Robert C Elston

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4666687/publications.pdf

Version: 2024-02-01

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	An Accidental Genetic Epidemiologist. Annual Review of Genomics and Human Genetics, 2020, 21, 15-36.	6.2	0
2	Local Ancestry Inference in Large Pedigrees. Scientific Reports, 2020, 10, 189.	3.3	3
3	ONETOOL for the analysis of family-based big data. Bioinformatics, 2018, 34, 2851-2853.	4.1	25
4	Applying family analyses to electronic health records to facilitate genetic research. Bioinformatics, 2018, 34, 635-642.	4.1	8
5	Fisherâ€™s influence on me. Genetic Epidemiology, 2018, 42, 849-853.	1.3	5
6	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	1.3	5
7	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
8	Statistical interactions and Bayes estimation of log odds in case-control studies. Statistical Methods in Medical Research, 2017, 26, 1021-1038.	1.5	3
9	On the association analysis of CNV data: a fast and robust family-based association method. BMC Bioinformatics, 2017, 18, 217.	2.6	1
10	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
11	A weighted U statistic for association analyses considering genetic heterogeneity. Statistics in Medicine, 2016, 35, 2802-2814.	1.6	7
12	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
13	Association Between Germline Mutation inVSIG10Land Familial Barrett Neoplasia. JAMA Oncology, 2016, 2, 1333.	7.1	23
14	Linkage and related analyses of Barrett's esophagus and its associated adenocarcinomas. Molecular Genetics & Genomic Medicine, 2016, 4, 407-419.	1.2	4
15	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
16	Joint modeling of longitudinal data and discrete-time survival outcome. Statistical Methods in Medical Research, 2016, 25, 1512-1526.	1.5	11
17	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. PLoS ONE, 2016, 11, e0146435.	2.5	2
18	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

#	Article	IF	Citations
19	On the Estimation of Heritability with Family-Based and Population-Based Samples. BioMed Research International, 2015, 2015, 1-9.	1.9	16
20	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
21	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
22	Novel approaches to the analysis of family data in genetic epidemiology. Frontiers in Genetics, 2015, 6, 27.	2.3	6
23	Putative Linkage Signals Identified for Breast Cancer in African American Families. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 442-447.	2.5	3
24	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
25	Analysis pipeline for the epistasis search Ã¢â‚¬â€œ statistical versus biological filtering. Frontiers in Genetics, 2014, 5, 106.	2.3	57
26	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
27	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
28	What Is the Significance of Difference in Phenotypic Variability across SNP Genotypes?. American Journal of Human Genetics, 2013, 93, 390-397.	6.2	39
29	Will Formal Genetics Become Dispensable?. Human Heredity, 2013, 76, 47-52.	0.8	8
30	Evaluation of removable statistical interaction for binary traits. Statistics in Medicine, 2013, 32, 1164-1190.	1.6	18
31	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
32	Linkage-Disequilibrium-Based Binning Misleads the Interpretation of Genome-wide Association Studies. American Journal of Human Genetics, 2012, 91, 965-968.	6.2	1
33	Power of Singleâ€•vs. Multiâ€Marker Tests of Association. Genetic Epidemiology, 2012, 36, 480-487.	1.3	12
34	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
35	Genetic Terminology. Methods in Molecular Biology, 2012, 850, 1-9.	0.9	16
36	A Non-Parametric Method for Building Predictive Genetic Tests on High-Dimensional Data. Human Heredity, 2011, 71, 161-170.	0.8	12

#	Article	IF	Citations
37	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
38	2010 William Allan Award Introduction: JÃ¼rg Ott. American Journal of Human Genetics, 2011, 88, 262-263.	6.2	1
39	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. Human Genetics, 2011, 130, 725-733.	3.8	79
40	Interrogating population structure and its impact on association tests. BMC Proceedings, 2011, 5, S25.	1.6	5
41	Testing gene-environment interactions in gene-based association studies. BMC Proceedings, 2011, 5, S26.	1.6	3
42	Detecting genetic interactions for quantitative traits with U-statistics. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	22
43	A Note on Comparing the Power of Test Statistics at Low Significance Levels. American Statistician, 2011, 65, 164-166.	1.6	8
44	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
45	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. Biometrics, 2010, 66, 586-593.	1.4	12
46	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
47	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
48	The Meaning of Interaction. Human Heredity, 2010, 70, 269-277.	0.8	115
49	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. BMC Proceedings, 2009, 3, S49.	1.6	13
50	Phase uncertainty in caseâ€control association studies. Genetic Epidemiology, 2009, 33, 463-478.	1.3	2
51	Choosing an optimal method to combine Pâ€values. Statistics in Medicine, 2009, 28, 1537-1553.	1.6	137
52	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
53	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
54	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

