Robert C Elston

List of Publications by Year
in descending order

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163 papers	5,528 citations	87888 38 h-index	98798 67 g-index
186 all docs	186 docs citations	186 times ranked	5394 citing authors

#	Article	IF	Citations
1	A comparison of sibâ€pair linkage tests for disease susceptibility loci. Genetic Epidemiology, 1985, 2, 85-97.	1.3	365
2	Haseman and Elston revisited. Genetic Epidemiology, 2000, 19, 1-17.	1.3	324
3	Hereditary nonpolyposis colorectal cancer (lynch syndromes I and II). I. Clinical description of resource. Cancer, 1985, 56, 934-938.	4.1	298
4	An autosomal screen for genes that predispose to celiac disease in the western counties of Ireland. Nature Genetics, 1996, 14, 329-333.	21.4	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. Cancer, 1985, 56, 939-951.	4.1	156
7	Choosing an optimal method to combine Pâ€values. Statistics in Medicine, 2009, 28, 1537-1553.	1.6	137
8	Lods, wrods, and mods: The interpretation of lod scores calculated under different models. Genetic Epidemiology, 1994, 11, 329-342.	1.3	133
9	Testing the association between polymorphic markers and quantitative traits in pedigrees. Genetic Epidemiology, 1987, 4, 193-201.	1.3	124
10	A Unified Association Analysis Approach for Family and Unrelated Samples Correcting for Stratification. American Journal of Human Genetics, 2008, 82, 352-365.	6.2	124
11	Genetic dissection of complex traits. Nature Genetics, 1996, 12, 355-356.	21.4	119
12	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). PLoS Genetics, 2015, 11, e1005352.	3.5	118
13	Novel recurrently mutated genes in African American colon cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1149-1154.	7.1	118
14	The Meaning of Interaction. Human Heredity, 2010, 70, 269-277.	0.8	115
15	A powerful method of combining measures of association and Hardyâ€“Weinberg disequilibrium for fineâ€mapping in caseâ€control studies. Statistics in Medicine, 2006, 25, 105-126.	1.6	99
16	Transmission/disequilibrium tests for quantitative traits. Genetic Epidemiology, 2001, 20, 57-74.	1.3	93
17	Adding Further Power to the Haseman and Elston Method for Detecting Linkage in Larger Sibships: Weighting Sums and Differences. Human Heredity, 2003, 55, 79-85.	0.8	91
18	Power and robustness of sib-pair linkage tests and extension to larger sibships. Communications in Statistics - Theory and Methods, 1982, 11, 449-484.	1.0	89

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19	Log-linear model-based multifactor dimensionality reduction method to detect geneâ€“gene interactions. Bioinformatics, 2007, 23, 2589-2595.	4.1	82
20	Linkage and association. Genetic Epidemiology, 1998, 15, 565-576.	1.3	81
21	Electrocardiographic Prediction of Abnormal Genotype in Congenital Long QT Syndrome: Experience in 101 Related Family Members. Journal of Cardiovascular Electrophysiology, 2001, 12, 455-461.	1.7	79
22	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. Human Genetics, 2011, 130, 725-733.	3.8	79
23	Genome Scan for Loci Predisposing to Anxiety Disorders Using a Novel Multivariate Approach: Strong Evidence for a Chromosome 4 Risk Locus. American Journal of Human Genetics, 2006, 78, 543-553.	6.2	76
24	Linkage Analysis of a Complex Disease through Use of Admixed Populations. American Journal of Human Genetics, 2004, 74, 1136-1153.	6.2	73
25	The Eiston-Stewart Algorithm for Continuous Genotypes and Environmental Factors. Human Heredity, 1992, 42, 16-27.	0.8	58
26	Analysis pipeline for the epistasis search Ã¢â‚¬â€œ statistical versus biological filtering. Frontiers in Genetics, 2014, 5, 106.	2.3	57
27	Segregation analysis of hereditary nonpolyposis colorectal cancer. Genetic Epidemiology, 1986, 3, 27-38.	1.3	55
28	A Faster and More General Hidden Markov Model Algorithm for Multipoint Likelihood Calculations. Human Heredity, 1997, 47, 197-202.	0.8	55
29	Genetic determinants of acute hypoxic ventilation: patterns of inheritance in mice. Journal of Applied Physiology, 2000, 88, 2310-2318.	2.5	55
30	Are Linkage Analysis and the Collection of Family Data Dead? Prospects for Family Studies in the Age of Genome-Wide Association. Human Heredity, 2007, 64, 91-96.	0.8	55
31	Genetic etiology of gastric carcinoma: I. Chronic atrophic gastritis. Genetic Epidemiology, 1986, 3, 213-224.	1.3	52
32	Using the Optimal Receiver Operating Characteristic Curve to Design a Predictive Genetic Test, Exemplified with Type 2 Diabetes. American Journal of Human Genetics, 2008, 82, 641-651.	6.2	52
33	Statistical validity of the Haseman-Elston sib-pair test in small samples. Genetic Epidemiology, 1993, 10, 593-598.	1.3	49
34	Twoâ€level Hasemanâ€Elston regression for general pedigree data analysis. Genetic Epidemiology, 2005, 29, 12-22.	1.3	46
35	Lung cancer histologic type and family history of cancer. Cancer, 1992, 69, 86-91.	4.1	45
36	Potential role of an additive genetic component in the cause of amyotrophic lateral sclerosis and parkinsonism-dementia in the western Pacific. American Journal of Medical Genetics Part A, 1993, 45, 68-76.	2.4	42

