

# Duncan C Thomas

## List of Publications by Year in descending order

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103  
papers

6,742  
citations

81900

39  
h-index

64796

79  
g-index

107  
all docs

107  
docs citations

107  
times ranked

9282  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene-environment-wide association studies: emerging approaches. <i>Nature Reviews Genetics</i> , 2010, 11, 259-272.	16.3	593
2	Exposure to Residential Electric and Magnetic Fields and Risk of Childhood Leukemia. <i>American Journal of Epidemiology</i> , 1991, 134, 923-937.	3.4	458
3	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	21.4	377
4	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.	3.8	294
5	SIMULTANEOUSLY MODELLING CENSORED SURVIVAL DATA AND REPEATEDLY MEASURED COVARIATES: A GIBBS SAMPLING APPROACH. <i>Statistics in Medicine</i> , 1996, 15, 1663-1685.	1.6	285
6	Dose to the Contralateral Breast From Radiotherapy and Risk of Second Primary Breast Cancer in the WECARE Study. <i>International Journal of Radiation Oncology Biology Physics</i> , 2008, 72, 1021-1030.	0.8	280
7	Modeling and E-M Estimation of Haplotype-Specific Relative Risks from Genotype Data for a Case-Control Study of Unrelated Individuals. <i>Human Heredity</i> , 2003, 55, 179-190.	0.8	249
8	Determining Risk of Colorectal Cancer and Starting Age of Screening Based on Lifestyle, Environmental, and Genetic Factors. <i>Gastroenterology</i> , 2018, 154, 2152-2164.e19.	1.3	226
9	Recent Developments in Genomewide Association Scans: A Workshop Summary and Review. <i>American Journal of Human Genetics</i> , 2005, 77, 337-345.	6.2	203
10	Population-Based Study of the Risk of Second Primary Contralateral Breast Cancer Associated With Carrying a Mutation in <i>BRCA1</i> or <i>BRCA2</i> . <i>Journal of Clinical Oncology</i> , 2010, 28, 2404-2410.	1.6	166
11	Point: population stratification: a problem for case-control studies of candidate-gene associations?. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2002, 11, 505-12.	2.5	154
12	Commentary: The concept of 'Mendelian Randomization'. <i>International Journal of Epidemiology</i> , 2004, 33, 21-25.	1.9	151
13	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , 2017, 186, 753-761.	3.4	150
14	Betting Odds and Genetic Associations. <i>Journal of the National Cancer Institute</i> , 2004, 96, 421-423.	6.3	144
15	Methods for Investigating Gene-Environment Interactions in Candidate Pathway and Genome-Wide Association Studies. <i>Annual Review of Public Health</i> , 2010, 31, 21-36.	17.4	138
16	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015, 6, 7138.	12.8	138
17	A Model to Determine Colorectal Cancer Risk Using Common Genetic Susceptibility Loci. <i>Gastroenterology</i> , 2015, 148, 1330-1339.e14.	1.3	129
18	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	6.3	129