#	Article	IF	Citations
55	Heritability of the Severity of Diabetic Retinopathy: The FIND-Eye Study. , 2008, 49, 3839.		163
56	Multistage Sampling for Genetic Studies. Annual Review of Genomics and Human Genetics, 2007, 8, 327-342.	6.2	26
57	Log-linear model-based multifactor dimensionality reduction method to detect geneâ€“gene interactions. Bioinformatics, 2007, 23, 2589-2595.	4.1	82
58	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
59	Adaptive Two-Stage Analysis of Genetic Association in Case-Control Designs. Human Heredity, 2007, 63, 175-186.	0.8	24
60	Improving Power in Contrasting Linkage-Disequilibrium Patterns between Cases and Controls. American Journal of Human Genetics, 2007, 80, 911-920.	6.2	38
61	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
62	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
63	Advances in statistical human genetics over the last 25 years. Statistics in Medicine, 2006, 25, 3049-3080.	1.6	24
64	Response to letter by Veronica J. Vieland and Susan E. Hodge. Genetic Epidemiology, 2005, 28, 286-287.	1.3	2
65	Twoâ€level Hasemanâ€Elston regression for general pedigree data analysis. Genetic Epidemiology, 2005, 29, 12-22.	1.3	46
66	Likelihood Modelling: Genetic Mapping of Complex Traits. , 2005, , 339-359.		0
67	Mathematical Assumptions versus Biological Reality: Myths in Affected Sib Pair Linkage Analysis. American Journal of Human Genetics, 2005, 76, 152-156.	6.2	34
68	A review of the 'Statistical Analysis for Genetic Epidemiology' (SAGE) software package. Human Genomics, 2004, 1, 456.	2.9	37
69	A Modified Revisited Haseman-Elston Method to Further Improve Power. Human Heredity, 2004, 57, 109-116.	0.8	25
70	Linkage Analysis of a Complex Disease through Use of Admixed Populations. American Journal of Human Genetics, 2004, 74, 1136-1153.	6.2	73
71	New multivariate test for linkage, with application to pleiotropy: Fuzzy Haseman-Elston. Genetic Epidemiology, 2003, 24, 253-264.	1.3	11
72	Regression Models for Linkage: Issues of Traits, Covariates, Heterogeneity, and Interaction. Human Heredity, 2003, 55, 86-96.	0.8	42

#	Article	IF	Citations
73	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
74	The Genetic Epidemiology of Age-Related Maculopathy. International Journal of Human Genetics, 2001, 1, 11-24.	0.1	2
75	Segregation Analysis of Gastric Cancer in a Japanese Population. International Journal of Human Genetics, 2001, 1, 263-270.	0.1	2
76	Introduction: Linkage Analyses of Single Regions. Genetic Epidemiology, 2001, 21, S79.	1.3	0
77	Segregation Analysis of Asthma and Respiratory Allergy in Populationâ€Based Samples of Families. Genetic Epidemiology, 2001, 21, S30-5.	1.3	2
78	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
79	Pooling Data and Linkage Analysis in the Chromosome 5q Candidate Region for Asthma. Genetic Epidemiology, 2001, 21, S103-8.	1.3	10
80	Localization of the Q1 Mutation by Cladistic Analysis. Genetic Epidemiology, 2001, 21, S594-9.	1.3	4
81	Linkage Disequilibrium Mapping of Complex Genetic Diseases Using Multiallelic Markers. Genetic Epidemiology, 2001, 21, S576-81.	1.3	2
82	Locating the Genes Underlying a Simulated Complex Disease by Discriminant Analysis. Genetic Epidemiology, 2001, 21, S516-S521.	1.3	10
83	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
84	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
85	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
86	Transmission/disequilibrium tests for quantitative traits. Genetic Epidemiology, 2001, 20, 57-74.	1.3	93
87	A PROBLEM IN ASCERTAINMENT. Communications in Statistics - Theory and Methods, 2001, 30, 1615-1631.	1.0	0
88	On the relative sample size required for multiple comparisons. , 2000, 19, 369-372.		41
89	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
90	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

