Ellen M Wijsman

List of Publications by Year
in descending order

150 papers	16,563 citations	41258 49 h-index	15683 125 g-index
156 all docs	156 docs citations	156 times ranked	17653 citing authors

#	Article	IF	Citations
1	Candidate gene for the chromosome 1 familial Alzheimer's disease locus. Science, 1995, 269, 973-977.	6.0	2,455
2	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
3	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	13.7	1,509
4	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	9.4	1,272
5	Genetic linkage evidence for a familial Alzheimer's disease locus on chromosome 14. Science, 1992, 258, 668-671.	6.0	904
6	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	2.6	819
7	A familial Alzheimer's disease locus on chromosome 1. Science, 1995, 269, 970-973.	6.0	768
8	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	1.4	538
9	Interactions of apolipoprotein E genotype, total cholesterol level, age, and sex in prediction of Alzheimer's disease. Neurology, 1995, 45, 1092-1096.	1.5	371
10	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	1.4	334
11	Genetic variation at the 22q11PRODH2/DGCR6locus presents an unusual pattern and increases susceptibility to schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3717-3722.	3.3	301
12	The Number of Trait Loci in Late-Onset Alzheimer Disease. American Journal of Human Genetics, 2000, 66, 196-204.	2.6	286
13	A putative RUNX1 binding site variant between SLC9A3R1 and NAT9 is associated with susceptibility to psoriasis. Nature Genetics, 2003, 35, 349-356.	9.4	284
14	Genome-Wide Association of Familial Late-Onset Alzheimer's Disease Replicates BIN1 and CLU and Nominates CUGBP2 in Interaction with APOE. PLoS Genetics, 2011, 7, e1001308.	1.5	223
15	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. Human Genetics, 2012, 131, 565-579.	1.8	180
16	Genetic analysis of simulated oligogenic traits in nuclear and extended pedigrees: Summary of GAW10 contributions. , 1997, 14, 719-735.		151
17	Comprehensive analysis of APOE and selected proximate markers for late-onset Alzheimer's disease: Patterns of linkage disequilibrium and disease/marker association. Genomics, 2007, 89, 655-665.	1.3	149
18	Modeling Phonological Core Deficits Within a Working Memory Architecture in Children and Adults With Developmental Dyslexia. Scientific Studies of Reading, 2006, 10, 165-198.	1.3	129

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19	Evidence for multiple loci from a genome scan of autism kindreds. Molecular Psychiatry, 2006, 11, 1049-1060.	4.1	115
20	Genetic Investigation of Quantitative Traits Related to Autism: Use of Multivariate Polygenic Models with Ascertainment Adjustment. American Journal of Human Genetics, 2005, 76, 68-81.	2.6	101
21	Replication of CNTNAP2 association with nonword repetition and support for FOXP2 association with timed reading and motor activities in a dyslexia family sample. Journal of Neurodevelopmental Disorders, 2011, 3, 39-49.	1.5	100
22	MCMC segregation and linkage analysis. Genetic Epidemiology, 1997, 14, 1011-1016.	0.6	99
23	Multipoint Oligogenic Analysis of Age-at-Onset Data with Applications to Alzheimer Disease Pedigrees. American Journal of Human Genetics, 1999, 64, 839-851.	2.6	92
24	Evidence for a Novel Late-Onset Alzheimer Disease Locus on Chromosome 19p13.2. American Journal of Human Genetics, 2004, 75, 398-409.	2.6	90
25	Genome Screens Using Linkage Disequilibrium Tests: Optimal Marker Characteristics and Feasibility. American Journal of Human Genetics, 1998, 63, 1872-1885.	2.6	88
26	The role of large pedigrees in an era of high-throughput sequencing. Human Genetics, 2012, 131, 1555-1563.	1.8	86
27	Apolipoprotein E genotypes in Parkinson's disease with and without dementia. Annals of Neurology, 1995, 37, 242-245.	2.8	82
28	Genetic association and linkage analysis of the apolipoprotein CII locus and familial Alzheimer's disease. Annals of Neurology, 1992, 31, 223-227.	2.8	79
29	Caseâ€control association testing in the presence of unknown relationships. Genetic Epidemiology, 2009, 33, 668-678.	0.6	79
30	Linkage between quantitative trait and marker loci: Methods using all relative pairs. Genetic Epidemiology, 1993, 10, 87-102.	0.6	76
31	Linkage analyses of four regions previously implicated in dyslexia: Confirmation of a locus on chromosome 15q. American Journal of Medical Genetics Part A, 2004, 131B, 67-75.	2.4	76
32	Evaluation of candidate genes forDYX1 andDYX2 in families with dyslexia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 556-560.	1.1	76
33	Local ancestry at APOE modifies Alzheimer's disease risk in Caribbean Hispanics. Alzheimer's and Dementia, 2019, 15, 1524-1532.	0.4	75
34	Bias in multipoint linkage analysis arising from map misspecification. Genetic Epidemiology, 2000, 19, 366-380.	0.6	73
35	Segregation Analysis of Phenotypic Components of Learning Disabilities. I. Nonword Memory and Digit Span. American Journal of Human Genetics, 2000, 67, 631-646.	2.6	73
36	Low Clusterin Levels in High-Density Lipoprotein Associate With Insulin Resistance, Obesity, and Dyslipoproteinemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2528-2534.	1.1	72