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19	Radiation Exposure, the ATM Gene, and Contralateral Breast Cancer in the Women's Environmental Cancer and Radiation Epidemiology Study. <i>Journal of the National Cancer Institute</i> , 2010, 102, 475-483.	6.3	121
20	Optimal two-stage genotyping designs for genome-wide association scans. <i>Genetic Epidemiology</i> , 2006, 30, 356-368.	1.3	119
21	Study design: Evaluating gene-environment interactions in the etiology of breast cancer – the WECARE study. <i>Breast Cancer Research</i> , 2004, 6, R199-214.	5.0	106
22	Processed meats and risk of childhood leukemia (California, USA). <i>Cancer Causes and Control</i> , 1994, 5, 195-202.	1.8	98
23	Bias and Efficiency in Family-Based Gene-Characterization Studies: Conditional, Prospective, Retrospective, and Joint Likelihoods. <i>American Journal of Human Genetics</i> , 2000, 66, 1119-1131.	6.2	98
24	Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. <i>Annual Review of Public Health</i> , 2017, 38, 279-294.	17.4	97
25	Sample size requirements to detect gene-environment interactions in genome-wide association studies. <i>Genetic Epidemiology</i> , 2011, 35, 201-210.	1.3	90
26	Bayesian Modeling of Complex Metabolic Pathways. <i>Human Heredity</i> , 2003, 56, 83-93.	0.8	88
27	Dysregulated lipid and fatty acid metabolism link perfluoroalkyl substances exposure and impaired glucose metabolism in young adults. <i>Environment International</i> , 2020, 145, 106091.	10.0	83
28	Hierarchical Bayes prioritization of marker associations from a genome-wide association scan for further investigation. <i>Genetic Epidemiology</i> , 2007, 31, 871-882.	1.3	77
29	Exposure to magnetic fields among electrical workers in relation to leukemia risk in Los Angeles County. <i>American Journal of Industrial Medicine</i> , 1994, 26, 47-60.	2.1	75
30	The Need for a Systematic Approach to Complex Pathways in Molecular Epidemiology. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 557-559.	2.5	60
31	Censored survival models for genetic epidemiology: A gibbs sampling approach. <i>Genetic Epidemiology</i> , 1994, 11, 171-188.	1.3	48
32	Are We Ready for Genome-wide Association Studies?: Table 1.. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 595-598.	2.5	48
33	Invited Commentary: GE-Whiz! Ratcheting Gene-Environment Studies up to the Whole Genome and the Whole Exposome. <i>American Journal of Epidemiology</i> , 2012, 175, 203-207.	3.4	47
34	Genetic epidemiology with a capital 'E'. <i>Genetic Epidemiology</i> , 2000, 19, 289-300.	1.3	45
35	Statistical Issues in Studies of the Long-Term Effects of Air Pollution: The Southern California Children's Health Study. <i>Statistical Science</i> , 2004, 19, 414.	2.8	45
36	Bayesian Spatial Modeling of Haplotype Associations. <i>Human Heredity</i> , 2003, 56, 32-40.	0.8	44

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37	Dissecting Effects of Complex Mixtures. <i>Epidemiology</i> , 2007, 18, 186-190.	2.7	44
38	Breast Cancer Family History and Contralateral Breast Cancer Risk in Young Women: An Update From the Women's Environmental Cancer and Radiation Epidemiology Study. <i>Journal of Clinical Oncology</i> , 2018, 36, 1513-1520.	1.6	44
39	Use of pathway information in molecular epidemiology. <i>Human Genomics</i> , 2009, 4, 21.	2.9	42
40	Methodological Issues in Multistage Genome-Wide Association Studies. <i>Statistical Science</i> , 2009, 24, 414-429.	2.8	41
41	Analysis of gene-smoking interaction in lung cancer. <i>Genetic Epidemiology</i> , 1997, 14, 199-214.	1.3	40
42	The Cardiopulmonary Effects of Ambient Air Pollution and Mechanistic Pathways: A Comparative Hierarchical Pathway Analysis. <i>PLoS ONE</i> , 2014, 9, e114913.	2.5	39
43	Efficient Genome-Wide Association Testing of Gene-Environment Interaction in Case-Parent Trios. <i>American Journal of Epidemiology</i> , 2010, 172, 116-122.	3.4	35
44	Near-roadway air pollution exposure and altered fatty acid oxidation among adolescents and young adults – The interplay with obesity. <i>Environment International</i> , 2019, 130, 104935.	10.0	35
45	Asthma Disease Status, COPD, and COVID-19 Severity in a Large Multiethnic Population. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2021, 9, 3621-3628.e2.	3.8	33
46	Bayesian Model Averaging in Time-Series Studies of Air Pollution and Mortality. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2007, 70, 311-315.	2.3	32
47	Bivariate survival models for analysis of genetic and environmental effects in twins. <i>Genetic Epidemiology</i> , 1990, 7, 121-135.	1.3	28
48	Association of Common Genetic Variants With Contralateral Breast Cancer Risk in the WECARE Study. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	28
49	Discovery of complex pathways from observational data. <i>Statistics in Medicine</i> , 2010, 29, 1998-2011.	1.6	27
50	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1370-1380.	2.5	27
51	Ambient air pollution and COVID-19 incidence during four 2020–2021 case surges. <i>Environmental Research</i> , 2022, 208, 112758.	7.5	27
52	Genome Scan of Complex Traits by Haplotype Sharing Correlation. <i>Genetic Epidemiology</i> , 2001, 21, S582-7.	1.3	23
53	Near-roadway air pollution associated with COVID-19 severity and mortality – Multiethnic cohort study in Southern California. <i>Environment International</i> , 2021, 157, 106862.	10.0	23
54	Methods for testing interactions, with applications to occupational exposures, smoking, and lung cancer. <i>American Journal of Industrial Medicine</i> , 1988, 13, 131-147.	2.1	21