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37	Regression Models for Linkage: Issues of Traits, Covariates, Heterogeneity, and Interaction. Human Heredity, 2003, 55, 86-96.	0.8	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?. American Journal of Human Genetics, 2013, 93, 390-397.	6.2	39
41	Generalized modulus power transformations. Communications in Statistics - Theory and Methods, 1988, 17, 2933-2952.	1.0	38
42	Improving Power in Contrasting Linkage-Disequilibrium Patterns between Cases and Controls. American Journal of Human Genetics, 2007, 80, 911-920.	6.2	38
43	A review of the 'Statistical Analysis for Genetic Epidemiology' (SAGE) software package. Human Genomics, 2004, 1, 456.	2.9	37
44	Effect of cohort differences in smoking prevalence on models of lung cancer susceptibility. Genetic Epidemiology, 1992, 9, 261-271.	1.3	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?. Nature Reviews Genetics, 2011, 12, 74-74.	16.3	35
47	Mathematical Assumptions versus Biological Reality: Myths in Affected Sib Pair Linkage Analysis. American Journal of Human Genetics, 2005, 76, 152-156.	6.2	34
48	Examination of Association with Candidate Genes for Diabetic Nephropathy in a Mexican American Population. Clinical Journal of the American Society of Nephrology: CJASN, 2010, 5, 1072-1078.	4.5	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. Genetic Epidemiology, 1990, 7, 453-466.	1.3	30
51	Haseman and Elston revisited: The effects of ascertainment and residual familial correlations on power to detect linkage. Genetic Epidemiology, 2000, 19, 456-460.	1.3	30
52	Genetic analysis of von Willebrand's disease in two large pedigrees: A multivariate approach. American Journal of Medical Genetics Part A, 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. Annual Review of Genomics and Human Genetics, 2007, 8, 327-342.	6.2	26

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55	A Modified Revisited Haseman-Elston Method to Further Improve Power. Human Heredity, 2004, 57, 109-116.	0.8	25
56	ONETOOL for the analysis of family-based big data. Bioinformatics, 2018, 34, 2851-2853.	4.1	25
57	Advances in statistical human genetics over the last 25 years. Statistics in Medicine, 2006, 25, 3049-3080.	1.6	24
58	Adaptive Two-Stage Analysis of Genetic Association in Case-Control Designs. Human Heredity, 2007, 63, 175-186.	0.8	24
59	A Genome-Wide Search for Linkage of Estimated Glomerular Filtration Rate (eGFR) in the Family Investigation of Nephropathy and Diabetes (FIND). PLoS ONE, 2013, 8, e81888.	2.5	24
60	Association Between Germline Mutation inVSIG10Land Familial Barrett Neoplasia. JAMA Oncology, 2016, 2, 1333.	7.1	23
61	Deriving components of genetic variance for multilocus models. Genetic Epidemiology, 1997, 14, 1131-1136.	1.3	22
62	Two-stage global search designs for linkage analysis II: Including discordant relative pairs in the study. Genetic Epidemiology, 2000, 18, 111-127.	1.3	22
63	Detecting genetic interactions for quantitative traits with U-statistics. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	22
64	Restrictions on Components of Variance for Epistatic Models. Theoretical Population Biology, 1998, 54, 161-174.	1.1	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. Genetic Epidemiology, 1986, 3, 147-152.	1.3	20
67	Association between polymorphic blood markers and risk factors for cardiovascular disease in a large pedigree. Genetic Epidemiology, 1987, 4, 267-275.	1.3	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. Genetics, 1985, 111, 597-615.	2.9	20
70	Segregation and linkage analyses of dopamineâ€Î²â€hydroxylase activity in a sixâ€generation pedigree. American Journal of Medical Genetics Part A, 1987, 27, 613-621.	2.4	19
71	Evidence for a dominant gene mechanism underlying coeliac disease in the West of Ireland. Genetic Epidemiology, 1991, 8, 13-27.	1.3	18
72	Evaluation of removable statistical interaction for binary traits. Statistics in Medicine, 2013, 32, 1164-1190.	1.6	18

