

Adam J De Smith

List of Publications by Year in descending order

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Version: 2024-02-01

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	Cancer health disparities in racial/ethnic minorities in the United States. <i>British Journal of Cancer</i> , 2021, 124, 315-332.	2.9	447
2	FCGR3B copy number variation is associated with susceptibility to systemic, but not organ-specific, autoimmunity. <i>Nature Genetics</i> , 2007, 39, 721-723.	9.4	421
3	A deletion of the HBII-85 class of small nucleolar RNAs (snoRNAs) is associated with hyperphagia, obesity and hypogonadism. <i>Human Molecular Genetics</i> , 2009, 18, 3257-3265.	1.4	253
4	Array CGH analysis of copy number variation identifies 1284 new genes variant in healthy white males: implications for association studies of complex diseases. <i>Human Molecular Genetics</i> , 2007, 16, 2783-2794.	1.4	200
5	PDGFR β demarcates the cardiogenic clonogenic Sca1 $^{+}$ stem/progenitor cell in adult murine myocardium. <i>Nature Communications</i> , 2015, 6, 6930.	5.8	130
6	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011, 29, 723-730.	9.4	113
7	A global DNA methylation and gene expression analysis of early human B-cell development reveals a demethylation signature and transcription factor network. <i>Nucleic Acids Research</i> , 2012, 40, 11339-11351.	6.5	95
8	GWAS in childhood acute lymphoblastic leukemia reveals novel genetic associations at chromosomes 17q12 and 8q24.21. <i>Nature Communications</i> , 2018, 9, 286.	5.8	75
9	Genetic Variation Associated with Longer Telomere Length Increases Risk of Chronic Lymphocytic Leukemia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1043-1049.	1.1	61
10	Common genetic variants associated with telomere length confer risk for neuroblastoma and other childhood cancers. <i>Carcinogenesis</i> , 2016, 37, 576-582.	1.3	60
11	Imprinted expression of UBE3A in non-neuronal cells from a Prader-Willi syndrome patient with an atypical deletion. <i>Human Molecular Genetics</i> , 2014, 23, 2364-2373.	1.4	58
12	In utero cytomegalovirus infection and development of childhood acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 1680-1684.	0.6	55
13	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. <i>PLoS ONE</i> , 2008, 3, e3104.	1.1	52
14	Novel childhood ALL susceptibility locus BMI1-PIP4K2A is specifically associated with the hyperdiploid subtype. <i>Blood</i> , 2013, 121, 4808-4809.	0.6	46
15	cnvHap: an integrative population and haplotype-based multiplatform model of SNPs and CNVs. <i>Nature Methods</i> , 2010, 7, 541-546.	9.0	44
16	Epigenetic remodeling in B-cell acute lymphoblastic leukemia occurs in two tracks and employs embryonic stem cell-like signatures. <i>Nucleic Acids Research</i> , 2015, 43, 2590-2602.	6.5	42
17	The role of KIR genes and their cognate HLA class I ligands in childhood acute lymphoblastic leukemia. <i>Blood</i> , 2014, 123, 2497-2503.	0.6	41
18	Periconceptual folate consumption is associated with neonatal DNA methylation modifications in neural crest regulatory and cancer development genes. <i>Epigenetics</i> , 2015, 10, 1166-1176.	1.3	41

