Duncan C Thomas

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95 papers	5,213 citations	37 h-index	71 g-index
107 ext. papers	6,060 ext. citations	5.2 avg, IF	5.74 L-index

#	Paper	IF	Citations
95	Gene--environment-wide association studies: emerging approaches. *Nature Reviews Genetics*, **2010**, 11, 259-72	30.1	488
94	Exposure to residential electric and magnetic fields and risk of childhood leukemia. *American Journal of Epidemiology*, **1991**, 134, 923-37	3.8	400
93	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. *Human Genetics*, **2012**, 131, 1565-89	6.3	258
92	Modeling and E-M estimation of haplotype-specific relative risks from genotype data for a case-control study of unrelated individuals. *Human Heredity*, **2003**, 55, 179-90	1.1	230
91	Simultaneously modelling censored survival data and repeatedly measured covariates: a Gibbs sampling approach. *Statistics in Medicine*, **1996**, 15, 1663-85	2.3	228
90	Dose to the contralateral breast from radiotherapy and risk of second primary breast cancer in the WECARE study. *International Journal of Radiation Oncology Biology Physics*, **2008**, 72, 1021-30	4	218
89	Recent developments in genomewide association scans: a workshop summary and review. *American Journal of Human Genetics*, **2005**, 77, 337-45	11	180
88	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
87	Population-based study of the risk of second primary contralateral breast cancer associated with carrying a mutation in BRCA1 or BRCA2. *Journal of Clinical Oncology*, **2010**, 28, 2404-10	2.2	137
86	Determining Risk of Colorectal Cancer and Starting Age of Screening Based on Lifestyle, Environmental, and Genetic Factors. *Gastroenterology*, **2018**, 154, 2152-2164.e19	13.3	131
85	Methods for investigating gene-environment interactions in candidate pathway and genome-wide association studies. *Annual Review of Public Health*, **2010**, 31, 21-36	20.6	113
84	Commentary: the concept of 'Mendelian Randomization'. *International Journal of Epidemiology*, **2004**, 33, 21-5	7.8	108
83	Optimal two-stage genotyping designs for genome-wide association scans. *Genetic Epidemiology*, **2006**, 30, 356-68	2.6	107
82	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106
81	Radiation exposure, the ATM Gene, and contralateral breast cancer in the women's environmental cancer and radiation epidemiology study. *Journal of the National Cancer Institute*, **2010**, 102, 475-83	9.7	101
80	Study design: evaluating gene-environment interactions in the etiology of breast cancer - the WECARE study. *Breast Cancer Research*, **2004**, 6, R199-214	8.3	94
79	A model to determine colorectal cancer risk using common genetic susceptibility loci. *Gastroenterology*, **2015**, 148, 1330-9.e14	13.3	89

78	Processed meats and risk of childhood leukemia (California, USA). *Cancer Causes and Control*, **1994**, 5, 195-202	2.8	88
77	Bias and efficiency in family-based gene-characterization studies: conditional, prospective, retrospective, and joint likelihoods. *American Journal of Human Genetics*, **2000**, 66, 1119-31	11	84
76	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. *American Journal of Epidemiology*, **2017**, 186, 753-761	3.8	78
75	Bayesian modeling of complex metabolic pathways. *Human Heredity*, **2003**, 56, 83-93	1.1	78
74	Sample size requirements to detect gene-environment interactions in genome-wide association studies. *Genetic Epidemiology*, **2011**, 35, 201-10	2.6	73
73	Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. *Annual Review of Public Health*, **2017**, 38, 279-294	20.6	68
72	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
71	Hierarchical Bayes prioritization of marker associations from a genome-wide association scan for further investigation. *Genetic Epidemiology*, **2007**, 31, 871-82	2.6	66
70	Exposure to magnetic fields among electrical workers in relation to leukemia risk in Los Angeles County. *American Journal of Industrial Medicine*, **1994**, 26, 47-60	2.7	60
69	Invited commentary: GE-Whiz! Ratcheting gene-environment studies up to the whole genome and the whole exposome. *American Journal of Epidemiology*, **2012**, 175, 203-7; discussion 208-9	3.8	41
68	Bayesian spatial modeling of haplotype associations. *Human Heredity*, **2003**, 56, 32-40	1.1	40
67	Methodological Issues in Multistage Genome-wide Association Studies. *Statistical Science*, **2009**, 24, 414-429	2.4	39
66	Use of pathway information in molecular epidemiology. *Human Genomics*, **2009**, 4, 21-42	6.8	38
65	Statistical Issues in Studies of the Long-Term Effects of Air Pollution: The Southern California Children's Health Study. *Statistical Science*, **2004**, 19, 414	2.4	37
64	Genetic epidemiology with a capital "E". *Genetic Epidemiology*, **2000**, 19, 289-300	2.6	37
63	Censored survival models for genetic epidemiology: a Gibbs sampling approach. *Genetic Epidemiology*, **1994**, 11, 171-88	2.6	35
62	Analysis of gene-smoking interaction in lung cancer. *Genetic Epidemiology*, **1997**, 14, 199-214	2.6	33
61	Efficient genome-wide association testing of gene-environment interaction in case-parent trios. *American Journal of Epidemiology*, **2010**, 172, 116-22	3.8	30

