W James Gauderman

List of Publications by Year in descending order

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		101543	5	6724
86	7,589	36		83
papers	citations	h-index		g-index
88	88	88		12475
all docs	docs citations	times ranked		citing authors

#	Article	IF	CITATIONS
1	The Effect of Air Pollution on Lung Development from 10 to 18 Years of Age. New England Journal of Medicine, 2004, 351, 1057-1067.	27.0	1,131
2	Effect of exposure to traffic on lung development from 10 to 18 years of age: a cohort study. Lancet, The, 2007, 369, 571-577.	13.7	617
3	Sample size requirements for matched caseâ€control studies of gene–environment interaction. Statistics in Medicine, 2002, 21, 35-50.	1.6	583
4	Sample Size Requirements for Association Studies of Gene-Gene Interaction. American Journal of Epidemiology, 2002, 155, 478-484.	3.4	553
5	Association of Improved Air Quality with Lung Development in Children. New England Journal of Medicine, 2015, 372, 905-913.	27.0	522
6	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
7	Association between Air Pollution and Lung Function Growth in Southern California Children. American Journal of Respiratory and Critical Care Medicine, 2002, 166, 76-84.	5.6	316
8	Gene-Environment Interaction in Genome-Wide Association Studies. American Journal of Epidemiology, 2008, 169, 219-226.	3.4	264
9	Testing association between disease and multiple SNPs in a candidate gene. Genetic Epidemiology, 2007, 31, 383-395.	1.3	193
10	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
11	Synergistic effect betweenlL-10 andbcl-2 genotypes in determining susceptibility to systemic lupus erythematosus. Arthritis and Rheumatism, 1998, 41, 596-602.	6.7	157
12	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
13	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
14	Candidate gene association analysis for a quantitative trait, using parent-offspring trios. Genetic Epidemiology, 2003, 25, 327-338.	1.3	127
15	Genetic ancestry influences asthma susceptibility and lung function among Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 228-235.	2.9	113
16	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
17	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 1373-1383.	5.6	107
18	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	21.4	106

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19	Finding Novel Genes by Testing GÂ×ÂE Interactions in a Genomeâ€Wide Association Study. Genetic Epidemiology, 2013, 37, 603-613.	1.3	100
20	Shift Work, Chronotype, and Melatonin Rhythm in Nurses. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1177-1186.	2.5	96
21	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
22	Association of Changes in Air Quality With Bronchitic Symptoms in Children in California, 1993-2012. JAMA - Journal of the American Medical Association, 2016, 315, 1491.	7.4	85
23	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
24	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
25	Trends in childhood leukemia incidence over two decades from 1992 to 2013. International Journal of Cancer, 2017, 140, 1000-1008.	5.1	77
26	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
27	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
28	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
29	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
30	Association between theRfp-Y haplotype and the incidence of Marek's disease in chickens. Immunogenetics, 1996, 44, 242-245.	2.4	55
31	Air Pollution and Lung Function in Minority Youth with Asthma in the GALA II (Genes–Environments) Tj ETQq1	1 0.78431 5.6	4 rgBT /Ove 54
32	Rising rates of acute lymphoblastic leukemia in Hispanic children: trends in incidence from 1992 to 2011. Blood, 2015, 125, 3033-3034.	1.4	53
33	Gene Expression Profiling in Blood Provides Reproducible Molecular Insights into Asthma Control. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 179-188.	5 . 6	49
34	Censored survival models for genetic epidemiology: A gibbs sampling approach. Genetic Epidemiology, 1994, 11, 171-188.	1.3	48
35	Analysis of gene-smoking interaction in lung cancer. Genetic Epidemiology, 1997, 14, 199-214.	1.3	40
36	Dietary nutrients associated with preservation of lung function in Hispanic and non-Hispanic white smokers from New Mexico. International Journal of COPD, 2017, Volume 12, 3171-3181.	2.3	40

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37	Efficient Genome-Wide Association Testing of Gene-Environment Interaction in Case-Parent Trios. American Journal of Epidemiology, 2010, 172, 116-122.	3.4	35
38	Detecting Gene–Environment Interactions for a Quantitative Trait in a Genomeâ€Wide Association Study. Genetic Epidemiology, 2016, 40, 394-403.	1.3	34
39	Genome-wide association study identifiesWNT7Bas a novel locus for central corneal thickness in Latinos. Human Molecular Genetics, 2016, 25, ddw319.	2.9	34
40	A Cross-Sectional Study Examining the Seroprevalence of Severe Acute Respiratory Syndrome Coronavirus 2 Antibodies in a University Student Population. Journal of Adolescent Health, 2020, 67, 763-768.	2.5	34
41	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	2.9	33
42	Longitudinal data analysis in pedigree studies. Genetic Epidemiology, 2003, 25, S18-S28.	1.3	32
43	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
44	Native American Ancestry Is Associated With Severe Diabetic Retinopathy in Latinos., 2014, 55, 6041.		27
45	Role of local CpG DNA methylation in mediating the 17q21 asthma susceptibility gasdermin B (GSDMB)/ORMDL sphingolipid biosynthesis regulator 3 (ORMDL3) expression quantitative trait locus. Journal of Allergy and Clinical Immunology, 2018, 141, 2282-2286.e6.	2.9	20
46	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
47	Age-Related Macular Degeneration and Quality of Life in Latinos. JAMA Ophthalmology, 2016, 134, 683.	2.5	18
48	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. British Journal of Cancer, 2016, 114, 221-229.	6.4	18
49	The Potential Effects of Policy-driven Air Pollution Interventions on Childhood Lung Development. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 438-444.	5.6	17
50	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
51	15q12 Variants, Sputum Gene Promoter Hypermethylation, and Lung Cancer Risk: A GWAS in Smokers. Journal of the National Cancer Institute, 2015, 107, .	6.3	16
52	Traffic-Related Pollutants: Exposure and Health Effects Among Hispanic Children. American Journal of Epidemiology, 2018, 187, 45-52.	3.4	16
53	Mapping the 17q12–21.1 Locus for Variants Associated with Early-Onset Asthma in African Americans. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 424-436.	5.6	16
54	Asthma and its relationship to mitochondrial copy number: Results from the Asthma Translational Genomics Collaborative (ATGC) of the Trans-Omics for Precision Medicine (TOPMed) program. PLoS ONE, 2020, 15, e0242364.	2.5	16

