Ellen M Wijsman

List of Publications by Year in Descending Order

150 papers	14,222 citations	49 h-index	118 g-index
156 ext. papers	15,556 ext. citations	7.2 avg, IF	5.39 L-index

#	Paper	IF	Citations
150	Analysis of individual families implicates noncoding DNA variation and multiple biological pathways in Alzheimer's disease risk. *Alzheimer's and Dementia*, **2020**, 16, e046456	1.2	
149	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	4.3	10
148	Local ancestry at APOE modifies Alzheimer's disease risk in Caribbean Hispanics. *Alzheimer's and Dementia*, **2019**, 15, 1524-1532	1.2	33
147	Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. *Genome Research*, **2019**, 29, 125-134	9.7	9
146	Association score testing for rare variants and binary traits in family data with shared controls. *Briefings in Bioinformatics*, **2019**, 20, 245-253	13.4	0
145	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimer's Disease Sequencing Project. *Dementia and Geriatric Cognitive Disorders*, **2018**, 45, 1-17	2.6	16
144	GIGI-Quick: a fast approach to impute missing genotypes in genome-wide association family data. *Bioinformatics*, **2018**, 34, 1591-1593	7.2	1
143	Association of rare missense variants in the second intracellular loop of Na1.7 sodium channels with familial autism. *Molecular Psychiatry*, **2018**, 23, 231-239	15.1	21
142	Variants regulating ZBTB4 are associated with age-at-onset of Alzheimer's disease. *Genes, Brain and Behavior*, **2018**, 17, e12429	3.6	7
141	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	2.6	1
140	Replication of a rare risk haplotype on 1p36.33 for autism spectrum disorder. *Human Genetics*, **2018** , 137, 807-815	6.3	1
139	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	2.3	5
138	Identity-by-descent estimation with population- and pedigree-based imputation in admixed family data. *BMC Proceedings*, **2016**, 10, 295-301	2.3	3
137	Estimating relationships between phenotypes and subjects drawn from admixed families. *BMC Proceedings*, **2016**, 10, 357-362	2.3	2
136	Family-based approaches: design, imputation, analysis, and beyond. *BMC Genetics*, **2016**, 17 Suppl 2, 9	2.6	9
135	Genetic Candidate Variants in Two Multigenerational Families with Childhood Apraxia of Speech. *PLoS ONE*, **2016**, 11, e0153864	3.7	25
134	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	6.3	7

133	Early event-related potentials to emotional faces differ for adults with autism spectrum disorder and by serotonin transporter genotype. *Clinical Neurophysiology*, **2016**, 127, 2436-47	4.3	12
132	PBAP: a pipeline for file processing and quality control of pedigree data with dense genetic markers. *Bioinformatics*, **2015**, 31, 3790-8	7.2	5
131	Whole exome sequencing in extended families with autism spectrum disorder implicates four candidate genes. *Human Genetics*, **2015**, 134, 1055-68	6.3	39
130	Family-based genome scan for age at onset of late-onset Alzheimer's disease in whole exome sequencing data. *Genes, Brain and Behavior*, **2015**, 14, 607-17	3.6	9
129	Identification and functional characterization of natural human melanocortin 1 receptor mutant alleles in Pakistani population. *Pigment Cell and Melanoma Research*, **2015**, 28, 730-5	4.5	4
128	Convergence of genes and cellular pathways dysregulated in autism spectrum disorders. *American Journal of Human Genetics*, **2014**, 94, 677-94	11	635
127	A statistical framework to guide sequencing choices in pedigrees. *American Journal of Human Genetics*, **2014**, 94, 257-67	11	20
126	Detection of Mendelian consistent genotyping errors in pedigrees. *Genetic Epidemiology*, **2014**, 38, 291-9	2.6	12
125	Visualization of haplotype sharing patterns in pedigree samples. *Human Heredity*, **2014**, 78, 1-8	1.1	
124	Combining family- and population-based imputation data for association analysis of rare and common variants in large pedigrees. *Genetic Epidemiology*, **2014**, 38, 579-90	2.6	20
123	Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. *BMC Proceedings*, **2014**, 8, S5	2.3	14
122	Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. *BMC Proceedings*, **2014**, 8, S19	2.3	6
121	Value of Mendelian laws of segregation in families: data quality control, imputation, and beyond. *Genetic Epidemiology*, **2014**, 38 Suppl 1, S21-8	2.6	2
120	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**, 165B, 345-56	3.5	11
119	Power of family-based association designs to detect rare variants in large pedigrees using imputed genotypes. *Genetic Epidemiology*, **2014**, 38, 1-9	2.6	23
118	Joint linkage and association analysis with exome sequence data implicates SLC25A40 in hypertriglyceridemia. *American Journal of Human Genetics*, **2013**, 93, 1035-45	11	35
117	GIGI: an approach to effective imputation of dense genotypes on large pedigrees. *American Journal of Human Genetics*, **2013**, 92, 504-16	11	51
116	Genome scan in familial late-onset Alzheimer's disease: a locus on chromosome 6 contributes to age-at-onset. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2013**, 162B, 201-12	3.5	4

