Andrew T Dewan

List of Publications by Year
in descending order

98 papers	4,820 citations	168829 31 h-index	111975 67 g-index
104 all docs	104 docs citations	104 times ranked	7747 citing authors

#	Article	IF	Citations
1	DNA Methylation, Preterm Birth and Blood Pressure in African American Children: The DPREG Study. Journal of Immigrant and Minority Health, 2022, 24, 334-341.	0.8	1
2	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. Leukemia, 2022, 36, 865-868.	3.3	9
3	Risk of lower respiratory tract infections: a genome-wide association study with Mendelian randomization analysis in three independent European populations. Clinical Microbiology and Infection, 2022, 28, 732.e1-732.e7.	2.8	2
4	Explaining sex differences in risk of bloodstream infections using mediation analysis in the population-based HUNT study in Norway. Scientific Reports, 2022, 12, 8436.	1.6	10
5	A pooled genome-wide association study identifies pancreatic cancer susceptibility loci on chromosome 19p12 and 19p13.3 in the full-Jewish population. Human Genetics, 2021, 140, 309-319.	1.8	2
6	Examining the effect of obesity-associated gene variants on breast cancer survivors in a randomized weight loss intervention. Breast Cancer Research and Treatment, 2021, 187, 487-497.	1.1	1
7	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
8	GWAS Identifies LINC01184/SLC12A2 as a Risk Locus for Skin and Soft Tissue Infections. Journal of Investigative Dermatology, 2021, 141, 2083-2086.e8.	0.3	4
9	Proteinarium: Multi-sample protein-protein interaction analysis and visualization tool. Genomics, 2020, 112, 4288-4296.	1.3	10
10	In-Depth Analysis of Genetic Variation Associated with Severe West Nile Viral Disease. Vaccines, 2020, 8, 744.	2.1	3
11	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003413.	3.9	15
12	Genetic Determinants of Blood Cell Traits Play a Role in Susceptibility to Acute Lymphoblastic Leukemia. Blood, 2020, 136, 10-11.	0.6	0
13	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0
14	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0
15	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0
16	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0
17	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0
18	Body mass index and risk of dying from a bloodstream infection: A Mendelian randomization study. , 2020, 17, e1003413.		0

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19	MendelProb: probability and sample size calculations for Mendelian studies of exome and whole genome sequence data. Bioinformatics, 2019, 35, 529-531.	1.8	0
20	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	0.6	37
21	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
22	Risks of preterm birth among nonâ€Hispanic black and nonâ€Hispanic white women: Effect modification by maternal age. Paediatric and Perinatal Epidemiology, 2019, 33, 346-356.	0.8	11
23	Associations between spousesâ€™ oxytocin receptor gene polymorphism, attachment security, and marital satisfaction. PLoS ONE, 2019, 14, e0213083.	1.1	14
24	RE: â€œRACIAL AND ETHNIC DIFFERENCES IN SOCIOECONOMIC POSITION AND RISK OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIAâ€• American Journal of Epidemiology, 2019, 188, 1192-1193.	1.6	5
25	GWAS in childhood acute lymphoblastic leukemia reveals novel genetic associations at chromosomes 17q12 and 8q24.21. Nature Communications, 2018, 9, 286.	5.8	75
26	Association of CACNA1C with bipolar disorder among the Pakistani population. Gene, 2018, 664, 119-126.	1.0	18
27	Statistical Analysis of Multiple Phenotypes in Genetic Epidemiologic Studies: From Cross-Phenotype Associations to Pleiotropy. American Journal of Epidemiology, 2018, 187, 855-863.	1.6	20
28	Anxiety and Depression Symptoms in a General Population and Future Risk of Bloodstream Infection: The HUNT Study. Psychosomatic Medicine, 2018, 80, 673-679.	1.3	18
29	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at PLEKHG1. Hypertension, 2018, 72, 408-416.	1.3	46
30	BMI1 enhancer polymorphism underlies chromosome 10p12.31 association with childhood acute lymphoblastic leukemia. International Journal of Cancer, 2018, 143, 2647-2658.	2.3	23
31	Identification of genetic variants associated with dengue or West Nile virus disease: a systematic review and meta-analysis. BMC Infectious Diseases, 2018, 18, 282.	1.3	30
32	Association of iron status with the risk of bloodstream infections: results from the prospective population-based HUNT Study in Norway. Intensive Care Medicine, 2018, 44, 1276-1283.	3.9	27
33	Gene-Gene and Gene-Environment Interactions. Methods in Molecular Biology, 2018, 1793, 89-110.	0.4	12
34	Parental Age and Risk of Pediatric Cancer in the Offspring: A Population-Based Record-Linkage Study in California. American Journal of Epidemiology, 2017, 186, 843-856.	1.6	26
35	Cesarean Section and Risk of Childhood Acute Lymphoblastic Leukemia in a Population-Based, Record-Linkage Study in California. American Journal of Epidemiology, 2017, 185, 96-105.	1.6	34
36	Impact of Sixteen Established Pancreatic Cancer Susceptibility Loci in American Jews. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1540-1548.	1.1	6

