

Robert C Elston

List of Publications by Year in descending order

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163
papers

5,528
citations

94269

37
h-index

102304

66
g-index

186
all docs

186
docs citations

186
times ranked

5394
citing authors

#	ARTICLE	IF	CITATIONS
1	A comparison of sib-pair linkage tests for disease susceptibility loci. <i>Genetic Epidemiology</i> , 1985, 2, 85-97.	0.6	365
2	Haseman and Elston revisited. <i>Genetic Epidemiology</i> , 2000, 19, 1-17.	0.6	324
3	Hereditary nonpolyposis colorectal cancer (lynch syndromes I and II). I. Clinical description of resource. <i>Cancer</i> , 1985, 56, 934-938.	2.0	298
4	An autosomal screen for genes that predispose to celiac disease in the western counties of Ireland. <i>Nature Genetics</i> , 1996, 14, 329-333.	9.4	173
5	Heritability of the Severity of Diabetic Retinopathy: The FIND-Eye Study. , 2008, 49, 3839.		163
6	Hereditary nonpolyposis colorectal cancer (lynch syndromes I and II). II. Biomarker studies. <i>Cancer</i> , 1985, 56, 939-951.	2.0	156
7	Choosing an optimal method to combine P values. <i>Statistics in Medicine</i> , 2009, 28, 1537-1553.	0.8	137
8	Lods, wrods, and mods: The interpretation of lod scores calculated under different models. <i>Genetic Epidemiology</i> , 1994, 11, 329-342.	0.6	133
9	Testing the association between polymorphic markers and quantitative traits in pedigrees. <i>Genetic Epidemiology</i> , 1987, 4, 193-201.	0.6	124
10	A Unified Association Analysis Approach for Family and Unrelated Samples Correcting for Stratification. <i>American Journal of Human Genetics</i> , 2008, 82, 352-365.	2.6	124
11	Genetic dissection of complex traits. <i>Nature Genetics</i> , 1996, 12, 355-356.	9.4	119
12	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). <i>PLoS Genetics</i> , 2015, 11, e1005352.	1.5	118
13	Novel recurrently mutated genes in African American colon cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1149-1154.	3.3	118
14	The Meaning of Interaction. <i>Human Heredity</i> , 2010, 70, 269-277.	0.4	115
15	A powerful method of combining measures of association and Hardy-Weinberg disequilibrium for fine-mapping in case-control studies. <i>Statistics in Medicine</i> , 2006, 25, 105-126.	0.8	99
16	Transmission/disequilibrium tests for quantitative traits. <i>Genetic Epidemiology</i> , 2001, 20, 57-74.	0.6	93
17	Adding Further Power to the Haseman and Elston Method for Detecting Linkage in Larger Sibships: Weighting Sums and Differences. <i>Human Heredity</i> , 2003, 55, 79-85.	0.4	91
18	Power and robustness of sib-pair linkage tests and extension to larger sibships. <i>Communications in Statistics - Theory and Methods</i> , 1982, 11, 449-484.	0.6	89