115	Evidence for involvement of GNB1L in autism. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 61-71	3.5	20
114	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. *Human Genetics*, **2012**, 131, 565-79	6.3	150
113	The role of large pedigrees in an era of high-throughput sequencing. *Human Genetics*, **2012**, 131, 1555-63	6.3	72
112	Identification of rare variants from exome sequence in a large pedigree with autism. *Human Heredity*, **2012**, 74, 153-64	1.1	7
111	Inheritance model introduces differential bias in CNV calls between parents and offspring. *Genetic Epidemiology*, **2012**, 36, 488-98	2.6	2
110	Cholesterol accumulation regulates expression of macrophage proteins implicated in proteolysis and complement activation. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2012**, 32, 2910-8	9.4	12
109	Individual common variants exert weak effects on the risk for autism spectrum disorders. *Human Molecular Genetics*, **2012**, 21, 4781-92	5.6	279
108	Genome-scan for IQ discrepancy in autism: evidence for loci on chromosomes 10 and 16. *Human Genetics*, **2011**, 129, 59-70	6.3	39
107	Genome scan for spelling deficits: effects of verbal IQ on models of transmission and trait gene localization. *Behavior Genetics*, **2011**, 41, 31-42	3.2	13
106	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	4.6	81
105	Genome scan of age-at-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**, 156B, 785-98	3.5	6
104	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	7.2	24
103	Estimation and visualization of identity-by-descent within pedigrees simplifies interpretation of complex trait analysis. *Human Heredity*, **2011**, 72, 289-97	1.1	8
102	Linkage and association of phospholipid transfer protein activity to LASS4. *Journal of Lipid Research* , **2011**, 52, 1837-46	6.3	17
101	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	6	179
100	Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, **2010**, 466, 368-72	50.4	1499
99	A genome-wide scan for common alleles affecting risk for autism. *Human Molecular Genetics*, **2010**, 19, 4072-82	5.6	443
98	Low clusterin levels in high-density lipoprotein associate with insulin resistance, obesity, and dyslipoproteinemia. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 2528-34	9.4	62