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55	Radiation Treatment, <i>ATM</i> , <i>BRCA1/2</i> , and <i>CHEK2</i> *1100delC Pathogenic Variants and Risk of Contralateral Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1275-1279.	6.3	21
56	Considerations in Determining Matching Criteria and Stratum Sizes for Case-control Studies. <i>International Journal of Epidemiology</i> , 1981, 10, 389-392.	1.9	20
57	Residential magnetic fields predicted from wiring configurations: II. Relationships to childhood leukemia. <i>Bioelectromagnetics</i> , 1999, 20, 414-422.	1.6	20
58	The use of hierarchical models for estimating relative risks of individual genetic variants: An application to a study of melanoma. <i>Statistics in Medicine</i> , 2008, 27, 1973-1992.	1.6	20
59	Using biological knowledge to discover higher order interactions in genetic association studies. <i>Genetic Epidemiology</i> , 2010, 34, 863-878.	1.3	20
60	Two-phase and family-based designs for next-generation sequencing studies. <i>Frontiers in Genetics</i> , 2013, 4, 276.	2.3	19
61	Bayes Estimates of Haplotype Effects. <i>Genetic Epidemiology</i> , 2001, 21, S712-7.	1.3	18
62	A latent unknown clustering integrating multi-omics data (LUCID) with phenotypic traits. <i>Bioinformatics</i> , 2020, 36, 842-850.	4.1	18
63	A Bayesian approach to multipoint mapping in nuclear families. <i>Genetic Epidemiology</i> , 1997, 14, 903-908.	1.3	17
64	A Unified Model for the Analysis of Gene-Environment Interaction. <i>American Journal of Epidemiology</i> , 2019, 188, 760-767.	3.4	15
65	Fitting models of carcinogenesis to a case-control study of breast cancer. <i>Journal of Chronic Diseases</i> , 1987, 40, 181S-189S.	1.2	14
66	Residential magnetic fields predicted from wiring configurations: I. Exposure model. <i>Bioelectromagnetics</i> , 1999, 20, 399-413.	1.6	14
67	Linkage Analysis of Urine Arsenic Species Patterns in the Strong Heart Family Study. <i>Toxicological Sciences</i> , 2015, 148, 89-100.	3.1	14
68	Toxicokinetic genetics: an approach to gene-environment and gene-gene interactions in complex metabolic pathways. <i>IARC (International Agency for Research on Cancer) Scientific Publications</i> , 2004, , 127-50.	0.4	14
69	Case-parents design for gene-environment interaction by Schaid. <i>Genetic Epidemiology</i> , 2000, 19, 461-463.	1.3	13
70	High-Volume ???-Omics??? Technologies and the Future of Molecular Epidemiology. <i>Epidemiology</i> , 2006, 17, 490-491.	2.7	13
71	Ascertainment Bias in Rate Ratio Estimation from Case-Sibling Control Studies of Variable Age-At-Onset Diseases. <i>Biometrics</i> , 1999, 55, 1129-1136.	1.4	12
72	Transcriptomic and metabolomic associations with exposures to air pollutants among young adults with childhood asthma history. <i>Environmental Pollution</i> , 2022, 299, 118903.	7.5	12

