Daniel E Weeks

List of Publications by Year in Descending Order

263 papers	18,393 citations	67 h-index	132 g-index
292 ext. papers	20,889 ext. citations	7.6 avg, IF	6.16 L-index

#	Paper	IF	Citations
263	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
262	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
261	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration: A Mendelian Randomization Study. *JAMA Ophthalmology*, **2021**,	3.9	2
260	An exploratory study of white blood cell proportions across preeclamptic and normotensive pregnancy by self-identified race in individuals with overweight or obesity. *Hypertension in Pregnancy*, **2021**, 40, 312-321	2	0
259	An Exploratory Study of Epigenetic Age in Preeclamptic and Normotensive Pregnancy Reveals Differences by Self-Reported Race but Not Pregnancy Outcome. *Reproductive Sciences*, **2021**, 28, 3519-3528	3	3
258	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
257	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. *American Journal of Epidemiology*, **2021**, 190, 1977-1992	3.8	3
256	Acute DNA Methylation Trajectories in Cerebrospinal Fluid and Associations With Outcomes Following Severe Traumatic Brain Injury in Adults. *Neurorehabilitation and Neural Repair*, **2021**, 35, 790-800	4.7	0
255	Genome-wide association studies in Samoans give insight into the genetic architecture of fasting serum lipid levels. *Journal of Human Genetics*, **2021**, 66, 111-121	4.3	2
254	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. *Journal of the American Statistical Association*, **2021**, 116, 531-545	2.8	1
253	ECHS1 disease in two unrelated families of Samoan descent: Common variant - rare disorder. *American Journal of Medical Genetics, Part A*, **2021**, 185, 157-167	2.5	3
252	A missense variant in CREBRF, rs373863828, is associated with fat-free mass, not fat mass in Samoan infants. *International Journal of Obesity*, **2021**, 45, 45-55	5.5	9
251	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. *Translational Vision Science and Technology*, **2021**, 10, 29	3.3	4
250	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
249	A murine model of the human CREBRFR457Q obesity-risk variant does not influence energy or glucose homeostasis in response to nutritional stress. *PLoS ONE*, **2021**, 16, e0251895	3.7	1
248	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. *Advances in Experimental Medicine and Biology*, **2021**, 1256, 191-200	3.6	1
247	Iron homeostasis pathway DNA methylation trajectories reveal a role for STEAP3 metalloreductase in patient outcomes after aneurysmal subarachnoid hemorrhage. **2021**, 1,		2

246	A missense variant in CREBRF is associated with taller stature in Samoans. *American Journal of Human Biology*, **2020**, 32, e23414	2.7	8
245	Methylation Data Processing Protocol and Comparison of Blood and Cerebral Spinal Fluid Following Aneurysmal Subarachnoid Hemorrhage. *Frontiers in Genetics*, **2020**, 11, 671	4.5	3
244	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. *Nature Machine Intelligence*, **2020**, 2, 141-150	22.5	35
243	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *Journal of Allergy and Clinical Immunology*, **2020**, 146, 671-675	11.5	7
242	Exploring the Paradoxical Relationship of a Creb 3 Regulatory Factor Missense Variant With Body Mass Index and Diabetes Among Samoans: Protocol for the Soifua Manuia (Good Health) Observational Cohort Study. *JMIR Research Protocols*, **2020**, 9, e17329	2	3
241	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
240	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nature Genetics*, **2020**, 52, 969-983	36.3	33
239	Genetic Variability and Trajectories of DNA Methylation May Support a Role for HAMP in Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. *Neurocritical Care*, **2020**, 32, 550-563	3.3	6
238	Genetic Variability in the Iron Homeostasis Pathway and Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. *Neurocritical Care*, **2020**, 33, 749-758	3.3	2
237	Evolutionary history of modern Samoans. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 9458-9465	11.5	3
236	Spinning convincing stories for both true and false association signals. *Genetic Epidemiology*, **2019**, 43, 356-364	2.6	5
235	Y chromosome mosaicism is associated with age-related macular degeneration. *European Journal of Human Genetics*, **2019**, 27, 36-41	5.3	27
234	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. *Lancet Respiratory Medicine,the*, **2019**, 7, 336-346	35.1	87
233	Linear mixed models for association analysis of quantitative traits with next-generation sequencing data. *Genetic Epidemiology*, **2019**, 43, 189-206	2.6	3
232	Genome-wide association study of maternal genetic effects and parent-of-origin effects on food allergy. *Medicine (United States)*, **2018**, 97, e0043	1.8	13
231	Genome-wide analysis of disease progression in age-related macular degeneration. *Human Molecular Genetics*, **2018**, 27, 929-940	5.6	37
230	Novel caries loci in children and adults implicated by genome-wide analysis of families. *BMC Oral Health*, **2018**, 18, 98	3.7	5
229	Re: "Widespread prevalence of a CREBRF variant among Māori and Pacific children is associated with weight and height in early childhood". *International Journal of Obesity*, **2018**, 42, 1389-1391	5.5	5