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37	Associations of obesity and lifestyle with the risk and mortality of bloodstream infection in a general population: a 15-year follow-up of 64â€‰027 individuals in the HUNT Study. International Journal of Epidemiology, 2017, 46, 1573-1581.	0.9	48
38	Genetic predisposition to elevated levels of C-reactive protein is associated with a decreased risk for preeclampsia. Hypertension in Pregnancy, 2017, 36, 30-35.	0.5	4
39	Epidemiology and outcome of sepsis in adult patients with Streptococcus pneumoniae infection in a Norwegian county 1993â€“2011: an observational study. BMC Infectious Diseases, 2016, 16, 223.	1.3	25
40	Genome-wide search identifies a gene-gene interaction between 20p13 and 2q14 in asthma. BMC Genetics, 2016, 17, 102.	2.7	9
41	Multiethnic genome-wide association study identifies ethnic-specific associations with body mass index in Hispanics and African Americans. BMC Genetics, 2016, 17, 78.	2.7	37
42	Exhaustive Genome-Wide Search for SNP-SNP Interactions Across 10 Human Diseases. G3: Genes, Genomes, Genetics, 2016, 6, 2043-2050.	0.8	16
43	dbPEC: a comprehensive literature-based database for preeclampsia related genes and phenotypes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw006.	1.4	9
44	The Impact of Infectious Disease Specialist Consultation for Staphylococcus aureus Bloodstream Infections: A Systematic Review. Open Forum Infectious Diseases, 2016, 3, ofw048.	0.4	60
45	Gene-based analysis identified the gene ZNF248 is associated with late-onset asthma in African Americans. Annals of Allergy, Asthma and Immunology, 2016, 117, 50-55.e2.	0.5	3
46	Birth weight and risk of paediatric Hodgkin lymphoma: Findings from a population-based record linkage study in California. European Journal of Cancer, 2016, 69, 19-27.	1.3	11
47	PIWI-Interacting RNAs in Gliomagenesis: Evidence from Post-GWAS and Functional Analyses. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1073-1080.	1.1	32
48	Genetic Risk Score for Essential Hypertension and Risk of Preeclampsia. American Journal of Hypertension, 2016, 29, 17-24.	1.0	19
49	Targeted Sequencing and Meta-Analysis of Preterm Birth. PLoS ONE, 2016, 11, e0155021.	1.1	13
50	Genome-Wide Gene by Environment Interaction Analysis Identifies Common SNPs at 17q21.2 that Are Associated with Increased Body Mass Index Only among Asthmatics. PLoS ONE, 2015, 10, e0144114.	1.1	14
51	Genetic Predisposition to Dyslipidemia and Risk of Preeclampsia. American Journal of Hypertension, 2015, 28, 915-923.	1.0	19
52	Confronting the missing epistasis problem: on the reproducibility of geneâ€“gene interactions. Human Genetics, 2015, 134, 837-849.	1.8	13
53	Neural-Specific Deletion of Htra2 Causes Cerebellar Neurodegeneration and Defective Processing of Mitochondrial OPA1. PLoS ONE, 2014, 9, e115789.	1.1	21
54	General, but not abdominal, overweight increases odds of asthma among Norwegian adolescents: the Youngâ€‹<scp>HUNT</scp> study. Acta Paediatrica, International Journal of Paediatrics, 2014, 103, 1270-1276.	0.7	8