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19	Log-linear model-based multifactor dimensionality reduction method to detect gene-gene interactions. <i>Bioinformatics</i> , 2007, 23, 2589-2595.	1.8	82
20	Linkage and association. , 1998, 15, 565-576.		81
21	Electrocardiographic Prediction of Abnormal Genotype in Congenital Long QT Syndrome: Experience in 101 Related Family Members. <i>Journal of Cardiovascular Electrophysiology</i> , 2001, 12, 455-461.	0.8	79
22	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. <i>Human Genetics</i> , 2011, 130, 725-733.	1.8	79
23	Genome Scan for Loci Predisposing to Anxiety Disorders Using a Novel Multivariate Approach: Strong Evidence for a Chromosome 4 Risk Locus. <i>American Journal of Human Genetics</i> , 2006, 78, 543-553.	2.6	76
24	Linkage Analysis of a Complex Disease through Use of Admixed Populations. <i>American Journal of Human Genetics</i> , 2004, 74, 1136-1153.	2.6	73
25	The Eiston-Stewart Algorithm for Continuous Genotypes and Environmental Factors. <i>Human Heredity</i> , 1992, 42, 16-27.	0.4	58
26	Analysis pipeline for the epistasis search - statistical versus biological filtering. <i>Frontiers in Genetics</i> , 2014, 5, 106.	1.1	57
27	Segregation analysis of hereditary nonpolyposis colorectal cancer. <i>Genetic Epidemiology</i> , 1986, 3, 27-38.	0.6	55
28	A Faster and More General Hidden Markov Model Algorithm for Multipoint Likelihood Calculations. <i>Human Heredity</i> , 1997, 47, 197-202.	0.4	55
29	Genetic determinants of acute hypoxic ventilation: patterns of inheritance in mice. <i>Journal of Applied Physiology</i> , 2000, 88, 2310-2318.	1.2	55
30	Are Linkage Analysis and the Collection of Family Data Dead? Prospects for Family Studies in the Age of Genome-Wide Association. <i>Human Heredity</i> , 2007, 64, 91-96.	0.4	55
31	Genetic etiology of gastric carcinoma: I. Chronic atrophic gastritis. <i>Genetic Epidemiology</i> , 1986, 3, 213-224.	0.6	52
32	Using the Optimal Receiver Operating Characteristic Curve to Design a Predictive Genetic Test, Exemplified with Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2008, 82, 641-651.	2.6	52
33	Statistical validity of the Haseman-Elston sib-pair test in small samples. <i>Genetic Epidemiology</i> , 1993, 10, 593-598.	0.6	49
34	Two-level Haseman-Elston regression for general pedigree data analysis. <i>Genetic Epidemiology</i> , 2005, 29, 12-22.	0.6	46
35	Lung cancer histologic type and family history of cancer. <i>Cancer</i> , 1992, 69, 86-91.	2.0	45
36	Potential role of an additive genetic component in the cause of amyotrophic lateral sclerosis and parkinsonism-dementia in the western Pacific. <i>American Journal of Medical Genetics Part A</i> , 1993, 45, 68-76.	2.4	42

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37	Regression Models for Linkage: Issues of Traits, Covariates, Heterogeneity, and Interaction. <i>Human Heredity</i> , 2003, 55, 86-96.	0.4	42
38	On the relative sample size required for multiple comparisons. , 2000, 19, 369-372.		41
39	Multipoint linkage disequilibrium mapping with particular reference to the African-American population. , 1999, 17, 79-101.		40
40	What Is the Significance of Difference in Phenotypic Variability across SNP Genotypes?. <i>American Journal of Human Genetics</i> , 2013, 93, 390-397.	2.6	39
41	Generalized modulus power transformations. <i>Communications in Statistics - Theory and Methods</i> , 1988, 17, 2933-2952.	0.6	38
42	Improving Power in Contrasting Linkage-Disequilibrium Patterns between Cases and Controls. <i>American Journal of Human Genetics</i> , 2007, 80, 911-920.	2.6	38
43	A review of the 'Statistical Analysis for Genetic Epidemiology' (SAGE) software package. <i>Human Genomics</i> , 2004, 1, 456.	1.4	37
44	Effect of cohort differences in smoking prevalence on models of lung cancer susceptibility. <i>Genetic Epidemiology</i> , 1992, 9, 261-271.	0.6	35
45	Genetic mapping of complex traits. , 1999, 18, 2961-2981.		35
46	Statistical interaction in human genetics: how should we model it if we are looking for biological interaction?. <i>Nature Reviews Genetics</i> , 2011, 12, 74-74.	7.7	35
47	Mathematical Assumptions versus Biological Reality: Myths in Affected Sib Pair Linkage Analysis. <i>American Journal of Human Genetics</i> , 2005, 76, 152-156.	2.6	34
48	Examination of Association with Candidate Genes for Diabetic Nephropathy in a Mexican American Population. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2010, 5, 1072-1078.	2.2	32
49	The study of candidate genes in drug trials: sample size considerations. , 1999, 18, 741-751.		31
50	Extensions to sib-pair linkage tests applicable to disorders characterized by delayed onset. <i>Genetic Epidemiology</i> , 1990, 7, 453-466.	0.6	30
51	Haseman and Elston revisited: The effects of ascertainment and residual familial correlations on power to detect linkage. <i>Genetic Epidemiology</i> , 2000, 19, 456-460.	0.6	30
52	Genetic analysis of von Willebrand's disease in two large pedigrees: A multivariate approach. <i>American Journal of Medical Genetics Part A</i> , 1980, 6, 279-293.	2.4	29
53	A multivariate logistic model (MLM) for analyzing binary family data. , 1998, 76, 428-437.		27
54	Multistage Sampling for Genetic Studies. <i>Annual Review of Genomics and Human Genetics</i> , 2007, 8, 327-342.	2.5	26