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55	A Unified Model for the Analysis of Gene-Environment Interaction. American Journal of Epidemiology, 2019, 188, 760-767.	3.4	15
56	Highâ€resolution MODIS aerosol retrieval during wildfire events in California for use in exposure assessment. Journal of Geophysical Research D: Atmospheres, 2013, 118, 11,242.	3.3	14
57	Satellite-Derived PM2.5 Composition and Its Differential Effect on Children's Lung Function. Remote Sensing, 2020, 12, 1028.	4.0	13
58	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
59	Childhood traffic-related air pollution and adverse changes in subclinical atherosclerosis measures from childhood to adulthood. Environmental Health, 2021, 20, 44.	4.0	13
60	Combined segregation and linkage analysis of late-onset Alzheimer's disease in Duke families using Gibbs sampling. Genetic Epidemiology, 1993, 10, 489-494.	1.3	12
61	Gene Coexpression Networks in Whole Blood Implicate Multiple Interrelated Molecular Pathways in Obesity in People with Asthma. Obesity, 2018, 26, 1938-1948.	3.0	11
62	Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739.	2.8	11
63	A generalized estimating equations approach to linkage analysis in sibships in relation to multiple markers and exposure factors. Genetic Epidemiology, 1999, 17, S737-42.	1.3	10
64	A genome-wide association study on medulloblastoma. Journal of Neuro-Oncology, 2020, 147, 309-315.	2.9	10
65	Should We Consider Gene×Environment Interaction in the Hunt for Quantitative Trait Loci?. Genetic Epidemiology, 2001, 21, S831-S836.	1.3	9
66	No Evidence of Gene–Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2971-2976.	2.5	9
67	Dietary Nutrient Intake, Ethnicity, and Epigenetic Silencing of Lung Cancer Genes Detected in Sputum in New Mexican Smokers. Cancer Prevention Research, 2018, 11, 93-102.	1.5	9
68	A joint test of linkage and gene×environment interaction, with affected sib pairs. Genetic Epidemiology, 1999, 17, S563-S568.	1.3	8
69	Genetic epidemiologic analysis of quantitative phenotypes using gibbs sampling. Genetic Epidemiology, 1995, 12, 753-758.	1.3	7
70	Functional informed genomeâ€wide interaction analysis of body mass index, diabetes and colorectal cancer risk. Cancer Medicine, 2020, 9, 3563-3573.	2.8	7
71	Joint segregation and linkage analysis of a quantitative trait compared to separate analyses. Genetic Epidemiology, 1997, 14, 993-998.	1.3	6
72	Combined Linkage and Association Analysis in Pedigrees. Genetic Epidemiology, 2001, 21, S358-S363.	1.3	6

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73	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	2.5	6
74	A bivariate genetic analysis of HDL- and LDL-cholesterol incorporating measured covariates: A gibbs sampling application. Genetic Epidemiology, 1993, 10, 623-628.	1.3	5
75	Twoâ€step hypothesis testing to detect geneâ€environment interactions in a genomeâ€wide scan with a survival endpoint. Statistics in Medicine, 2022, 41, 1644-1657.	1.6	5
76	A two-step approach to testing overall effect of gene–environment interaction for multiple phenotypes. Bioinformatics, 2021, 36, 5640-5648.	4.1	4
77	Hierarchical Bayesian estimation of covariate effects on airway and alveolar nitric oxide. Scientific Reports, 2021, 11, 17180.	3.3	3
78	A method for simulating familial disease data with variable age at onset and genetic and environmental effects. Statistics and Computing, 1995, 5, 237-243.	1.5	2
79	Association tests using unaffected-sibling versus pseudo-sibling controls. Genetic Epidemiology, 1999, 17, S731-S736.	1.3	2
80	Immune factors preceding diagnosis of glioma: a Prostate Lung Colorectal Ovarian Cancer Screening Trial nested case–control study. Neuro-Oncology Advances, 2019, 1, vdz031.	0.7	2
81	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
82	Association between the Rfp-Y haplotype and the incidence of Marek?s disease in chickens. Immunogenetics, 1996, 44, 242-245.	2.4	1
83	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. Blood, 2014, 124, 135-135.	1.4	1
84	A Scalable Hierarchical Lasso for Gene–Environment Interactions. Journal of Computational and Graphical Statistics, 2022, 31, 1091-1103.	1.7	1
85	E-Cigarettes, Cigarettes, and the Prevalence of Adolescent Tobacco Use., 2017,, 101-110.		0
86	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	6.3	0