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37	Apolipoprotein E genotypes and age of onset in early-onset familial Alzheimer's disease. Annals of Neurology, 1995, 38, 678-680.	2.8	68
38	Multipoint Linkage Analysis with Many Multiallelic or Dense Diallelic Markers: Markov Chainâ€“Monte Carlo Provides Practical Approaches for Genome Scans on General Pedigrees. American Journal of Human Genetics, 2006, 79, 846-858.	2.6	67
39	APOE and other loci affect age-at-onset in Alzheimer's disease families with PS2 mutation. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 132B, 14-20.	1.1	65
40	Î²APP mRNA transcription is increased in cultured fibroblasts from the familial Alzheimer's disease-1 family. Molecular Brain Research, 1995, 28, 319-337.	2.5	64
41	Evaluation of locus heterogeneity and EXT1 mutations in 34 families with hereditary multiple exostoses. Human Mutation, 1998, 11, 231-239.	1.1	63
42	Presence of Large Deletions in Kindreds with Autism. American Journal of Human Genetics, 2002, 71, 100-115.	2.6	63
43	Relationship Inference from Trios of Individuals, in the Presence of Typing Error. American Journal of Human Genetics, 2002, 70, 170-180.	2.6	62
44	A genome scan in multigenerational families with dyslexia: Identification of a novel locus on chromosome 2q that contributes to phonological decoding efficiency. Molecular Psychiatry, 2005, 10, 699-711.	4.1	61
45	Familial aggregation of dyslexia phenotypes. Behavior Genetics, 2000, 30, 385-396.	1.4	59
46	Two sites in the MAPT region confer genetic risk for Guam ALS/PDC and dementia. Human Molecular Genetics, 2007, 16, 295-306.	1.4	59
47	A deductive method of haplotype analysis in pedigrees. American Journal of Human Genetics, 1987, 41, 356-73.	2.6	59
48	Influence of apolipoprotein E genotype on the transmission of Alzheimer disease in a community-based sample. American Journal of Human Genetics, 1996, 58, 191-200.	2.6	59
49	GIGI: An Approach to Effective Imputation of Dense Genotypes on Large Pedigrees. American Journal of Human Genetics, 2013, 92, 504-516.	2.6	57
50	Genome-wide scan in a large complex pedigree with predominantly male schizophrenics from the island of Kosrae: evidence for linkage to chromosome 2q. Molecular Psychiatry, 2003, 8, 695-705.	4.1	54
51	Whole exome sequencing in extended families with autism spectrum disorder implicates four candidate genes. Human Genetics, 2015, 134, 1055-1068.	1.8	49
52	Genome-scan for IQ discrepancy in autism: evidence for loci on chromosomes 10 and 16. Human Genetics, 2011, 129, 59-70.	1.8	44
53	Genomewide scan for real-word reading subphenotypes of dyslexia: Novel chromosome 13 locus and genetic complexity. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 15-27.	1.1	43
54	Linkage of Low-Density Lipoprotein Size to the Lipoprotein Lipase Gene in Heterozygous Lipoprotein Lipase Deficiency. American Journal of Human Genetics, 1999, 64, 608-618.	2.6	42