#	Article	IF	Citations
91	Two-stage global search designs for linkage analysis I: Use of the mean statistic for affected sib pairs. , 2000, 18, 97-110.		20
92	Haseman and Elston revisited. Genetic Epidemiology, 2000, 19, 1-17.	1.3	324
93	Model-free sib-pair linkage analysis: Combining full-sib and half-sib pairs. Genetic Epidemiology, 2000, 19, 30-51.	1.3	6
94	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
95	Mulitpoint admixture mapping. Genetic Epidemiology, 2000, 19, 464-467.	1.3	12
96	A Century of Biometrical Genetics. Biometrics, 2000, 56, 659-666.	1.4	3
97	Adding power to Haseman and Elston's (1972) method. GeneScreen, 2000, 1, 63-64.	0.6	7
98	Genetic determinants of acute hypoxic ventilation: patterns of inheritance in mice. Journal of Applied Physiology, 2000, 88, 2310-2318.	2.5	55
99	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
100	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
101	Multipoint linkage disequilibrium mapping with particular reference to the African-American population. , 1999, 17, 79-101.		40
102	Fieller's theorem and linkage disequilibrium mapping. , 1999, 17, 237-252.		21
103	The study of candidate genes in drug trials: sample size considerations. , 1999, 18, 741-751.		31
104	Genetic mapping of complex traits. , 1999, 18, 2961-2981.		35
105	Model-based and model-free multipoint genome-wide linkage analysis of alcoholism. Genetic Epidemiology, 1999, 17, S175-S180.	1.3	1
106	Association and linkage analysis of ICDâ€10 diagnosis for alcoholism. Genetic Epidemiology, 1999, 17, S343-7.	1.3	3
107	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
108	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. Genetic Epidemiology, 1999, 17, S157-S161.	1.3	7

#	Article	IF	Citations
109	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
110	A multivariate logistic model (MLM) for analyzing binary family data. , 1998, 76, 428-437.		27
111	Using family history information to distinguish true and false positive model-free linkage results. , 1998, 15, 183-192.		5
112	Analysis of Swedish male breast cancer family data: A simple way to incorporate a common sibling effect. , 1998, 15, 201-212.		5
113	Linkage and association. Genetic Epidemiology, 1998, 15, 565-576.	1.3	81
114	Restrictions on Components of Variance for Epistatic Models. Theoretical Population Biology, 1998, 54, 161-174.	1.1	21
115	A Faster and More General Hidden Markov Model Algorithm for Multipoint Likelihood Calculations. Human Heredity, 1997, 47, 197-202.	0.8	55
116	Alternative test for linkage between two loci. Genetic Epidemiology, 1997, 14, 117-131.	1.3	9
117	Deriving components of genetic variance for multilocus models. Genetic Epidemiology, 1997, 14, 1131-1136.	1.3	22
118	Modeling age of onset and residual familial correlations for the linkage analysis of bipolar disorder. Genetic Epidemiology, 1997, 14, 675-680.	1.3	6
119	Model-free age-of-onset methods applied to the linkage of bipolar disorder. Genetic Epidemiology, 1997, 14, 711-716.	1.3	9
120	False discoveries in genome scanning. Genetic Epidemiology, 1997, 14, 779-784.	1.3	16
121	False discoveries in genome scanning. Genetic Epidemiology, 1997, 14, 779-784.	1.3	1
122	Association within twin pairs for a dichotomous trait. , 1996, 13, 489-499.		14
123	Genetic dissection of complex traits. Nature Genetics, 1996, 12, 355-356.	21.4	119
124	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
125	Statistical validity for testing associations between genetic markers and quantitative traits in family data. Genetic Epidemiology, 1995, 12, 145-161.	1.3	6
126	Model-free association analysis of a rare Disease. Genetic Epidemiology, 1995, 12, 571-575.	1.3	7