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55	A Modified Revisited Haseman-Elston Method to Further Improve Power. <i>Human Heredity</i> , 2004, 57, 109-116.	0.4	25
56	ONETOOL for the analysis of family-based big data. <i>Bioinformatics</i> , 2018, 34, 2851-2853.	1.8	25
57	Advances in statistical human genetics over the last 25 years. <i>Statistics in Medicine</i> , 2006, 25, 3049-3080.	0.8	24
58	Adaptive Two-Stage Analysis of Genetic Association in Case-Control Designs. <i>Human Heredity</i> , 2007, 63, 175-186.	0.4	24
59	A Genome-Wide Search for Linkage of Estimated Glomerular Filtration Rate (eGFR) in the Family Investigation of Nephropathy and Diabetes (FIND). <i>PLoS ONE</i> , 2013, 8, e81888.	1.1	24
60	Association Between Germline Mutation in <i>V51G10L</i> and Familial Barrett Neoplasia. <i>JAMA Oncology</i> , 2016, 2, 1333.	3.4	23
61	Deriving components of genetic variance for multilocus models. <i>Genetic Epidemiology</i> , 1997, 14, 1131-1136.	0.6	22
62	Two-stage global search designs for linkage analysis II: Including discordant relative pairs in the study. <i>Genetic Epidemiology</i> , 2000, 18, 111-127.	0.6	22
63	Detecting genetic interactions for quantitative traits with U-statistics. <i>Genetic Epidemiology</i> , 2011, 35, n/a-n/a.	0.6	22
64	Restrictions on Components of Variance for Epistatic Models. <i>Theoretical Population Biology</i> , 1998, 54, 161-174.	0.5	21
65	Fieller's theorem and linkage disequilibrium mapping. , 1999, 17, 237-252.		21
66	Determination of the order of loci on the short arm of chromosome 11 using two and three locus linkage analyses of pedigree and sib pair data. <i>Genetic Epidemiology</i> , 1986, 3, 147-152.	0.6	20
67	Association between polymorphic blood markers and risk factors for cardiovascular disease in a large pedigree. <i>Genetic Epidemiology</i> , 1987, 4, 267-275.	0.6	20
68	Two-stage global search designs for linkage analysis I: Use of the mean statistic for affected sib pairs. , 2000, 18, 97-110.		20
69	CELLULAR GENES IN THE MOUSE REGULATE IN TRANS THE EXPRESSION OF ENDOGENOUS MOUSE MAMMARY TUMOR VIRUSES. <i>Genetics</i> , 1985, 111, 597-615.	1.2	20
70	Segregation and linkage analyses of dopamine- β -hydroxylase activity in a six-generation pedigree. <i>American Journal of Medical Genetics Part A</i> , 1987, 27, 613-621.	2.4	19
71	Evidence for a dominant gene mechanism underlying coeliac disease in the West of Ireland. <i>Genetic Epidemiology</i> , 1991, 8, 13-27.	0.6	18
72	Evaluation of removable statistical interaction for binary traits. <i>Statistics in Medicine</i> , 2013, 32, 1164-1190.	0.8	18

