association study of acute lymphoblastic leukemia in children with Down syndrome. Blood Advances, 2022, 6, 4132-4136.	2.5	1
5	Investigating DNA methylation as a mediator of genetic risk in childhood acute lymphoblastic leukemia. Human Molecular Genetics, 2022, 31, 3741-3756.	1.4	0
6	Variant to function mapping at single-cell resolution through network propagation. Nature Biotechnology, 2022, 40, 1644-1653.	9.4	25
7	Trends in Acute Lymphoblastic Leukemia Incidence in the United States by Race/Ethnicity From 2000 to 2016. American Journal of Epidemiology, 2021, 190, 519-527.	1.6	23
8	Cancer health disparities in racial/ethnic minorities in the United States. British Journal of Cancer, 2021, 124, 315-332.	2.9	447
9	The genome-wide impact of trisomy 21 on DNA methylation and its implications for hematopoiesis. Nature Communications, 2021, 12, 821.	5.8	32
10	In utero and early-life exposure to thirdhand smoke causes profound changes to the immune system. Clinical Science, 2021, 135, 1053-1063.	1.8	8
11	Epigenetic Biomarkers of Prenatal Tobacco Smoke Exposure Are Associated with Gene Deletions in Childhood Acute Lymphoblastic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1517-1525.	1.1	7
12	Exploring the genetic and epigenetic origins of juvenile myelomonocytic leukemia using newborn screening samples. Leukemia, 2021, , .	3.3	9
13	Genetic determinants of blood-cell traits influence susceptibility to childhood acute lymphoblastic leukemia. American Journal of Human Genetics, 2021, 108, 1823-1835.	2.6	37
14	Evaluation of DNA Methylation at Birth in Monozygotic Twin Pairs Discordant for Acute Lymphoblastic Leukemia. Blood, 2021, 138, 2278-2278.	0.6	3
15	Epigenome-Wide Association Study of Acute Lymphoblastic Leukemia in Children with Down Syndrome. Blood, 2021, 138, 214-214.	0.6	0
16	Whole-Exome Sequencing in Multiplex Families to Identify Novel AYA Classical Hodgkin Lymphoma Predisposition Genes. Blood, 2021, 138, 3499-3499.	0.6	1
17	The Effect of Cytomegalovirus on Pediatric Acute Lymphoblastic Leukemia. Blood, 2021, 138, 2281-2281.	0.6	1
18	Common genetic variation and risk of osteosarcoma in a multi-ethnic pediatric and adolescent population. Bone, 2020, 130, 115070.	1.4	22

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19	European genetic ancestry associated with risk of childhood ependymoma. Neuro-Oncology, 2020, 22, 1637-1646.	0.6	16
20	Genetic predisposition to longer telomere length and risk of childhood, adolescent and adult-onset ependymoma. Acta Neuropathologica Communications, 2020, 8, 173.	2.4	15
21	Pediatric glioma and medulloblastoma risk and population demographics: a Poisson regression analysis. Neuro-Oncology Advances, 2020, 2, vdaa089.	0.4	6
22	Germline cancer predisposition variants and pediatric glioma: a population-based study in California. Neuro-Oncology, 2020, 22, 864-874.	0.6	24
23	History of Early Childhood Infections and Acute Lymphoblastic Leukemia Risk Among Children in a US Integrated Health-Care System. American Journal of Epidemiology, 2020, 189, 1076-1085.	1.6	5
24	Germline variants in predisposition genes in children with Down syndrome and acute lymphoblastic leukemia. Blood Advances, 2020, 4, 672-675.	2.5	5
25	Genetic Alterations Precede DNA Methylation Changes in Juvenile Myelomonocytic Leukemia. Blood, 2020, 136, 19-20.	0.6	0
26	Genetic Determinants of Blood Cell Traits Play a Role in Susceptibility to Acute Lymphoblastic Leukemia. Blood, 2020, 136, 10-11.	0.6	0
27	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	0.6	37
28	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
29	Germline genetic landscape of pediatric central nervous system tumors. Neuro-Oncology, 2019, 21, 1376-1388.	0.6	24
30	HGG-11. GERMLINE GENETIC PREDISPOSITION TO PEDIATRIC GLIOMA. Neuro-Oncology, 2019, 21, ii89-ii89.	0.6	0
31	Increased neonatal level of arginase 2 in cases of childhood acute lymphoblastic leukemia implicates immunosuppression in the etiology. Haematologica, 2019, 104, e514-e516.	1.7	8
32	Predisposing germline mutations in high hyperdiploid acute lymphoblastic leukemia in children. Genes Chromosomes and Cancer, 2019, 58, 723-730.	1.5	17
33	The Genome-Wide Impact of Trisomy 21 on DNA Methylation and Its Implications for Hematologic Malignancies. Blood, 2019, 134, 2510-2510.	0.6	2
34	GWAS in childhood acute lymphoblastic leukemia reveals novel genetic associations at chromosomes 17q12 and 8q24.21. Nature Communications, 2018, 9, 286.	5.8	75
35	A germ-line deletion of APOBEC3B does not contribute to subtype-specific childhood acute lymphoblastic leukemia etiology. Haematologica, 2018, 103, e29-e31.	1.7	1
36	PDTM-01. GERMLINE GENETIC PREDISPOSITION TO PEDIATRIC GLIOMA. Neuro-Oncology, 2018, 20, vi203-vi203.	0.6	0