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19	A Heritable Missense Polymorphism in <i>CDKN2A</i> Confers Strong Risk of Childhood Acute Lymphoblastic Leukemia and Is Preferentially Selected during Clonal Evolution. <i>Cancer Research</i> , 2015, 75, 4884-4894.	0.4	38
20	Novel association approach for variable number tandem repeats (VNTRs) identifies <i>DOCK5</i> as a susceptibility gene for severe obesity. <i>Human Molecular Genetics</i> , 2012, 21, 3727-3738.	1.4	37
21	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. <i>Blood</i> , 2019, 134, 1227-1237.	0.6	37
22	Genetic determinants of blood-cell traits influence susceptibility to childhood acute lymphoblastic leukemia. <i>American Journal of Human Genetics</i> , 2021, 108, 1823-1835.	2.6	37
23	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. <i>PLoS ONE</i> , 2013, 8, e58048.	1.1	33
24	Genetic contribution to variation in DNA methylation at maternal smoking-sensitive loci in exposed neonates. <i>Epigenetics</i> , 2016, 11, 664-673.	1.3	32
25	The genome-wide impact of trisomy 21 on DNA methylation and its implications for hematopoiesis. <i>Nature Communications</i> , 2021, 12, 821.	5.8	32
26	Genomic ancestry and somatic alterations correlate with age at diagnosis in Hispanic children with B-cell acute lymphoblastic leukemia. <i>American Journal of Hematology</i> , 2014, 89, 721-725.	2.0	30
27	<i>GATA3</i> risk alleles are associated with ancestral components in Hispanic children with ALL. <i>Blood</i> , 2013, 122, 3385-3387.	0.6	29
28	Correlates of Prenatal and Early-Life Tobacco Smoke Exposure and Frequency of Common Gene Deletions in Childhood Acute Lymphoblastic Leukemia. <i>Cancer Research</i> , 2017, 77, 1674-1683.	0.4	28
29	To ERV Is Human: A Phenotype-Wide Scan Linking Polymorphic Human Endogenous Retrovirus-K Insertions to Complex Phenotypes. <i>Frontiers in Genetics</i> , 2018, 9, 298.	1.1	26
30	Variant to function mapping at single-cell resolution through network propagation. <i>Nature Biotechnology</i> , 2022, 40, 1644-1653.	9.4	25
31	Germline genetic landscape of pediatric central nervous system tumors. <i>Neuro-Oncology</i> , 2019, 21, 1376-1388.	0.6	24
32	Germline cancer predisposition variants and pediatric glioma: a population-based study in California. <i>Neuro-Oncology</i> , 2020, 22, 864-874.	0.6	24
33	<i>BMI1</i> enhancer polymorphism underlies chromosome 10p12.31 association with childhood acute lymphoblastic leukemia. <i>International Journal of Cancer</i> , 2018, 143, 2647-2658.	2.3	23
34	Trends in Acute Lymphoblastic Leukemia Incidence in the United States by Race/Ethnicity From 2000 to 2016. <i>American Journal of Epidemiology</i> , 2021, 190, 519-527.	1.6	23
35	Common genetic variation and risk of osteosarcoma in a multi-ethnic pediatric and adolescent population. <i>Bone</i> , 2020, 130, 115070.	1.4	22
36	Genetic determinants of childhood and adult height associated with osteosarcoma risk. <i>Cancer</i> , 2018, 124, 3742-3752.	2.0	20

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37	Heritable variation at the chromosome 21 gene ERG is associated with acute lymphoblastic leukemia risk in children with and without Down syndrome. <i>Leukemia</i> , 2019, 33, 2746-2751.	3.3	18
38	Predisposing germline mutations in high hyperdiploid acute lymphoblastic leukemia in children. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 723-730.	1.5	17
39	European genetic ancestry associated with risk of childhood ependymoma. <i>Neuro-Oncology</i> , 2020, 22, 1637-1646.	0.6	16
40	Genetic predisposition to longer telomere length and risk of childhood, adolescent and adult-onset ependymoma. <i>Acta Neuropathologica Communications</i> , 2020, 8, 173.	2.4	15
41	Non-additive and epistatic effects of HLA polymorphisms contributing to risk of adult glioma. <i>Journal of Neuro-Oncology</i> , 2017, 135, 237-244.	1.4	13
42	<i>PTPRG</i> inhibition by DNA methylation and cooperation with <i>RAS</i> gene activation in childhood acute lymphoblastic leukemia. <i>International Journal of Cancer</i> , 2014, 135, 1101-1109.	2.3	12
43	Clonal and microclonal mutational heterogeneity in high hyperdiploid acute lymphoblastic leukemia. <i>Oncotarget</i> , 2016, 7, 72733-72745.	0.8	12
44	Implications of copy number variation in people with chromosomal abnormalities: potential for greater variation in copy number state may contribute to variability of phenotype. <i>The HUGO Journal</i> , 2010, 4, 1-9.	4.1	10
45	Accurate Single-Nucleotide Polymorphism Allele Assignment in Trisomic or Duplicated Regions by Using a Single Base Extension Assay with MALDI-TOF Mass Spectrometry. <i>Clinical Chemistry</i> , 2011, 57, 1188-1195.	1.5	10
46	Exploring the genetic and epigenetic origins of juvenile myelomonocytic leukemia using newborn screening samples. <i>Leukemia</i> , 2021, , .	3.3	9
47	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2022, 36, 865-868.	3.3	9
48	Increased neonatal level of arginase 2 in cases of childhood acute lymphoblastic leukemia implicates immunosuppression in the etiology. <i>Haematologica</i> , 2019, 104, e514-e516.	1.7	8
49	<i>In utero</i> and early-life exposure to thirdhand smoke causes profound changes to the immune system. <i>Clinical Science</i> , 2021, 135, 1053-1063.	1.8	8
50	Epigenetic Biomarkers of Prenatal Tobacco Smoke Exposure Are Associated with Gene Deletions in Childhood Acute Lymphoblastic Leukemia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1517-1525.	1.1	7
51	Pediatric glioma and medulloblastoma risk and population demographics: a Poisson regression analysis. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa089.	0.4	6
52	Investigation of the HIN200 Locus in UK SLE Families Identifies Novel Copy Number Variants. <i>Annals of Human Genetics</i> , 2011, 75, 383-397.	0.3	5
53	History of Early Childhood Infections and Acute Lymphoblastic Leukemia Risk Among Children in a US Integrated Health-Care System. <i>American Journal of Epidemiology</i> , 2020, 189, 1076-1085.	1.6	5
54	Germline variants in predisposition genes in children with Down syndrome and acute lymphoblastic leukemia. <i>Blood Advances</i> , 2020, 4, 672-675.	2.5	5