97	Genetic and nongenetic sources of variation in phospholipid transfer protein activity. *Journal of Lipid Research*, **2010**, 51, 983-90	6.3	25
96	The N141I mutation in PSEN2: implications for the quintessential case of Alzheimer disease. *Archives of Neurology*, **2010**, 67, 631-3		13
95	Linkage and association analyses identify a candidate region for apoB level on chromosome 4q32.3 in FCHL families. *Human Genetics*, **2010**, 127, 705-19	6.3	11
94	Joint linkage and segregation analysis under multiallelic trait inheritance: simplifying interpretations for complex traits. *Genetic Epidemiology*, **2010**, 34, 344-53	2.6	8
93	Evidence for three loci modifying age-at-onset of Alzheimer's disease in early-onset PSEN2 families. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1031-41	3.5	17
92	Contrasting identity-by-descent estimators, association studies, and linkage analyses using the Framingham Heart Study data. *BMC Proceedings*, **2009**, 3 Suppl 7, S102	2.3	4
91	Identification of novel susceptibility loci for Guam neurodegenerative disease: challenges of genome scans in genetic isolates. *Human Molecular Genetics*, **2009**, 18, 3725-38	5.6	31
90	Case-control association testing in the presence of unknown relationships. *Genetic Epidemiology*, **2009**, 33, 668-78	2.6	63
89	A common VLDLR polymorphism interacts with APOE genotype in the prediction of carotid artery disease risk. *Journal of Lipid Research*, **2008**, 49, 588-96	6.3	24
88	Genome scan of a nonword repetition phenotype in families with dyslexia: evidence for multiple loci. *Behavior Genetics*, **2008**, 38, 462-75	3.2	23
87	Empirical significance values for linkage analysis: trait simulation using posterior model distributions from MCMC oligogenic segregation analysis. *Genetic Epidemiology*, **2008**, 32, 119-31	2.6	17
86	Two sites in the MAPT region confer genetic risk for Guam ALS/PDC and dementia. *Human Molecular Genetics*, **2007**, 16, 295-306	5.6	50
85	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 Suppl 1, S93	2.3	13
84	Evaluation of candidate genes for DYX1 and DYX2 in families with dyslexia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2007**, 144B, 556-60	3.5	67
83	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, 103-14	2.6	23
82	Replicating genotype-phenotype associations. *Nature*, **2007**, 447, 655-60	50.4	1363
81	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. *Nature Genetics*, **2007**, 39, 319-28	36.3	1083
80	Accounting for epistasis in linkage analysis of general pedigrees. *Human Heredity*, **2007**, 63, 144-52	1.1	9

79	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 Alzheimer's disease. *Human Heredity*, **2007**, 63, 26-34	1.1	7
78	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. *BMC Proceedings*, **2007**, 1 Suppl 1, S1	2.3	6
77	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, 655-65	4.3	118
76	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	3.5	35
75	Segregation analysis of a complex quantitative trait: approaches for identifying influential data points. *Human Heredity*, **2006**, 61, 80-6	1.1	11
74	Modeling Phonological Core Deficits Within a Working Memory Architecture in Children and Adults With Developmental Dyslexia. *Scientific Studies of Reading*, **2006**, 10, 165-198	3.8	114
73	Multipoint linkage analysis with many multiallelic or dense diallelic markers: Markov chain-Monte Carlo provides practical approaches for genome scans on general pedigrees. *American Journal of Human Genetics*, **2006**, 79, 846-58	11	62
72	Evidence for multiple loci from a genome scan of autism kindreds. *Molecular Psychiatry*, **2006**, 11, 1049-60, 979	15.1	97
71	Evidence for genetic linkage of autism to chromosomes 7 and 4. *Molecular Psychiatry*, **2006**, 11, 979-979	15.1	3
70	MCMC multilocus lod scores: application of a new approach. *Human Heredity*, **2005**, 59, 98-108	1.1	15
69	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	11	86
68	Gene mapping and the transition from STRPs to SNPs **2005**,		1
67	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	15.1	54
66	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 Suppl 1, S7-28	2.6	24
65	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	3.5	61
64	Genome scan for quantitative trait loci influencing HDL levels: evidence for multilocus inheritance in familial combined hyperlipidemia. *Human Genetics*, **2005**, 117, 494-505	6.3	21
63	Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. *BMC Genetics*, **2005**, 6 Suppl 1, S11	2.6	14
62	Low-density lipoprotein particle size loci in familial combined hyperlipidemia: evidence for multiple loci from a genome scan. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2004**, 24, 1942-50	9.4	35