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73	Confidence bands for the growth of head circumference in achondroplastic children during the first year of life. <i>American Journal of Medical Genetics Part A</i> , 1980, 7, 529-536.	2.4	17
74	Confidence limits based on the first occurrence of an event. <i>Statistics in Medicine</i> , 1993, 12, 685-690.	0.8	17
75	Single-marker and two-marker association tests for unphased case-control genotype data, with a power comparison. <i>Genetic Epidemiology</i> , 2010, 34, 67-77.	0.6	17
76	False discoveries in genome scanning. <i>Genetic Epidemiology</i> , 1997, 14, 779-784.	0.6	16
77	Linkage of chromosome 1 markers to alcoholism-related phenotypes by sib pair linkage analysis of principal components. <i>Genetic Epidemiology</i> , 1999, 17, S271-6.	0.6	16
78	The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. <i>PLoS Genetics</i> , 2014, 10, e1004641.	1.5	16
79	On the Estimation of Heritability with Family-Based and Population-Based Samples. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	16
80	Genetic Terminology. <i>Methods in Molecular Biology</i> , 2012, 850, 1-9.	0.4	16
81	The power of independent types of genetic information to detect association in a case-control study design. <i>Genetic Epidemiology</i> , 2008, 32, 731-756.	0.6	15
82	A Likelihood Ratio-Based Mann-Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. <i>Genetic Epidemiology</i> , 2012, 36, 583-593.	0.6	15
83	Association within twin pairs for a dichotomous trait. , 1996, 13, 489-499.		14
84	A bivariate problem in human genetics: Ascertainment of families through a correlated trait. <i>American Journal of Medical Genetics Part A</i> , 1984, 18, 435-448.	2.4	13
85	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. <i>BMC Proceedings</i> , 2009, 3, S49.	1.8	13
86	Multipoint admixture mapping. <i>Genetic Epidemiology</i> , 2000, 19, 464-467.	0.6	12
87	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. <i>Biometrics</i> , 2010, 66, 586-593.	0.8	12
88	A Non-Parametric Method for Building Predictive Genetic Tests on High-Dimensional Data. <i>Human Heredity</i> , 2011, 71, 161-170.	0.4	12
89	Power of Single-vs. Multi-Marker Tests of Association. <i>Genetic Epidemiology</i> , 2012, 36, 480-487.	0.6	12
90	Regression toward the mean in 2 \times 2 crossover designs with baseline measurements. <i>Statistics in Medicine</i> , 1992, 11, 727-741.	0.8	11

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91	Major gene segregation of actinic prurigo among North American Indians in Saskatchewan. American Journal of Medical Genetics Part A, 2000, 92, 212-219.	2.4	11
92	New multivariate test for linkage, with application to pleiotropy: Fuzzy Haseman-Elston. Genetic Epidemiology, 2003, 24, 253-264.	0.6	11
93	Joint modeling of longitudinal data and discrete-time survival outcome. Statistical Methods in Medical Research, 2016, 25, 1512-1526.	0.7	11
94	Description of a large pedigree with an adverse lipoprotein cholesterol phenotype: The Bogalusa Heart Study. Genetic Epidemiology, 1986, 3, 241-253.	0.6	10
95	Pooling Data and Linkage Analysis in the Chromosome 5q Candidate Region for Asthma. Genetic Epidemiology, 2001, 21, S103-8.	0.6	10
96	Locating the Genes Underlying a Simulated Complex Disease by Discriminant Analysis. Genetic Epidemiology, 2001, 21, S516-S521.	0.6	10
97	Family-Based Rare Variant Association Analysis: A Fast and Efficient Method of Multivariate Phenotype Association Analysis. Genetic Epidemiology, 2016, 40, 502-511.	0.6	10
98	Predicting Barrett's Esophagus in Families: An Esophagus Translational Research Network (BETRNet) Model Fitting Clinical Data to a Familial Paradigm. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 727-735.	1.1	10
99	Alternative test for linkage between two loci. , 1997, 14, 117-131.		9
100	Model-free age-of-onset methods applied to the linkage of bipolar disorder. Genetic Epidemiology, 1997, 14, 711-716.	0.6	9
101	A Note on Comparing the Power of Test Statistics at Low Significance Levels. American Statistician, 2011, 65, 164-166.	0.9	8
102	Will Formal Genetics Become Dispensable?. Human Heredity, 2013, 76, 47-52.	0.4	8
103	On the Analysis of a Repeated Measure Design in Genome-Wide Association Analysis. International Journal of Environmental Research and Public Health, 2014, 11, 12283-12303.	1.2	8
104	Applying family analyses to electronic health records to facilitate genetic research. Bioinformatics, 2018, 34, 635-642.	1.8	8
105	INHERITANCE OF ADRENAL PHENYLETHANOLAMINE <i>N</i> -METHYLTRANSFERASE ACTIVITY IN THE RAT. Genetics, 1984, 108, 633-649.	1.2	8
106	Genetic etiology of gastric carcinoma: II. Segregation analysis of gastric pH, nitrate, and nitrite. Genetic Epidemiology, 1987, 4, 103-114.	0.6	7
107	A major gene model for the familial aggregation of plasma IgA concentration. American Journal of Medical Genetics Part A, 1987, 27, 857-866.	2.4	7
108	Model-free association analysis of a rare Disease. Genetic Epidemiology, 1995, 12, 571-575.	0.6	7