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73	A generalized estimating equations approach to fitting major gene models in segregation analysis of continuous phenotypes. <i>Genetic Epidemiology</i> , 1993, 10, 61-74.	1.3	11
74	Multistage sampling for latent variable models. <i>Lifetime Data Analysis</i> , 2007, 13, 565-581.	0.9	11
75	A generalized estimating equations approach to linkage analysis in sibships in relation to multiple markers and exposure factors. <i>Genetic Epidemiology</i> , 1999, 17, S737-42.	1.3	10
76	A joint test of linkage and gene–environment interaction, with affected sib pairs. <i>Genetic Epidemiology</i> , 1999, 17, S563-S568.	1.3	8
77	What Does “Precision Medicine” Have to Say About Prevention?. <i>Epidemiology</i> , 2017, 28, 479-483.	2.7	8
78	Genetic epidemiologic analysis of quantitative phenotypes using gibbs sampling. <i>Genetic Epidemiology</i> , 1995, 12, 753-758.	1.3	7
79	Some Contributions of Statistics to Environmental Epidemiology. <i>Journal of the American Statistical Association</i> , 2000, 95, 315-319.	3.1	7
80	Empirical Hierarchical Bayes Approach to Gene–Environment Interactions: Development and Application to Genome–Wide Association Studies of Lung Cancer in TRICL. <i>Genetic Epidemiology</i> , 2013, 37, 551-559.	1.3	7
81	GWASeq: targeted re-sequencing follow up to GWAS. <i>BMC Genomics</i> , 2016, 17, 176.	2.8	7
82	International Genetic Epidemiology Society: Commentary on Darkness in El Dorado by Patrick Tierney. <i>Genetic Epidemiology</i> , 2001, 21, 81-104.	1.3	6
83	Two-stage family-based designs for sequencing studies. <i>BMC Proceedings</i> , 2014, 8, S32.	1.6	6
84	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1077-1089.	2.5	6
85	A bivariate genetic analysis of HDL- and LDL-cholesterol incorporating measured covariates: A gibbs sampling application. <i>Genetic Epidemiology</i> , 1993, 10, 623-628.	1.3	5
86	Joint Analysis for Integrating Two Related Studies of Different Data Types and Different Study Designs Using Hierarchical Modeling Approaches. <i>Human Heredity</i> , 2012, 74, 83-96.	0.8	5
87	Inclusion of biological knowledge in a Bayesian shrinkage model for joint estimation of SNP effects. <i>Genetic Epidemiology</i> , 2017, 41, 320-331.	1.3	5
88	Association of a Pathway-Specific Genetic Risk Score With Risk of Radiation-Associated Contralateral Breast Cancer. <i>JAMA Network Open</i> , 2019, 2, e1912259.	5.9	5
89	Viewpoint: using gene–environment interactions to dissect the effects of complex mixtures. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2007, 17, S71-S74.	3.9	4
90	Complex System Approaches to Genetic Analysis. <i>Advances in Genetics</i> , 2010, 72, 47-71.	1.8	4

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91	Genetic Epidemiology with a Capital E: Where Will We Be in Another 10 Years?. Genetic Epidemiology, 2012, 36, 179-182.	1.3	4
92	Re: "Risk of Premenopausal Breast Cancer and Use of Electric Blankets". American Journal of Epidemiology, 1995, 142, 448-449.	3.4	3
93	Next-Generation Sequencing Studies: Optimal Design and Analysis, Missing Heritability and Rare Variants. Current Epidemiology Reports, 2014, 1, 213-219.	2.4	3
94	Association tests using unaffected-sibling versus pseudo-sibling controls. Genetic Epidemiology, 1999, 17, S731-S736.	1.3	2
95	A Bayesian Hierarchical Model for Relating Multiple SNPs within Multiple Genes to Disease Risk. International Journal of Genomics, 2013, 2013, 1-10.	1.6	2
96	Measurement error in spatial exposure models: study design implications. Environmetrics, 2013, 24, 518-520.	1.4	2
97	Estimating the Effect of Targeted Screening Strategies. Epidemiology, 2017, 28, 470-478.	2.7	2
98	Some Contributions of Statistics to Environmental Epidemiology. Journal of the American Statistical Association, 2000, 95, 315.	3.1	1
99	Discussion on "Statistical Issues Arising in the Women's Health Initiative". Biometrics, 2005, 61, 930-933.	1.4	0
100	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.	1.8	0
101	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. PLoS Computational Biology, 2021, 17, e1007948.	3.2	0
102	Longer- and Shorter-term Air Pollution Exposure Associated with COVID-19 Severity and Mortality: A Large Cohort Study in Southern California. ISEE Conference Abstracts, 2021, 2021, .	0.0	0
103	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	6.3	0