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55	Novel gene identified in an exomeâ€wide association study of tanning dependence. Experimental Dermatology, 2014, 23, 757-759.	1.4	54
56	Bioinformatic Approach to the Genetics of Preeclampsia. Obstetrics and Gynecology, 2014, 123, 1155-1161.	1.2	36
57	Leptin Signaling and Hyperparathyroidism: Clinical and Genetic Associations. Journal of the American College of Surgeons, 2014, 218, 1239-1250e4.	0.2	8
58	Pathway-based genetic analysis of preterm birth. Genomics, 2013, 101, 163-170.	1.3	51
59	Association between the SERPINE1 (PAI-1) 4G/5G insertion/deletion promoter polymorphism (rs1799889) and pre-eclampsia: a systematic review and meta-analysis. Molecular Human Reproduction, 2013, 19, 136-143.	1.3	31
60	Genomeâ€Wide Association Study of Preâ€Eclampsia Detects Novel Maternal Single Nucleotide Polymorphisms and Copyâ€Number Variants in Subsets of the Hyperglycemia and Adverse Pregnancy Outcome (HAPO) Study Cohort. Annals of Human Genetics, 2013, 77, 277-287.	0.3	55
61	Genome-wide association study identifies a maternal copy-number deletion in PSG11 enriched among preeclampsia patients. BMC Pregnancy and Childbirth, 2012, 12, 61.	0.9	68
62	Association of maternalAGTR1polymorphisms and preeclampsia: a systematic review and meta-analysis. Journal of Maternal-Fetal and Neonatal Medicine, 2012, 25, 2676-2680.	0.7	25
63	Whole-exome sequencing of a pedigree segregating asthma. BMC Medical Genetics, 2012, 13, 95.	2.1	42
64	Genetic Signatures of Exceptional Longevity in Humans. PLoS ONE, 2012, 7, e29848.	1.1	340
65	Leveraging Ethnic Group Incidence Variation to Investigate Genetic Susceptibility to Glioma: A Novel Candidate SNP Approach. Frontiers in Genetics, 2012, 3, 203.	1.1	12
66	Stage and Gene Specific Signatures Defined by Histones H3K4me2 and H3K27me3 Accompany Mammalian Retina Maturation In Vivo. PLoS ONE, 2012, 7, e46867.	1.1	47
67	A Comparison of Association Methods Correcting for Population Stratification in Caseâ€“Control Studies. Annals of Human Genetics, 2011, 75, 418-427.	0.3	83
68	Attempted Replication of 50 Reported Asthma Risk Genes Identifies a SNP in RAD50 as Associated with Childhood Atopic Asthma. Human Heredity, 2011, 71, 97-105.	0.4	40
69	A pilot genome-wide association study shows genomic variants enriched in the non-tumor cells of patients with well-differentiated neuroendocrine tumors of the ileum. Endocrine-Related Cancer, 2011, 18, 171-180.	1.6	22
70	Association between reduced copy-number at T-cell receptor gamma (TCRÎ³) and childhood allergic asthma: A possible role for somatic mosaicism. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 690, 89-94.	0.4	11
71	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	9.4	357
72	PDE11A associations with asthma: Results of a genome-wide association scan. Journal of Allergy and Clinical Immunology, 2010, 126, 871-873.e9.	1.5	45