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55	Techniques for estimating genetic admixture and applications to the problem of the origin of the Icelanders and the Ashkenazi Jews. Human Genetics, 1984, 67, 441-448.	1.8	41
56	Evidence Against Linkage of Familial Combined Hyperlipidemia to the Apolipoprotein AI-CIII-AIV Gene Complex. Arteriosclerosis, Thrombosis, and Vascular Biology, 1998, 18, 215-226.	1.1	41
57	Extended Intermarker Linkage Disequilibrium in the Afrikaners. Genome Research, 2002, 12, 956-961.	2.4	38
58	Low-Density Lipoprotein Particle Size Loci in Familial Combined Hyperlipidemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 1942-1950.	1.1	37
59	Identification of novel susceptibility loci for Guam neurodegenerative disease: challenges of genome scans in genetic isolates. Human Molecular Genetics, 2009, 18, 3725-3738.	1.4	37
60	Joint Linkage and Association Analysis with Exome Sequence Data Implicates SLC25A40 in Hypertriglyceridemia. American Journal of Human Genetics, 2013, 93, 1035-1045.	2.6	36
61	Toward localization of the Werner syndrome gene by linkage disequilibrium and ancestral haplotyping: lessons learned from analysis of 35 chromosome 8p11.1-21.1 markers. American Journal of Human Genetics, 1996, 58, 1286-302.	2.6	35
62	Oligogenic segregation analysis of hereditary prostate cancer pedigrees: Evidence for multiple loci affecting age at onset. International Journal of Cancer, 2003, 105, 630-635.	2.3	34
63	Genetic Candidate Variants in Two Multigenerational Families with Childhood Apraxia of Speech. PLoS ONE, 2016, 11, e0153864.	1.1	33
64	Segregation analysis of phenotypic components of learning disabilities. II. Phonological decoding. American Journal of Medical Genetics Part A, 2003, 121B, 60-70.	2.4	32
65	Characteristics of genetic markers and maps for cost-effective genome screens using diallelic markers. Genetic Epidemiology, 2002, 22, 205-220.	0.6	30
66	Association of rare missense variants in the second intracellular loop of NaV1.7 sodium channels with familial autism. Molecular Psychiatry, 2018, 23, 231-239.	4.1	30
67	Genome Scan of a Nonword Repetition Phenotype in Families with Dyslexia: Evidence for Multiple Loci. Behavior Genetics, 2008, 38, 462-475.	1.4	29
68	Familial aggregation of dyslexia phenotypes. II: Paired correlated measures. American Journal of Medical Genetics Part A, 2002, 114, 471-478.	2.4	28
69	Comparison of single-nucleotide polymorphisms and microsatellite markers for linkage analysis in the COGA and simulated data sets for Genetic Analysis Workshop 14: Presentation Groups 1, 2, and 3. Genetic Epidemiology, 2005, 29, S7-S28.	0.6	28
70	Evidence for involvement of GNB1L in autism. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 61-71.	1.1	28
71	Combining Familyâ€•and Populationâ€Based Imputation Data for Association Analysis of Rare and Common Variants in Large Pedigrees. Genetic Epidemiology, 2014, 38, 579-590.	0.6	28
72	Power of Familyâ€Based Association Designs to Detect Rare Variants in Large Pedigrees Using Imputed Genotypes. Genetic Epidemiology, 2014, 38, 1-9.	0.6	27