61	Familial aggregation patterns in mathematical ability. *Behavior Genetics*, **2004**, 34, 51-62	3.2	5
60	Joint oligogenic segregation and linkage analysis using bayesian Markov chain Monte Carlo methods. *Molecular Biotechnology*, **2004**, 28, 205-26	3	26
59	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		61
58	Evidence for a novel late-onset Alzheimer disease locus on chromosome 19p13.2. *American Journal of Human Genetics*, **2004**, 75, 398-409	11	82
57	Evidence of linkage of HDL level variation to APOC3 in two samples with different ascertainment. *Human Genetics*, **2003**, 113, 522-33	6.3	25
56	A score for Bayesian genome screening. *Genetic Epidemiology*, **2003**, 24, 181-90	2.6	14
55	Summary of Group 8: Development and extension of linkage methods. *Genetic Epidemiology*, **2003**, 25 Suppl 1, S64-71	2.6	7
54	Oligogenic segregation analysis of hereditary prostate cancer pedigrees: evidence for multiple loci affecting age at onset. *International Journal of Cancer*, **2003**, 105, 630-5	7.5	30
53	Segregation analysis of phenotypic components of learning disabilities. II. Phonological decoding. *American Journal of Medical Genetics Part A*, **2003**, 121B, 60-70		26
52	Approaches to mapping genetically correlated complex traits. *BMC Genetics*, **2003**, 4 Suppl 1, S71	2.6	7
51	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, 643	15.1	50
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, 643-643	15.1	2
49	A putative RUNX1 binding site variant between SLC9A3R1 and NAT9 is associated with susceptibility to psoriasis. *Nature Genetics*, **2003**, 35, 349-56	36.3	248
48	Familial aggregation of dyslexia phenotypes. II: paired correlated measures. *American Journal of Medical Genetics Part A*, **2002**, 114, 471-8		25
47	Characteristics of genetic markers and maps for cost-effective genome screens using diallelic markers. *Genetic Epidemiology*, **2002**, 22, 205-20	2.6	28
46	Genetic variation at the 22q11 PRODH2/DGCR6 locus presents an unusual pattern and increases susceptibility to schizophrenia. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 3717-22	11.5	278
45	Extended intermarker linkage disequilibrium in the Afrikaners. *Genome Research*, **2002**, 12, 956-61	9.7	32
44	Joint linkage and segregation analysis using Markov chain Monte Carlo methods. *Methods in Molecular Biology*, **2002**, 195, 139-61	1.4	11

43	Relationship inference from trios of individuals, in the presence of typing error. *American Journal of Human Genetics*, **2002**, 70, 170-80	11	58
42	Presence of large deletions in kindreds with autism. *American Journal of Human Genetics*, **2002**, 71, 100-15	11	56
41	The importance of connections: joining components of the Hutterite pedigree. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S230-5	2.6	10
40	On estimating the proportion of variance in a phenotypic trait attributable to a measured locus. *Human Heredity*, **2001**, 51, 145-9	1.1	5
39	Bias in multipoint linkage analysis arising from map misspecification. *Genetic Epidemiology*, **2000**, 19, 366-80	2.6	66
38	Monte Carlo Markov chain methods and model selection in genetic epidemiology. *Computational Statistics and Data Analysis*, **2000**, 32, 349-360	1.6	1
37	Familial aggregation of dyslexia phenotypes. *Behavior Genetics*, **2000**, 30, 385-96	3.2	55
36	The number of trait loci in late-onset Alzheimer disease. *American Journal of Human Genetics*, **2000**, 66, 196-204	11	257
35	Segregation analysis of phenotypic components of learning disabilities. I. Nonword memory and digit span. *American Journal of Human Genetics*, **2000**, 67, 631-46	11	60
34	Linkage of low-density lipoprotein size to the lipoprotein lipase gene in heterozygous lipoprotein lipase deficiency. *American Journal of Human Genetics*, **1999**, 64, 608-18	11	35
33	Multipoint oligogenic analysis of age-at-onset data with applications to Alzheimer disease pedigrees. *American Journal of Human Genetics*, **1999**, 64, 839-51	11	82
32	Evaluation of locus heterogeneity and EXT1 mutations in 34 families with hereditary multiple exostoses. *Human Mutation*, **1998**, 11, 231-9	4.7	54
31	Semiparametric estimation of major gene effects for age of onset. *Genetic Epidemiology*, **1998**, 15, 279-92	2.6	17
30	Pedigree analysis package (PAP) vs. MORGAN: model selection and hypothesis testing on a large pedigree. *Genetic Epidemiology*, **1998**, 15, 355-69	2.6	11
29	Genome screens using linkage disequilibrium tests: optimal marker characteristics and feasibility. *American Journal of Human Genetics*, **1998**, 63, 1872-85	11	82
28	Evidence against linkage of familial combined hyperlipidemia to the apolipoprotein AI-CIII-AIV gene complex. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **1998**, 18, 215-26	9.4	40
27	Monte Carlo Markov chain methods and model selection in Genetic analysis. *Animal Biotechnology*, **1997**, 8, 129-144	1.4	
26	MCMC segregation and linkage analysis. *Genetic Epidemiology*, **1997**, 14, 1011-6	2.6	93