60	Breast Cancer Family History and Contralateral Breast Cancer Risk in Young Women: An Update From the Women's Environmental Cancer and Radiation Epidemiology Study. *Journal of Clinical Oncology*, **2018**, 36, 1513-1520	2.2	29
59	Dysregulated lipid and fatty acid metabolism link perfluoroalkyl substances exposure and impaired glucose metabolism in young adults. *Environment International*, **2020**, 145, 106091	12.9	27
58	The cardiopulmonary effects of ambient air pollution and mechanistic pathways: a comparative hierarchical pathway analysis. *PLoS ONE*, **2014**, 9, e114913	3.7	26
57	Discovery of complex pathways from observational data. *Statistics in Medicine*, **2010**, 29, 1998-2011	2.3	25
56	Bivariate survival models for analysis of genetic and environmental effects in twins. *Genetic Epidemiology*, **1990**, 7, 121-35	2.6	25
55	Bayesian model averaging in time-series studies of air pollution and mortality. *Journal of Toxicology and Environmental Health - Part A: Current Issues*, **2007**, 70, 311-5	3.2	23
54	Association of Common Genetic Variants With Contralateral Breast Cancer Risk in the WECARE Study. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	22
53	The use of hierarchical models for estimating relative risks of individual genetic variants: an application to a study of melanoma. *Statistics in Medicine*, **2008**, 27, 1973-92	2.3	20
52	Genome scan of complex traits by haplotype sharing correlation. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S582-7	2.6	20
51	Residential magnetic fields predicted from wiring configurations: II. Relationships to childhood leukemia. *Bioelectromagnetics*, **1999**, 20, 414-422	1.6	18
50	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1370-1380	4	17
49	Considerations in determining matching criteria and stratum sizes for case-control studies. *International Journal of Epidemiology*, **1981**, 10, 389-92	7.8	17
48	Near-roadway air pollution exposure and altered fatty acid oxidation among adolescents and young adults - The interplay with obesity. *Environment International*, **2019**, 130, 104935	12.9	16
47	Two-phase and family-based designs for next-generation sequencing studies. *Frontiers in Genetics*, **2013**, 4, 276	4.5	16
46	Methods for testing interactions, with applications to occupational exposures, smoking, and lung cancer. *American Journal of Industrial Medicine*, **1988**, 13, 131-47	2.7	16
45	Using biological knowledge to discover higher order interactions in genetic association studies. *Genetic Epidemiology*, **2010**, 34, 863-78	2.6	15
44	Bayes estimates of haplotype effects. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S712-7	2.6	15
43	Linkage Analysis of Urine Arsenic Species Patterns in the Strong Heart Family Study. *Toxicological Sciences*, **2015**, 148, 89-100	4.4	14

42	Toxicokinetic genetics: an approach to gene-environment and gene-gene interactions in complex metabolic pathways. *Iarc (international Agency for Research on Cancer) Scientific Publications*, **2004**, 127-50		14
41	A Bayesian approach to multipoint mapping in nuclear families. *Genetic Epidemiology*, **1997**, 14, 903-8	2.6	13
40	Case-parents design for gene-environment interaction by Schaid. *Genetic Epidemiology*, **2000**, 19, 461-3	2.6	12
39	Residential magnetic fields predicted from wiring configurations: I. Exposure model. *Bioelectromagnetics*, **1999**, 20, 399-413	1.6	12
38	Ascertainment bias in rate ratio estimation from case-sibling control studies of variable age-at-onset diseases. *Biometrics*, **1999**, 55, 1129-36	1.8	11
37	Fitting models of carcinogenesis to a case-control study of breast cancer. *Journal of Chronic Diseases*, **1987**, 40 Suppl 2, 181S-189S		11
36	Multistage sampling for latent variable models. *Lifetime Data Analysis*, **2007**, 13, 565-81	1.3	10
35	High-volume "-omics" technologies and the future of molecular epidemiology. *Epidemiology*, **2006**, 17, 490-1	3.1	10
34	Asthma Disease Status, COPD, and COVID-19 Severity in a Large Multiethnic Population. *Journal of Allergy and Clinical Immunology: in Practice*, **2021**, 9, 3621-3628.e2	5.4	10
33	A generalized estimating equations approach to linkage analysis in sibships in relation to multiple markers and exposure factors. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S737-42	2.6	9
32	A latent unknown clustering integrating multi-omics data (LUCID) with phenotypic traits. *Bioinformatics*, **2020**, 36, 842-850	7.2	9
31	GWASeq: targeted re-sequencing follow up to GWAS. *BMC Genomics*, **2016**, 17, 176	4.5	7
30	What Does "Precision Medicine" Have to Say About Prevention?. *Epidemiology*, **2017**, 28, 479-483	3.1	6
29	Radiation Treatment, ATM, BRCA1/2, and CHEK2*1100delC Pathogenic Variants and Risk of Contralateral Breast Cancer. *Journal of the National Cancer Institute*, **2020**, 112, 1275-1279	9.7	6
28	Two-stage family-based designs for sequencing studies. *BMC Proceedings*, **2014**, 8, S32	2.3	6
27	Genetic epidemiologic analysis of quantitative phenotypes using Gibbs sampling. *Genetic Epidemiology*, **1995**, 12, 753-8	2.6	6
26	Empirical hierarchical bayes approach to gene-environment interactions: development and application to genome-wide association studies of lung cancer in TRICL. *Genetic Epidemiology*, **2013**, 37, 551-559	2.6	5
25	Joint analysis for integrating two related studies of different data types and different study designs using hierarchical modeling approaches. *Human Heredity*, **2012**, 74, 83-96	1.1	5