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55	Somatic Mutation Allelic Ratio Test Using ddPCR (SMART-ddPCR): An Accurate Method for Assessment of Preferential Allelic Imbalance in Tumor DNA. <i>PLoS ONE</i> , 2015, 10, e0143343.	1.1	4
56	Two HLA Class II Gene Variants Are Independently Associated with Pediatric Osteosarcoma Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1151-1158.	1.1	4
57	Tobacco Smoke and Ras Mutations Among Latino and Non-Latino Children with Acute Lymphoblastic Leukemia. <i>Archives of Medical Research</i> , 2016, 47, 677-683.	1.5	3
58	Evaluation of DNA Methylation at Birth in Monozygotic Twin Pairs Discordant for Acute Lymphoblastic Leukemia. <i>Blood</i> , 2021, 138, 2278-2278.	0.6	3
59	Interaction between maternal killer immunoglobulin-like receptors and offspring HLAs and susceptibility of childhood ALL. <i>Blood Advances</i> , 2022, 6, 3756-3766.	2.5	3
60	The Genome-Wide Impact of Trisomy 21 on DNA Methylation and Its Implications for Hematologic Malignancies. <i>Blood</i> , 2019, 134, 2510-2510.	0.6	2
61	A germ-line deletion of APOBEC3B does not contribute to subtype-specific childhood acute lymphoblastic leukemia etiology. <i>Haematologica</i> , 2018, 103, e29-e31.	1.7	1
62	Missense SNP rs3731249 Explains the CDKN2A Association with Childhood ALL and Shows Risk Allele Selection in Tumors with Somatic CDKN2A Alterations. <i>Blood</i> , 2014, 124, 129-129.	0.6	1
63	Whole-Exome Sequencing in Multiplex Families to Identify Novel AYA Classical Hodgkin Lymphoma Predisposition Genes. <i>Blood</i> , 2021, 138, 3499-3499.	0.6	1
64	The Effect of Cytomegalovirus on Pediatric Acute Lymphoblastic Leukemia. <i>Blood</i> , 2021, 138, 2281-2281.	0.6	1
65	Mitochondrial 1555 G>A variant as a potential risk factor for childhood glioblastoma. <i>Neuro-Oncology Advances</i> , 2022, 4, v045.	0.4	1
66	Epigenome-wide association study of acute lymphoblastic leukemia in children with Down syndrome. <i>Blood Advances</i> , 2022, 6, 4132-4136.	2.5	1
67	PDTM-01. GERMLINE GENETIC PREDISPOSITION TO PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2018, 20, vi203-vi203.	0.6	0
68	HGG-11. GERMLINE GENETIC PREDISPOSITION TO PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2019, 21, ii89-ii89.	0.6	0
69	Somatic and Germline Mutational Heterogeneity in High Hyperdiploid Acute Lymphoblastic Leukemia. <i>Blood</i> , 2016, 128, 1727-1727.	0.6	0
70	Germline GAB2 Mutations in Childhood Acute Lymphoblastic Leukemia. <i>Blood</i> , 2018, 132, 388-388.	0.6	0
71	Epigenome-Wide Association Study of Acute Lymphoblastic Leukemia in Children with Down Syndrome. <i>Blood</i> , 2021, 138, 214-214.	0.6	0
72	Genetic Alterations Precede DNA Methylation Changes in Juvenile Myelomonocytic Leukemia. <i>Blood</i> , 2020, 136, 19-20.	0.6	0

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73	Genetic Determinants of Blood Cell Traits Play a Role in Susceptibility to Acute Lymphoblastic Leukemia. <i>Blood</i> , 2020, 136, 10-11.	0.6	0
74	Investigating DNA methylation as a mediator of genetic risk in childhood acute lymphoblastic leukemia. <i>Human Molecular Genetics</i> , 2022, 31, 3741-3756.	1.4	0