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109	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. <i>Genetic Epidemiology</i> , 1999, 17, S157-S161.	0.6	7
110	Adding power to Haseman and Elston's (1972) method. <i>GeneScreen</i> , 2000, 1, 63-64.	0.7	7
111	A weighted U statistic for association analyses considering genetic heterogeneity. <i>Statistics in Medicine</i> , 2016, 35, 2802-2814.	0.8	7
112	Statistical validity for testing associations between genetic markers and quantitative traits in family data. <i>Genetic Epidemiology</i> , 1995, 12, 145-161.	0.6	6
113	Modeling age of onset and residual familial correlations for the linkage analysis of bipolar disorder. <i>Genetic Epidemiology</i> , 1997, 14, 675-680.	0.6	6
114	Model-free sib-pair linkage analysis: Combining full-sib and half-sib pairs. <i>Genetic Epidemiology</i> , 2000, 19, 30-51.	0.6	6
115	Segregation analyses of asthma and respiratory allergy: The Humboldt family study. <i>American Journal of Medical Genetics Part A</i> , 2001, 104, 23-30.	2.4	6
116	Novel approaches to the analysis of family data in genetic epidemiology. <i>Frontiers in Genetics</i> , 2015, 6, 27.	1.1	6
117	Genomic regions associated with susceptibility to Barrett's esophagus and esophageal adenocarcinoma in African Americans: The cross BETRNet admixture study. <i>PLoS ONE</i> , 2017, 12, e0184962.	1.1	6
118	The HGAR1 familial hypercholesterolemia pedigree. <i>Genetic Epidemiology</i> , 1993, 10, 529-531.	0.6	5
119	Using family history information to distinguish true and false positive model-free linkage results. , 1998, 15, 183-192.		5
120	Analysis of Swedish male breast cancer family data: A simple way to incorporate a common sibling effect. , 1998, 15, 201-212.		5
121	Bagging Optimal ROC Curve Method for Predictive Genetic Tests, with an Application for Rheumatoid Arthritis. <i>Journal of Biopharmaceutical Statistics</i> , 2010, 20, 401-414.	0.4	5
122	Interrogating population structure and its impact on association tests. <i>BMC Proceedings</i> , 2011, 5, S25.	1.8	5
123	Fisher's influence on me. <i>Genetic Epidemiology</i> , 2018, 42, 849-853.	0.6	5
124	Adjustment for covariates using summary statistics of genome-wide association studies. <i>Genetic Epidemiology</i> , 2018, 42, 812-825.	0.6	5
125	A multivariate analysis of familial associations of lipoprotein levels in the Lipid Research Clinics Collaborative Family Study: I. Familial correlation and regression analyses. <i>Genetic Epidemiology</i> , 1985, 2, 283-300.	0.6	4
126	Effects of marker information on sib-pair linkage analysis of a rare disease. <i>Genetic Epidemiology</i> , 1995, 12, 625-630.	0.6	4

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127	Localization of the Q1 Mutation by Cladistic Analysis. <i>Genetic Epidemiology</i> , 2001, 21, S594-9.	0.6	4
128	What We Know and What We Need to Know About Familial Gastroesophageal Reflux Disease and Barrett's Esophagus. <i>Clinical Gastroenterology and Hepatology</i> , 2014, 12, 1664-1666.	2.4	4
129	Linkage and related analyses of Barrett's esophagus and its associated adenocarcinomas. <i>Molecular Genetics & Genomic Medicine</i> , 2016, 4, 407-419.	0.6	4
130	Combining two-point genetic linkage analyses using mapping functions. <i>Genetic Epidemiology</i> , 1994, 11, 1-17.	0.6	3
131	Association and linkage analysis of ICD-10 diagnosis for alcoholism. <i>Genetic Epidemiology</i> , 1999, 17, S343-7.	0.6	3
132	Improving the power for disease locus detection in affected sib-pair studies by using two-locus analysis and multiple regression methods. <i>Genetic Epidemiology</i> , 1999, 17, S521-6.	0.6	3
133	A Century of Biometrical Genetics. <i>Biometrics</i> , 2000, 56, 659-666.	0.8	3
134	Testing gene-environment interactions in gene-based association studies. <i>BMC Proceedings</i> , 2011, 5, S26.	1.8	3
135	Putative Linkage Signals Identified for Breast Cancer in African American Families. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 442-447.	1.1	3
136	Statistical interactions and Bayes estimation of log odds in case-control studies. <i>Statistical Methods in Medical Research</i> , 2017, 26, 1021-1038.	0.7	3
137	How Consistent are Genetic Factors in Explaining Leisure-Time Physical Activity and Sport Participation? The Portuguese Healthy Families Study. <i>Twin Research and Human Genetics</i> , 2018, 21, 369-377.	0.3	3
138	Local Ancestry Inference in Large Pedigrees. <i>Scientific Reports</i> , 2020, 10, 189.	1.6	3
139	Likelihood Models for Multivariate Traits in Human Genetics1. <i>Biometrical Journal</i> , 1985, 27, 553-563.	0.6	2
140	A method to assess the environment for genetic studies: The common environment index and the household relationships interview. <i>American Journal of Medical Genetics Part A</i> , 1985, 21, 325-335.	2.4	2
141	Testing specific hypotheses by fitting underlying distributions to categorical data. <i>Journal of Biopharmaceutical Statistics</i> , 1994, 4, 53-64.	0.4	2
142	The Genetic Epidemiology of Age-Related Maculopathy. <i>International Journal of Human Genetics</i> , 2001, 1, 11-24.	0.1	2
143	Segregation Analysis of Gastric Cancer in a Japanese Population. <i>International Journal of Human Genetics</i> , 2001, 1, 263-270.	0.1	2
144	Segregation Analysis of Asthma and Respiratory Allergy in Population-Based Samples of Families. <i>Genetic Epidemiology</i> , 2001, 21, S30-5.	0.6	2