24	International Genetic Epidemiology Society: commentary on Darkness in El Dorado by Patrick Tierney. *Genetic Epidemiology*, **2001**, 21, 81-104	2.6	5
23	Some Contributions of Statistics to Environmental Epidemiology. *Journal of the American Statistical Association*, **2000**, 95, 315-319	2.8	5
22	A joint test of linkage and gene x environment interaction, with affected sib pairs. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S563-8	2.6	5
21	A bivariate genetic analysis of HDL- and LDL-cholesterol incorporating measured covariates: a Gibbs sampling application. *Genetic Epidemiology*, **1993**, 10, 623-8	2.6	5
20	Inclusion of biological knowledge in a Bayesian shrinkage model for joint estimation of SNP effects. *Genetic Epidemiology*, **2017**, 41, 320-331	2.6	4
19	Complex system approaches to genetic analysis Bayesian approaches. *Advances in Genetics*, **2010**, 72, 47-71	3.3	4
18	Viewpoint: using gene-environment interactions to dissect the effects of complex mixtures. *Journal of Exposure Science and Environmental Epidemiology*, **2007**, 17 Suppl 2, S71-4	6.7	4
17	A generalized estimating equations approach to fitting major gene models in segregation analysis of continuous phenotypes. *Genetic Epidemiology*, **1993**, 10, 61-74	2.6	4
16	Near-roadway air pollution associated with COVID-19 severity and mortality - Multiethnic cohort study in Southern California. *Environment International*, **2021**, 157, 106862	12.9	3
15	Next-Generation Sequencing Studies: Optimal Design and Analysis, Missing Heritability and Rare Variants. *Current Epidemiology Reports*, **2014**, 1, 213-219	2.9	2
14	A Bayesian Hierarchical Model for Relating Multiple SNPs within Multiple Genes to Disease Risk. *International Journal of Genomics*, **2013**, 2013, 406217	2.5	2
13	Measurement Error in Spatial Exposure Models: Study Design Implications. *Environmetrics*, **2013**, 24, 518-520	1.3	2
12	Ambient air pollution and COVID-19 incidence during four 2020-2021 case surges.. *Environmental Research*, **2022**, 208, 112758	7.9	2
11	Estimating the Effect of Targeted Screening Strategies: An Application to Colonoscopy and Colorectal Cancer. *Epidemiology*, **2017**, 28, 470-478	3.1	2
10	A Unified Model for the Analysis of Gene-Environment Interaction. *American Journal of Epidemiology*, **2019**, 188, 760-767	3.8	2
9	Association of a Pathway-Specific Genetic Risk Score With Risk of Radiation-Associated Contralateral Breast Cancer. *JAMA Network Open*, **2019**, 2, e1912259	10.4	1
8	Association tests using unaffected-sibling versus pseudo-sibling controls. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S731-6	2.6	1
7	Re: "A population-based case-cohort evaluation of the efficacy of mammographic screening for breast cancer". *American Journal of Epidemiology*, **1995**, 142, 448-50	3.8	1

6	Transcriptomic and metabolomic associations with exposures to air pollutants among young adults with childhood asthma history.. *Environmental Pollution*, **2022**, 299, 118903	9.3	1
5	Some Contributions of Statistics to Environmental Epidemiology		1
4	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**, OF1-OF13	4	0
3	Re: Kheifets et al. (2017): Residential magnetic fields exposure and childhood leukemia: a population-based case-control study in California. *Cancer Causes and Control*, **2018**, 29, 609-610	2.8	
2	Discussion on "Statistical Issues Arising in the Women's Health Initiative". *Biometrics*, **2005**, 61, 930-933	1.8	
1	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. *PLoS Computational Biology*, **2021**, 17, e1007948	5	