228	Discordant association of the CREBRF rs373863828 A allele with increased BMI and protection from type 2 diabetes in Māori and Pacific (Polynesian) people living in Aotearoa/New Zealand. *Diabetologia*, **2018**, 61, 1603-1613	10.3	35
227	Statistics for X-chromosome associations. *Genetic Epidemiology*, **2018**, 42, 539-550	2.6	8
226	The Mega2R package: R tools for accessing and processing genetic data in common formats. *F1000Research*, **2018**, 7, 1352	3.6	1
225	The Mega2R package: R tools for accessing and processing genetic data in common formats. *F1000Research*, **2018**, 7, 1352	3.6	1
224	An epigenome-wide association study of total serum IgE in Hispanic children. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 571-577	11.5	41
223	Genetic risk models: Influence of model size on risk estimates and precision. *Genetic Epidemiology*, **2017**, 41, 282-296	2.6	2
222	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. *Nature Communications*, **2017**, 8, 15608	17.4	16
221	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics*, **2017**, 206, 119-133	4	31
220	A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for next-generation sequencing. *Genetic Epidemiology*, **2017**, 41, 18-34	2.6	2
219	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. *European Journal of Human Genetics*, **2017**, 25, 350-359	5.3	2
218	Genetic pleiotropy between age-related macular degeneration and 16 complex diseases and traits. *Genome Medicine*, **2017**, 9, 29	14.4	41
217	Joint Analysis of Nuclear and Mitochondrial Variants in Age-Related Macular Degeneration Identifies Novel Loci TRPM1 and ABHD2/RLBP1 **2017**, 58, 4027-4038		13
216	A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. *Genetic Epidemiology*, **2016**, 40, 702-721	2.6	10
215	A thrifty variant in CREBRF strongly influences body mass index in Samoans. *Nature Genetics*, **2016**, 48, 1049-1054	36.3	135
214	The impact of genotype calling errors on family-based studies. *Scientific Reports*, **2016**, 6, 28323	4.9	8
213	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. *Genetic Epidemiology*, **2016**, 40, 161-71	2.6	3
212	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. *Nature Genetics*, **2016**, 48, 134-43	36.3	769
211	Enhanced B Cell Alloantigen Presentation and Its Epigenetic Dysregulation in Liver Transplant Rejection. *American Journal of Transplantation*, **2016**, 16, 497-508	8.7	11

210	Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. *Genetic Epidemiology*, **2016**, 40, 133-43	2.6	10
209	Epigenome-wide association study links site-specific DNA methylation changes with cow's milk allergy. *Journal of Allergy and Clinical Immunology*, **2016**, 138, 908-911.e9	11.5	37
208	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. *Nature Communications*, **2015**, 6, 6304	17.4	152
207	dbVOR: a database system for importing pedigree, phenotype and genotype data and exporting selected subsets. *BMC Bioinformatics*, **2015**, 16, 91	3.6	1
206	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. *Genetics*, **2015**, 201, 1329-39	4	12
205	Genetic ME-a visualization application for merging and editing pedigrees for genetic studies. *BMC Research Notes*, **2015**, 8, 241	2.3	
204	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. *Human Heredity*, **2015**, 80, 126-38	1.1	7
203	Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. *Human Heredity*, **2015**, 80, 79-89	1.1	
202	Identification of epidermal growth factor receptor (EGFR) genetic variants that modify risk for head and neck squamous cell carcinoma. *Cancer Letters*, **2015**, 357, 549-56	9.9	11
201	Predisposition to Childhood Otitis Media and Genetic Polymorphisms within the Toll-Like Receptor 4 (TLR4) Locus. *PLoS ONE*, **2015**, 10, e0132551	3.7	28
200	Prevalence of adiposity and associated cardiometabolic risk factors in the Samoan genome-wide association study. *American Journal of Human Biology*, **2014**, 26, 491-501	2.7	45
199	Rare and common variants in extracellular matrix gene Fibrillin 2 (FBN2) are associated with macular degeneration. *Human Molecular Genetics*, **2014**, 23, 5827-37	5.6	34
198	Endophenotypes for Age-Related Macular Degeneration: Extending Our Reach into the Preclinical Stages of Disease. *Journal of Clinical Medicine*, **2014**, 3, 1335-56	5.1	8
197	Mega2: validated data-reformatting for linkage and association analyses. *Source Code for Biology and Medicine*, **2014**, 9, 26	1.9	7
196	Stratified randomization controls better for batch effects in 450K methylation analysis: a cautionary tale. *Frontiers in Genetics*, **2014**, 5, 354	4.5	31
195	Genetic-based prediction of disease traits: prediction is very difficult, especially about the future. *Frontiers in Genetics*, **2014**, 5, 162	4.5	42
194	Generalized functional linear models for gene-based case-control association studies. *Genetic Epidemiology*, **2014**, 38, 622-637	2.6	20
193	Genome-wide association study of primary dentition pit-and-fissure and smooth surface caries. *Caries Research*, **2014**, 48, 330-8	4.2	25