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73	Optimizing selection of restriction enzyme in the search for ONA variants. Nucleic Acids Research, 1984, 12, 9209-9226.	6.5	26
74	Evidence of linkage of HDL level variation to APOC3 in two samples with different ascertainment. Human Genetics, 2003, 113, 522-533.	1.8	26
75	Joint Oligogenic Segregation and Linkage Analysis Using Bayesian Markov Chain Monte Carlo Methods. Molecular Biotechnology, 2004, 28, 205-226.	1.3	26
76	Genetic and nongenetic sources of variation in phospholipid transfer protein activity. Journal of Lipid Research, 2010, 51, 983-990.	2.0	26
77	Identification of Genetic Loci Underlying the Phenotypic Constructs of Autism Spectrum Disorders. Journal of the American Academy of Child and Adolescent Psychiatry, 2011, 50, 687-696.e13.	0.3	26
78	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	1.3	26
79	MCMC-based linkage analysis for complex traits on general pedigrees: multipoint analysis with a two-locus model and a polygenic component. Genetic Epidemiology, 2007, 31, 103-114.	0.6	24
80	A common VLDLR polymorphism interacts with APOE genotype in the prediction of carotid artery disease risk. Journal of Lipid Research, 2008, 49, 588-596.	2.0	24
81	Recurrence risk of a new dominant mutation in children of unaffected parents. American Journal of Human Genetics, 1991, 48, 654-61.	2.6	24
82	Linkage and association of phospholipid transfer protein activity to LASS4. Journal of Lipid Research, 2011, 52, 1837-1846.	2.0	23
83	Monte Carlo analysis on a large pedigree. Genetic Epidemiology, 1993, 10, 677-682.	0.6	22
84	Semiparametric estimation of major gene effects for age of onset. Genetic Epidemiology, 1998, 15, 279-298.	0.6	22
85	Evidence for three loci modifying ageâ€¤atâ€¤onset of Alzheimer's disease in earlyâ€¤onset PSEN2 families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1031-1041.	1.1	22
86	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	0.7	22
87	Genome scan for quantitative trait loci influencing HDL levels: evidence for multilocus inheritance in familial combined hyperlipidemia. Human Genetics, 2005, 117, 494-505.	1.8	21
88	A Statistical Framework to Guide Sequencing Choices in Pedigrees. American Journal of Human Genetics, 2014, 94, 257-267.	2.6	21
89	The use of nonmetric variation in estimating human population admixture: A test case with Brazilian blacks, whites, and mulattos. American Journal of Physical Anthropology, 1986, 70, 395-405.	2.1	19
90	The c-fos gene and early-onset familial Alzheimer's disease. Neuroscience Letters, 1993, 160, 33-36.	1.0	19

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91	Empirical significance values for linkage analysis: trait simulation using posterior model distributions from MCMC oligogenic segregation analysis. Genetic Epidemiology, 2008, 32, 119-131.	0.6	18
92	MCMC Multilocus Lod Scores: Application of a New Approach. Human Heredity, 2005, 59, 98-108.	0.4	17
93	Genome Scan for Spelling Deficits: Effects of Verbal IQ on Models of Transmission and Trait Gene Localization. Behavior Genetics, 2011, 41, 31-42.	1.4	17
94	Detection of Mendelian Consistent Genotyping Errors in Pedigrees. Genetic Epidemiology, 2014, 38, 291-299.	0.6	17
95	Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. BMC Proceedings, 2014, 8, S5.	1.8	16
96	Early event-related potentials to emotional faces differ for adults with autism spectrum disorder and by serotonin transporter genotype. Clinical Neurophysiology, 2016, 127, 2436-2447.	0.7	16
97	Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. Genome Research, 2019, 29, 125-134.	2.4	16
98	The N141I Mutation in PSEN2. Archives of Neurology, 2010, 67, 631-3.	4.9	15
99	A score for Bayesian genome screening. Genetic Epidemiology, 2003, 24, 181-190.	0.6	14
100	Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. BMC Genetics, 2005, 6, S11.	2.7	14
101	Comparison of multipoint linkage analyses for quantitative traits in the CEPH data: parametric LOD scores, variance components LOD scores, and Bayes factors. BMC Proceedings, 2007, 1, S93.	1.8	14
102	Cholesterol Accumulation Regulates Expression of Macrophage Proteins Implicated in Proteolysis and Complement Activation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 2910-2918.	1.1	14
103	Pedigree analysis package (PAP) vs. MORGAN: Model selection and hypothesis testing on a large pedigree. , 1998, 15, 355-369.		13
104	Linkage and association analyses identify a candidate region for apoB level on chromosome 4q32.3 in FCHL families. Human Genetics, 2010, 127, 705-719.	1.8	13
105	Familyâ€based genome scan for age at onset of lateâ€onset Alzheimer's disease in whole exome sequencing data. Genes, Brain and Behavior, 2015, 14, 607-617.	1.1	13
106	Family-based approaches: design, imputation, analysis, and beyond. BMC Genetics, 2016, 17, 9.	2.7	13
107	Joint Linkage and Segregation Analysis Using Markov Chain Monte Carlo Methods. , 2002, 195, 139-161.		12
108	Genome scan for cognitive trait loci of dyslexia: Rapid naming and rapid switching of letters, numbers, and colors. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 345-356.	1.1	12