25	Genetic analysis of simulated oligogenic traits in nuclear and extended pedigrees: summary of GAW10 contributions. *Genetic Epidemiology*, **1997**, 14, 719-35	2.6	131
24	Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. *Genetic Epidemiology*, **1997**, 14, 999-1004	2.6	4
23	Pedigree analysis package vs. MIXD: fitting the mixed model on a large pedigree. *Genetic Epidemiology*, **1996**, 13, 91-106	2.6	9
22	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	11	52
21	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	11	31
20	Interactions of apolipoprotein E genotype, total cholesterol level, age, and sex in prediction of Alzheimer's disease: a case-control study. *Neurology*, **1995**, 45, 1092-6	6.5	342
19	Beta APP mRNA transcription is increased in cultured fibroblasts from the familial Alzheimer's disease-1 family. *Molecular Brain Research*, **1995**, 28, 319-37		58
18	Candidate gene for the chromosome 1 familial Alzheimer's disease locus. *Science*, **1995**, 269, 973-7	33.3	2156
17	A familial Alzheimer's disease locus on chromosome 1. *Science*, **1995**, 269, 970-3	33.3	663
16	Apolipoprotein E genotypes in Parkinson's disease with and without dementia. *Annals of Neurology*, **1995**, 37, 242-5	9.4	59
15	Apolipoprotein E genotypes and age of onset in early-onset familial Alzheimer's disease. *Annals of Neurology*, **1995**, 38, 678-80	9.4	59
14	Alzheimer's disease and the family effect. *Nature Genetics*, **1994**, 8, 115	36.3	10
13	The c-fos gene and early-onset familial Alzheimer's disease. *Neuroscience Letters*, **1993**, 160, 33-6	3.3	18
12	Linkage between quantitative trait and marker loci: methods using all relative pairs. *Genetic Epidemiology*, **1993**, 10, 87-102	2.6	59
11	Genetic analysis of Alzheimer's disease: a summary of contributions to GAW8. *Genetic Epidemiology*, **1993**, 10, 349-60	2.6	5
10	The Seattle Alzheimer's disease data set. *Genetic Epidemiology*, **1993**, 10, 365-9	2.6	
9	Monte Carlo analysis on a large pedigree. *Genetic Epidemiology*, **1993**, 10, 677-82	2.6	19
8	Genetic linkage evidence for a familial Alzheimer's disease locus on chromosome 14. *Science*, **1992**, 258, 668-71	33.3	805

7	Genetic association and linkage analysis of the apolipoprotein CII locus and familial Alzheimer's disease. *Annals of Neurology*, **1992**, 31, 223-7	9.4	72
6	Recurrence risk of a new dominant mutation in children of unaffected parents. *American Journal of Human Genetics*, **1991**, 48, 654-61	11	23
5	Characteristics of familial Alzheimer's disease in nine kindreds of Volga German ancestry. *Progress in Clinical and Biological Research*, **1989**, 317, 229-34		7
4	A deductive method of haplotype analysis in pedigrees. *American Journal of Human Genetics*, **1987**, 41, 356-73	11	51
3	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	2.5	14
2	Optimizing selection of restriction enzymes in the search for DNA variants. *Nucleic Acids Research*, **1984**, 12, 9209-26	20.1	25
1	Techniques for estimating genetic admixture and applications to the problem of the origin of the Icelanders and the Ashkenazi Jews. *Human Genetics*, **1984**, 67, 441-8	6.3	33