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73	Confidence bands for the growth of head circumference in achondroplastic children during the first year of life. American Journal of Medical Genetics Part A, 1980, 7, 529-536.	2.4	17
74	Confidence limits based on the first occurrence of an event. Statistics in Medicine, 1993, 12, 685-690.	1.6	17
75	Singleâ€marker and twoâ€marker association tests for unphased caseâ€control genotype data, with a power comparison. Genetic Epidemiology, 2010, 34, 67-77.	1.3	17
76	False discoveries in genome scanning. Genetic Epidemiology, 1997, 14, 779-784.	1.3	16
77	Linkage of chromosome 1 markers to alcoholismâ€related phenotypes by sib pair linkage analysis of principal components. Genetic Epidemiology, 1999, 17, S271-6.	1.3	16
78	The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. PLoS Genetics, 2014, 10, e1004641.	3.5	16
79	On the Estimation of Heritability with Family-Based and Population-Based Samples. BioMed Research International, 2015, 2015, 1-9.	1.9	16
80	Genetic Terminology. Methods in Molecular Biology, 2012, 850, 1-9.	0.9	16
81	The power of independent types of genetic information to detect association in a caseâ€control study design. Genetic Epidemiology, 2008, 32, 731-756.	1.3	15
82	A Likelihood Ratioâ€Based Mannâ€Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. Genetic Epidemiology, 2012, 36, 583-593.	1.3	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. American Journal of Medical Genetics Part A, 1984, 18, 435-448.	2.4	13
85	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. BMC Proceedings, 2009, 3, S49.	1.6	13
86	Mulitpoint admixture mapping. Genetic Epidemiology, 2000, 19, 464-467.	1.3	12
87	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. Biometrics, 2010, 66, 586-593.	1.4	12
88	A Non-Parametric Method for Building Predictive Genetic Tests on High-Dimensional Data. Human Heredity, 2011, 71, 161-170.	0.8	12
89	Power of Singleâ€vs. Multiâ€Marker Tests of Association. Genetic Epidemiology, 2012, 36, 480-487.	1.3	12
90	Regression toward the mean in 2 Ã— 2 crossover designs with baseline measurements. Statistics in Medicine, 1992, 11, 727-741.	1.6	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.	1.3	11
93	Joint modeling of longitudinal data and discrete-time survival outcome. Statistical Methods in Medical Research, 2016, 25, 1512-1526.	1.5	11
94	Description of a large pedigree with an adverse lipoprotein cholesterol phenotype: The Bogalusa Heart Study. Genetic Epidemiology, 1986, 3, 241-253.	1.3	10
95	Pooling Data and Linkage Analysis in the Chromosome 5q Candidate Region for Asthma. Genetic Epidemiology, 2001, 21, S103-8.	1.3	10
96	Locating the Genes Underlying a Simulated Complex Disease by Discriminant Analysis. Genetic Epidemiology, 2001, 21, S516-S521.	1.3	10
97	Familyâ€Based Rare Variant Association Analysis: A Fast and Efficient Method of Multivariate Phenotype Association Analysis. Genetic Epidemiology, 2016, 40, 502-511.	1.3	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.	2.5	10
99	Alternative test for linkage between two loci. Genetic Epidemiology, 1997, 14, 117-131.	1.3	9
100	Model-free age-of-onset methods applied to the linkage of bipolar disorder. Genetic Epidemiology, 1997, 14, 711-716.	1.3	9
101	A Note on Comparing the Power of Test Statistics at Low Significance Levels. American Statistician, 2011, 65, 164-166.	1.6	8
102	Will Formal Genetics Become Dispensable?. Human Heredity, 2013, 76, 47-52.	0.8	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.	2.6	8
104	Applying family analyses to electronic health records to facilitate genetic research. Bioinformatics, 2018, 34, 635-642.	4.1	8
105	INHERITANCE OF ADRENAL PHENYLETHANOLAMINE N-METHYLTRANSFERASE ACTIVITY IN THE RAT. Genetics, 1984, 108, 633-649.	2.9	8
106	Genetic etiology of gastric carcinoma: II. Segregation analysis of gastric pH, nitrate, and nitrite. Genetic Epidemiology, 1987, 4, 103-114.	1.3	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.	1.3	7