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109	Alzheimer's disease and the family effect. Nature Genetics, 1994, 8, 115-115.	9.4	11
110	The Importance of Connections: Joining Components of the Hutterite Pedigree. Genetic Epidemiology, 2001, 21, S230-5.	0.6	11
111	Segregation Analysis of a Complex Quantitative Trait: Approaches for Identifying Influential Data Points. Human Heredity, 2006, 61, 80-86.	0.4	11
112	Identification of Rare Variants from Exome Sequence in a Large Pedigree with Autism. Human Heredity, 2012, 74, 153-164.	0.4	10
113	Pedigree analysis package vs. MIXD: Fitting the mixed model on a large pedigree. , 1996, 13, 91-106.		9
114	Accounting for Epistasis in Linkage Analysis of General Pedigrees. Human Heredity, 2007, 63, 144-152.	0.4	9
115	Joint linkage and segregation analysis under multiallelic trait inheritance: simplifying interpretations for complex traits. Genetic Epidemiology, 2010, 34, 344-353.	0.6	9
116	Estimation and Visualization of Identity-by-Descent within Pedigrees Simplifies Interpretation of Complex Trait Analysis. Human Heredity, 2011, 72, 289-297.	0.4	9
117	Multipoint genome-wide linkage scan for nonword repetition in a multigenerational family further supports chromosome 13q as a locus for verbal trait disorders. Human Genetics, 2016, 135, 1329-1341.	1.8	9
118	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. BMC Proceedings, 2007, 1, S1.	1.8	8
119	Genome scan of ageâ€atâ€onset in the NIMH Alzheimer disease sample uncovers multiple loci, along with evidence of both genetic and sample heterogeneity. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 785-798.	1.1	8
120	Variants regulating ZBTB4 are associated with ageâ€atâ€onset of Alzheimer's disease. Genes, Brain and Behavior, 2018, 17, e12429.	1.1	8
121	Characteristics of familial Alzheimer's disease in nine kindreds of Volga German ancestry. Progress in Clinical and Biological Research, 1989, 317, 229-34.	0.2	8
122	Genetic analysis of Alzheimer's disease: A summary of contributions to GAW8. Genetic Epidemiology, 1993, 10, 349-360.	0.6	7
123	Summary of Group 8: Development and extension of linkage methods. Genetic Epidemiology, 2003, 25, S64-S71.	0.6	7
124	Approaches to mapping genetically correlated complex traits. BMC Genetics, 2003, 4, S71.	2.7	7
125	Accounting for Linkage Disequilibrium among Markers in Linkage Analysis: Impact of Haplotype Frequency Estimation and Molecular Haplotypes for a Gene in a Candidate Region for Alzheimerâ€™s Disease. Human Heredity, 2007, 63, 26-34.	0.4	7
126	Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. BMC Proceedings, 2014, 8, S19.	1.8	7