#	Article	IF	Citations
127	Effects of marker information on sib-pair linkage analysis of a rare disease. Genetic Epidemiology, 1995, 12, 625-630.	1.3	4
128	Testing specific hypotheses by fitting underlying distributions to categorical data. Journal of Biopharmaceutical Statistics, 1994, 4, 53-64.	0.8	2
129	Combining two-point genetic linkage analyses using mapping functions. Genetic Epidemiology, 1994, 11, 1-17.	1.3	3
130	Lods, wrods, and mods: The interpretation of lod scores calculated under different models. Genetic Epidemiology, 1994, 11, 329-342.	1.3	133
131	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
132	The HGAR1 familial hypercholesterolemia pedigree. Genetic Epidemiology, 1993, 10, 529-531.	1.3	5
133	Statistical validity of the Haseman-Elston sib-pair test in small samples. Genetic Epidemiology, 1993, 10, 593-598.	1.3	49
134	Confidence limits based on the first occurrence of an event. Statistics in Medicine, 1993, 12, 685-690.	1.6	17
135	The Eiston-Stewart Algorithm for Continuous Genotypes and Environmental Factors. Human Heredity, 1992, 42, 16-27.	0.8	58
136	Regression toward the mean in 2 Ã— 2 crossover designs with baseline measurements. Statistics in Medicine, 1992, 11, 727-741.	1.6	11
137	Effect of cohort differences in smoking prevalence on models of lung cancer susceptibility. Genetic Epidemiology, 1992, 9, 261-271.	1.3	35
138	Lung cancer histologic type and family history of cancer. Cancer, 1992, 69, 86-91.	4.1	45
139	Evidence for a dominant gene mechanism underlying coeliac disease in the West of Ireland. Genetic Epidemiology, 1991, 8, 13-27.	1.3	18
140	Extensions to sib-pair linkage tests applicable to disorders characterized by delayed onset. Genetic Epidemiology, 1990, 7, 453-466.	1.3	30
141	Generalized modulus power transformations. Communications in Statistics - Theory and Methods, 1988, 17, 2933-2952.	1.0	38
142	Pedigree discriminant analysis of two French Canadian Tay-Sachs families. Genetic Epidemiology, 1987, 4, 77-85.	1.3	1
143	Genetic etiology of gastric carcinoma: II. Segregation analysis of gastric pH, nitrate, and nitrite. Genetic Epidemiology, 1987, 4, 103-114.	1.3	7
144	Testing the association between polymorphic markers and quantitative traits in pedigrees. Genetic Epidemiology, 1987, 4, 193-201.	1.3	124

#	Article	IF	Citations
145	Association between polymorphic blood markers and risk factors for cardiovascular disease in a large pedigree. Genetic Epidemiology, 1987, 4, 267-275.	1.3	20
146	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
147	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
148	Segregation analysis of hereditary nonpolyposis colorectal cancer. Genetic Epidemiology, 1986, 3, 27-38.	1.3	55
149	Genetic etiology of gastric carcinoma: I. Chronic atrophic gastritis. Genetic Epidemiology, 1986, 3, 213-224.	1.3	52
150	Description of a large pedigree with an adverse lipoprotein cholesterol phenotype: The Bogalusa Heart Study. Genetic Epidemiology, 1986, 3, 241-253.	1.3	10
151	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
152	Likelihood Models for Multivariate Traits in Human Genetics1. Biometrical Journal, 1985, 27, 553-563.	1.0	2
153	A comparison of sibâ€pair linkage tests for disease susceptibility loci. Genetic Epidemiology, 1985, 2, 85-97.	1.3	365
154	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
155	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
156	Hereditary nonpolyposis colorectal cancer (lynch syndromes I and II). I. Clinical description of resource. Cancer, 1985, 56, 934-938.	4.1	298
157	Hereditary nonpolyposis colorectal cancer (lynch syndromes I and II). II. Biomarker studies. Cancer, 1985, 56, 939-951.	4.1	156
158	CELLULAR GENES IN THE MOUSE REGULATE IN TRANS THE EXPRESSION OF ENDOGENOUS MOUSE MAMMARY TUMOR VIRUSES. Genetics, 1985, 111, 597-615.	2.9	20
159	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
160	INHERITANCE OF ADRENAL PHENYLETHANOLAMINE N-METHYLTRANSFERASE ACTIVITY IN THE RAT. Genetics, 1984, 108, 633-649.	2.9	8
161	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
162	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

#	Article	IF	Citations
163	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