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37	Genetic determinants of childhood and adult height associated with osteosarcoma risk. Cancer, 2018, 124, 3742-3752.	2.0	20
38	BMI1 enhancer polymorphism underlies chromosome 10p12.31 association with childhood acute lymphoblastic leukemia. International Journal of Cancer, 2018, 143, 2647-2658.	2.3	23
39	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
40	To ERV Is Human: A Phenotype-Wide Scan Linking Polymorphic Human Endogenous Retrovirus-K Insertions to Complex Phenotypes. Frontiers in Genetics, 2018, 9, 298.	1.1	26
41	Germline GAB2 Mutations in Childhood Acute Lymphoblastic Leukemia. Blood, 2018, 132, 388-388.	0.6	0
42	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
43	In utero cytomegalovirus infection and development of childhood acute lymphoblastic leukemia. Blood, 2017, 129, 1680-1684.	0.6	55
44	Non-additive and epistatic effects of HLA polymorphisms contributing to risk of adult glioma. Journal of Neuro-Oncology, 2017, 135, 237-244.	1.4	13
45	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
46	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
47	Common genetic variants associated with telomere length confer risk for neuroblastoma and other childhood cancers. Carcinogenesis, 2016, 37, 576-582.	1.3	60
48	Genetic contribution to variation in DNA methylation at maternal smoking-sensitive loci in exposed neonates. Epigenetics, 2016, 11, 664-673.	1.3	32
49	Clonal and microclonal mutational heterogeneity in high hyperdiploid acute lymphoblastic leukemia. Oncotarget, 2016, 7, 72733-72745.	0.8	12
50	Somatic and Germline Mutational Heterogeneity in High Hyperdiploid Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1727-1727.	0.6	0
51	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
52	PDGFRÎ± demarcates the cardiogenic clonogenic Sca1+ stem/progenitor cell in adult murine myocardium. Nature Communications, 2015, 6, 6930.	5.8	130
53	Periconceptional folate consumption is associated with neonatal DNA methylation modifications in neural crest regulatory and cancer development genes. Epigenetics, 2015, 10, 1166-1176.	1.3	41
54	Epigenetic remodeling in B-cell acute lymphoblastic leukemia occurs in two tracks and employs embryonic stem cell-like signatures. Nucleic Acids Research, 2015, 43, 2590-2602.	6.5	42

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55	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
56	The role of KIR genes and their cognate HLA class I ligands in childhood acute lymphoblastic leukemia. Blood, 2014, 123, 2497-2503.	0.6	41
57	PTPRG inhibition by DNA methylation and cooperation with RAS gene activation in childhood acute lymphoblastic leukemia. International Journal of Cancer, 2014, 135, 1101-1109.	2.3	12
58	Imprinted expression of UBE3A in non-neuronal cells from a Praderâ€“Willi syndrome patient with an atypical deletion. Human Molecular Genetics, 2014, 23, 2364-2373.	1.4	58
59	Genomic ancestry and somatic alterations correlate with age at diagnosis in Hispanic children with Bâ€cell acute lymphoblastic leukemia. American Journal of Hematology, 2014, 89, 721-725.	2.0	30
60	Missense SNP rs3731249 Explains the CDKN2A Association with Childhood ALL and Shows Risk Allele Selection in Tumors with Somatic CDKN2A Alterations. Blood, 2014, 124, 129-129.	0.6	1
61	Novel childhood ALL susceptibility locus BMI1-PIP4K2A is specifically associated with the hyperdiploid subtype. Blood, 2013, 121, 4808-4809.	0.6	46
62	GATA3 risk alleles are associated with ancestral components in Hispanic children with ALL. Blood, 2013, 122, 3385-3387.	0.6	29
63	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. PLoS ONE, 2013, 8, e58048.	1.1	33
64	A global DNA methylation and gene expression analysis of early human B-cell development reveals a demethylation signature and transcription factor network. Nucleic Acids Research, 2012, 40, 11339-11351.	6.5	95
65	Novel association approach for variable number tandem repeats (VNTRs) identifies DOCK5 as a susceptibility gene for severe obesity. Human Molecular Genetics, 2012, 21, 3727-3738.	1.4	37
66	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. Nature Biotechnology, 2011, 29, 723-730.	9.4	113
67	Investigation of the HIN200 Locus in UK SLE Families Identifies Novel Copy Number Variants. Annals of Human Genetics, 2011, 75, 383-397.	0.3	5
68	Accurate Single-Nucleotide Polymorphism Allele Assignment in Trisomic or Duplicated Regions by Using a Single Baseâ€Extension Assay with MALDI-TOF Mass Spectrometry. Clinical Chemistry, 2011, 57, 1188-1195.	1.5	10
69	Implications of copy number variation in people with chromosomal abnormalities: potential for greater variation in copy number state may contribute to variability of phenotype. The HUGO Journal, 2010, 4, 1-9.	4.1	10
70	cnvHap: an integrative population and haplotypeâ€based multiplatform model of SNPs and CNVs. Nature Methods, 2010, 7, 541-546.	9.0	44
71	A deletion of the HBII-85 class of small nucleolar RNAs (snoRNAs) is associated with hyperphagia, obesity and hypogonadism. Human Molecular Genetics, 2009, 18, 3257-3265.	1.4	253
72	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. PLoS ONE, 2008, 3, e3104.	1.1	52

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73	Array CGH analysis of copy number variation identifies 1284 new genes variant in healthy white males: implications for association studies of complex diseases. Human Molecular Genetics, 2007, 16, 2783-2794.	1.4	200
74	FCGR3B copy number variation is associated with susceptibility to systemic, but not organ-specific, autoimmunity. Nature Genetics, 2007, 39, 721-723.	9.4	421