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127	Genetic Analysis Workshop 19: methods and strategies for analyzing human sequence and gene expression data in extended families and unrelated individuals. BMC Proceedings, 2016, 10, 67-70.	1.8	7
128	Genome-wide scan in a large complex pedigree with predominantly male schizophrenics from the island of Kosrae: evidence for linkage to chromosome 2q. Molecular Psychiatry, 2003, 8, 643-643.	4.1	6
129	Familial Aggregation Patterns in Mathematical Ability. Behavior Genetics, 2004, 34, 51-62.	1.4	6
130	PBAP: a pipeline for file processing and quality control of pedigree data with dense genetic markers. Bioinformatics, 2015, 31, 3790-3798.	1.8	6
131	On Estimating the Proportion of Variance in a Phenotypic Trait Attributable to a Measured Locus. Human Heredity, 2001, 51, 145-149.	0.4	5
132	Evidence for genetic linkage of autism to chromosomes 7 and 4. Molecular Psychiatry, 2006, 11, 979-979.	4.1	5
133	Contrasting identity-by-descent estimators, association studies, and linkage analyses using the Framingham Heart Study data. BMC Proceedings, 2009, 3, S102.	1.8	5
134	Genome scan in familial lateâ€onset Alzheimer's disease: A locus on chromosome 6 contributes to ageâ€atâ€onset. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 201-212.	1.1	5
135	Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. Genetic Epidemiology, 1997, 14, 999-1004.	0.6	4
136	Identification and functional characterization of natural human melanocortin 1 receptor mutant alleles in Pakistani population. Pigment Cell and Melanoma Research, 2015, 28, 730-735.	1.5	4
137	Identity-by-descent estimation with population- and pedigree-based imputation in admixed family data. BMC Proceedings, 2016, 10, 295-301.	1.8	4
138	Estimating relationships between phenotypes and subjects drawn from admixed families. BMC Proceedings, 2016, 10, 357-362.	1.8	4
139	Replication of a rare risk haplotype on 1p36.33 for autism spectrum disorder. Human Genetics, 2018, 137, 807-815.	1.8	4
140	Gene mapping and the transition from STRPs to SNPs. , 2005, , .		3
141	Value of Mendelian Laws of Segregation in Families: Data Quality Control, Imputation, and Beyond. Genetic Epidemiology, 2014, 38, S21-8.	0.6	3
142	Analysis of pedigree data in populations with multiple ancestries: Strategies for dealing with admixture in Caribbean Hispanic families from the ADSP. Genetic Epidemiology, 2018, 42, 500-515.	0.6	3
143	Monte Carlo Markov chain methods and model selection in genetic epidemiology. Computational Statistics and Data Analysis, 2000, 32, 349-360.	0.7	2
144	Inheritance Model Introduces Differential Bias in <scp>CNV</scp> Calls Between Parents and Offspring. Genetic Epidemiology, 2012, 36, 488-498.	0.6	2

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145	Association score testing for rare variants and binary traits in family data with shared controls. Briefings in Bioinformatics, 2019, 20, 245-253.	3.2	2
146	GIGI-Quick: a fast approach to impute missing genotypes in genome-wide association family data. Bioinformatics, 2018, 34, 1591-1593.	1.8	1
147	The Seattle Alzheimer's disease data set. Genetic Epidemiology, 1993, 10, 365-369.	0.6	0
148	Monte Carlo Markov chain methods and model selection in Genetic analysis. Animal Biotechnology, 1997, 8, 129-144.	0.7	0
149	Visualization of Haplotype Sharing Patterns in Pedigree Samples. Human Heredity, 2014, 78, 1-8.	0.4	0
150	Analysis of individual families implicates noncoding DNA variation and multiple biological pathways in Alzheimerâ€™s disease risk. Alzheimer's and Dementia, 2020, 16, e046456.	0.4	0