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109	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. Genetic Epidemiology, 1999, 17, S157-S161.	1.3	7
110	Adding power to Haseman and Elston's (1972) method. GeneScreen, 2000, 1, 63-64.	0.6	7
111	A weighted U statistic for association analyses considering genetic heterogeneity. Statistics in Medicine, 2016, 35, 2802-2814.	1.6	7
112	Statistical validity for testing associations between genetic markers and quantitative traits in family data. Genetic Epidemiology, 1995, 12, 145-161.	1.3	6
113	Modeling age of onset and residual familial correlations for the linkage analysis of bipolar disorder. Genetic Epidemiology, 1997, 14, 675-680.	1.3	6
114	Model-free sib-pair linkage analysis: Combining full-sib and half-sib pairs. Genetic Epidemiology, 2000, 19, 30-51.	1.3	6
115	Segregation analyses of asthma and respiratory allergy: The Humboldt family study. American Journal of Medical Genetics Part A, 2001, 104, 23-30.	2.4	6
116	Novel approaches to the analysis of family data in genetic epidemiology. Frontiers in Genetics, 2015, 6, 27.	2.3	6
117	Genomic regions associated with susceptibility to Barrettâ€™s esophagus and esophageal adenocarcinoma in African Americans: The cross BETRNet admixture study. PLoS ONE, 2017, 12, e0184962.	2.5	6
118	The HGAR1 familial hypercholesterolemia pedigree. Genetic Epidemiology, 1993, 10, 529-531.	1.3	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. Journal of Biopharmaceutical Statistics, 2010, 20, 401-414.	0.8	5
122	Interrogating population structure and its impact on association tests. BMC Proceedings, 2011, 5, S25.	1.6	5
123	Fisherâ€™s influence on me. Genetic Epidemiology, 2018, 42, 849-853.	1.3	5
124	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	1.3	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. Genetic Epidemiology, 1985, 2, 283-300.	1.3	4
126	Effects of marker information on sib-pair linkage analysis of a rare disease. Genetic Epidemiology, 1995, 12, 625-630.	1.3	4