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73	Five classic articles in genetic epidemiology. Yale Journal of Biology and Medicine, 2010, 83, 87-90.	0.2	2
74	Mitochondrial DNA Variants of Respiratory Complex I that Uniquely Characterize Haplogroup T2 Are Associated with Increased Risk of Age-Related Macular Degeneration. PLoS ONE, 2009, 4, e5508.	1.1	89
75	Common variants on chromosome 2 and risk of primary open-angle glaucoma in the Afro-Caribbean population of Barbados. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17105-17110.	3.3	44
76	p53 responsive elements in human retrotransposons. Oncogene, 2009, 28, 3857-3865.	2.6	88
77	Detecting essential and removable interactions in genome-wide association studies. Statistics and Its Interface, 2009, 2, 161-170.	0.2	8
78	Further mapping of 10q26 supports strong association of HTRA1 polymorphisms with age-related macular degeneration. Vision Research, 2008, 48, 685-689.	0.7	44
79	HTRA1Variants in Exudative Age-Related Macular Degeneration and Interactions with Smoking andCFH. , 2008, 49, 2357.		81
80	Genomewide Association Studies. , 2008, , 225-238.		4
81	Joint effects of polymorphisms in the HTRA1, LOC387715/ARMS2, and CFH genes on AMD in a Caucasian population. Molecular Vision, 2008, 14, 1395-400.	1.1	47
82	Two genetic pathways for age-related macular degeneration. Current Opinion in Genetics and Development, 2007, 17, 228-233.	1.5	31
83	Linkage Disequilibrium Mapping for Complex Disease Genes. Methods in Molecular Biology, 2007, 376, 85-107.	0.4	5
84	HTRA1 promoter polymorphism predisposes Japanese to age-related macular degeneration. Molecular Vision, 2007, 13, 545-8.	1.1	61
85	HTRA1 Promoter Polymorphism in Wet Age-Related Macular Degeneration. Science, 2006, 314, 989-992.	6.0	812
86	A Variant of the HTRA1 Gene Increases Susceptibility to Age-Related Macular Degeneration. Science, 2006, 314, 992-993.	6.0	735
87	Reanalysis of a Genome Scan for Schizophrenia Loci Using Multigenic Methods. Human Heredity, 2004, 57, 191-194.	0.4	3
88	X-Linked High Myopia Associated With Cone Dysfunction. JAMA Ophthalmology, 2004, 122, 897.	2.6	74
89	Evidence for a putative bipolar disorder locus on 2p13â€“16 and other potential loci on 4q31, 7q34, 8q13, 9q31, 10q21â€“24, 13q32, 14q21 and 17q11â€“12. Molecular Psychiatry, 2003, 8, 333-342.	4.1	118
90	Mutations in the Î³-Actin Gene (ACTG1) Are Associated with Dominant Progressive Deafness (DFNA20/26). American Journal of Human Genetics, 2003, 73, 1082-1091.	2.6	170

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91	The Map Problem: A Comparison of Genetic and Sequence-Based Physical Maps. American Journal of Human Genetics, 2002, 70, 101-107.	2.6	29
92	Refined Mapping of Suggestive Linkage to Renal Function in African Americans: The HyperGEN Study. American Journal of Human Genetics, 2002, 71, 204-205.	2.6	14
93	Map Error Reduction: Using Genetic and Sequence-Based Physical Maps to Order Closely Linked Markers. Human Heredity, 2002, 54, 34-44.	0.4	6
94	A Genome Scan for Renal Function among Hypertensives: the HyperGEN Study. American Journal of Human Genetics, 2001, 68, 136-144.	2.6	68
95	Linkage of Left Ventricular Contractility to Chromosome 11 in Humans. Hypertension, 2001, 38, 767-772.	1.3	29
96	Further refinement of the MYP2 locus for autosomal dominant high myopia by linkage disequilibrium analysis. Ophthalmic Genetics, 2001, 22, 69-75.	0.5	44
97	Evidence for genetic heterogeneity in families with congenital motor nystagmus (CN). Ophthalmic Genetics, 2000, 21, 227-233.	0.5	9
98	Linkage Disequilibrium Mapping for Complex Disease Genes. , 0, , 85-108.		0