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145	Linkage Disequilibrium Mapping of Complex Genetic Diseases Using Multiallelic Markers. <i>Genetic Epidemiology</i> , 2001, 21, S576-81.	0.6	2
146	Response to letter by Veronica J. Vieland and Susan E. Hodge. <i>Genetic Epidemiology</i> , 2005, 28, 286-287.	0.6	2
147	Phase uncertainty in case-control association studies. <i>Genetic Epidemiology</i> , 2009, 33, 463-478.	0.6	2
148	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. <i>PLoS ONE</i> , 2016, 11, e0146435.	1.1	2
149	Pedigree discriminant analysis of two French Canadian Tay-Sachs families. <i>Genetic Epidemiology</i> , 1987, 4, 77-85.	0.6	1
150	Model-based and model-free multipoint genome-wide linkage analysis of alcoholism. <i>Genetic Epidemiology</i> , 1999, 17, S175-S180.	0.6	1
151	Comparison of Marker Intervals and Number of Sib Pairs Used for Linkage Analysis on Simulated Nuclear Family Data. <i>Genetic Epidemiology</i> , 2001, 21, S748-S753.	0.6	1
152	2010 William Allan Award Introduction: J. Arg Ott. <i>American Journal of Human Genetics</i> , 2011, 88, 262-263.	2.6	1
153	Linkage-Disequilibrium-Based Binning Misleads the Interpretation of Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2012, 91, 965-968.	2.6	1
154	Reply to Ashktorab et al.: Mutational landscape of colon cancers in African Americans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2853-E2853.	3.3	1
155	On the association analysis of CNV data: a fast and robust family-based association method. <i>BMC Bioinformatics</i> , 2017, 18, 217.	1.2	1
156	Major gene segregation of actinic prurigo among North American Indians in Saskatchewan. <i>American Journal of Medical Genetics Part A</i> , 2000, 92, 212-219.	2.4	1
157	False discoveries in genome scanning., 1997, 14, 779.		1
158	Authors' reply: Confidence limits based on the first occurrence of an event. V.T. George and R.C. Elton. <i>Statistics in Medicine</i> , 12, 685-690 (1993). <i>Statistics in Medicine</i> , 1998, 17, 945-945.	0.8	0
159	Introduction: Linkage Analyses of Single Regions. <i>Genetic Epidemiology</i> , 2001, 21, S79.	0.6	0
160	Impact of Preadjusting a Quantitative Phenotype Prior to Sib-Pair Linkage Analysis when Gene-Environment Interaction Exists. <i>Genetic Epidemiology</i> , 2001, 21, S837-S842.	0.6	0
161	A PROBLEM IN ASCERTAINMENT. <i>Communications in Statistics - Theory and Methods</i> , 2001, 30, 1615-1631.	0.6	0
162	Likelihood Modelling: Genetic Mapping of Complex Traits. , 2005, , 339-359.		0

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163	An Accidental Genetic Epidemiologist. Annual Review of Genomics and Human Genetics, 2020, 21, 15-36.	2.5	0