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127	Localization of the Q1 Mutation by Cladistic Analysis. Genetic Epidemiology, 2001, 21, S594-9.	1.3	4
128	What We Know and What We Need to Know About Familial Gastroesophageal Reflux Disease and Barrett's Esophagus. Clinical Gastroenterology and Hepatology, 2014, 12, 1664-1666.	4.4	4
129	Linkage and related analyses of Barrett's esophagus and its associated adenocarcinomas. Molecular Genetics & Genomic Medicine, 2016, 4, 407-419.	1.2	4
130	Combining two-point genetic linkage analyses using mapping functions. Genetic Epidemiology, 1994, 11, 1-17.	1.3	3
131	Association and linkage analysis of ICDâ€10 diagnosis for alcoholism. Genetic Epidemiology, 1999, 17, S343-7.	1.3	3
132	Improving the power for disease locus detection in affectedâ€sibâ€pair studies by using twoâ€locus analysis and multiple regression methods. Genetic Epidemiology, 1999, 17, S521-6.	1.3	3
133	A Century of Biometrical Genetics. Biometrics, 2000, 56, 659-666.	1.4	3
134	Testing gene-environment interactions in gene-based association studies. BMC Proceedings, 2011, 5, S26.	1.6	3
135	Putative Linkage Signals Identified for Breast Cancer in African American Families. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 442-447.	2.5	3
136	Statistical interactions and Bayes estimation of log odds in case-control studies. Statistical Methods in Medical Research, 2017, 26, 1021-1038.	1.5	3
137	How Consistent are Genetic Factors in Explaining Leisure-Time Physical Activity and Sport Participation? The Portuguese Healthy Families Study. Twin Research and Human Genetics, 2018, 21, 369-377.	0.6	3
138	Local Ancestry Inference in Large Pedigrees. Scientific Reports, 2020, 10, 189.	3.3	3
139	Likelihood Models for Multivariate Traits in Human Genetics1. Biometrical Journal, 1985, 27, 553-563.	1.0	2
140	A method to assess the environment for genetic studies: The common environment index and the household relationships interview. American Journal of Medical Genetics Part A, 1985, 21, 325-335.	2.4	2
141	Testing specific hypotheses by fitting underlying distributions to categorical data. Journal of Biopharmaceutical Statistics, 1994, 4, 53-64.	0.8	2
142	The Genetic Epidemiology of Age-Related Maculopathy. International Journal of Human Genetics, 2001, 1, 11-24.	0.1	2
143	Segregation Analysis of Gastric Cancer in a Japanese Population. International Journal of Human Genetics, 2001, 1, 263-270.	0.1	2
144	Segregation Analysis of Asthma and Respiratory Allergy in Populationâ€Based Samples of Families. Genetic Epidemiology, 2001, 21, S30-5.	1.3	2

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145	Linkage Disequilibrium Mapping of Complex Genetic Diseases Using Multiallelic Markers. Genetic Epidemiology, 2001, 21, S576-81.	1.3	2
146	Response to letter by Veronica J. Vieland and Susan E. Hodge. Genetic Epidemiology, 2005, 28, 286-287.	1.3	2
147	Phase uncertainty in caseâ€control association studies. Genetic Epidemiology, 2009, 33, 463-478.	1.3	2
148	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. PLoS ONE, 2016, 11, e0146435.	2.5	2
149	Pedigree discriminant analysis of two French Canadian Tay-Sachs families. Genetic Epidemiology, 1987, 4, 77-85.	1.3	1
150	Model-based and model-free multipoint genome-wide linkage analysis of alcoholism. Genetic Epidemiology, 1999, 17, S175-S180.	1.3	1
151	Comparison of Marker Intervals and Number of Sib Pairs Used for Linkage Analysis on Simulated Nuclear Family Data. Genetic Epidemiology, 2001, 21, S748-S753.	1.3	1
152	2010 William Allan Award Introduction: JÃ¼rg Ott. American Journal of Human Genetics, 2011, 88, 262-263.	6.2	1
153	Linkage-Disequilibrium-Based Binning Misleads the Interpretation of Genome-wide Association Studies. American Journal of Human Genetics, 2012, 91, 965-968.	6.2	1
154	Reply to Ashktorab et al.: Mutational landscape of colon cancers in African Americans. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2853-E2853.	7.1	1
155	On the association analysis of CNV data: a fast and robust family-based association method. BMC Bioinformatics, 2017, 18, 217.	2.6	1
156	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	1
157	False discoveries in genome scanning. Genetic Epidemiology, 1997, 14, 779-784.	1.3	1
158	Authors' reply: Confidence limits based on the first occurrence of an event. V.T. George and R.C. Elton.Statistics in Medicine,12, 685-690 (1993). Statistics in Medicine, 1998, 17, 945-945.	1.6	0
159	Introduction: Linkage Analyses of Single Regions. Genetic Epidemiology, 2001, 21, S79.	1.3	0
160	Impact of Preadjusting a Quantitative Phenotype Prior to Sib-Pair Linkage Analysis when GeneÃ—Environment Interaction Exists. Genetic Epidemiology, 2001, 21, S837-S842.	1.3	0
161	A PROBLEM IN ASCERTAINMENT. Communications in Statistics - Theory and Methods, 2001, 30, 1615-1631.	1.0	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.	6.2	0