192	Genome-wide association study of periodontal health measured by probing depth in adults ages 18-49 years. *G3: Genes, Genomes, Genetics*, **2014**, 4, 307-14	3.2	46
191	A genome-wide association study of chronic otitis media with effusion and recurrent otitis media identifies a novel susceptibility locus on chromosome 2. *JARO - Journal of the Association for Research in Otolaryngology*, **2013**, 14, 791-800	3.3	34
190	Clustering tooth surfaces into biologically informative caries outcomes. *Journal of Dental Research*, **2013**, 92, 32-7	8.1	24
189	GWAS of dental caries patterns in the permanent dentition. *Journal of Dental Research*, **2013**, 92, 38-44	8.1	59
188	Seven new loci associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 433-9, 439e1-2	36.3	577
187	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 1375-9	36.3	130
186	ADCYAP1R1 and asthma in Puerto Rican children. *American Journal of Respiratory and Critical Care Medicine*, **2013**, 187, 584-8	10.2	75
185	Genome-wide association studies of pit-and-fissure- and smooth-surface caries in permanent dentition. *Journal of Dental Research*, **2013**, 92, 432-7	8.1	48
184	Demographic, socioeconomic, and behavioral factors affecting patterns of tooth decay in the permanent dentition: principal components and factor analyses. *Community Dentistry and Oral Epidemiology*, **2013**, 41, 364-73	2.8	17
183	INSIG2 variants, dietary patterns and metabolic risk in Samoa. *European Journal of Clinical Nutrition*, **2013**, 67, 101-7	5.2	14
182	Replication of a genome-wide association study of birth weight in preterm neonates. *Journal of Pediatrics*, **2012**, 160, 19-24.e4	3.6	14
181	Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. *BMC Oral Health*, **2012**, 12, 7	3.7	27
180	Genome-wide association scan of dental caries in the permanent dentition. *BMC Oral Health*, **2012**, 12, 57	3.7	53
179	Effects of smoking and genotype on the PSR index of periodontal disease in adults aged 18-49. *International Journal of Environmental Research and Public Health*, **2012**, 9, 2839-50	4.6	11
178	ASTN1 and alcohol dependence: family-based association analysis in multiplex alcohol dependence families. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 445-55	3.5	14
177	Common variants in FTO are not significantly associated with obesity-related phenotypes among Samoans of Polynesia. *Annals of Human Genetics*, **2012**, 76, 17-24	2.2	12
176	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. *International Journal of Epidemiology*, **2012**, 41, 250-62	7.8	70
175	Evaluation of 15 functional candidate genes for association with chronic otitis media with effusion and/or recurrent otitis media (COME/ROM). *PLoS ONE*, **2011**, 6, e22297	3.7	27

174	Enhanced genetic maps from family-based disease studies: population-specific comparisons. *BMC Medical Genetics*, **2011**, 12, 15	2.1	3
173	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. *Human Mutation*, **2011**, 32, 1407-16	4.7	99
172	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. *American Journal of Epidemiology*, **2011**, 173, 1357-64	3.8	67
171	Genome-wide association scan for childhood caries implicates novel genes. *Journal of Dental Research*, **2011**, 90, 1457-62	8.1	84
170	Coordinated conditional simulation with SLINK and SUP of many markers linked or associated to a trait in large pedigrees. *Human Heredity*, **2011**, 71, 126-34	1.1	14
169	Role of African ancestry and gene-environment interactions in predicting preterm birth. *Obstetrics and Gynecology*, **2011**, 118, 1081-1089	4.9	16
168	Dissection of chromosome 16p12 linkage peak suggests a possible role for CACNG3 variants in age-related macular degeneration susceptibility **2011**, 52, 1748-54		8
167	NOD2 gene polymorphism rs2066844 associates with need for combined liver-intestine transplantation in children with short-gut syndrome. *American Journal of Gastroenterology*, **2011**, 106, 157-65	0.7	38
166	Genetic variants near TIMP3 and high-density lipoprotein-associated loci influence susceptibility to age-related macular degeneration. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 7401-6	11.5	417
165	Association tests using kernel-based measures of multi-locus genotype similarity between individuals. *Genetic Epidemiology*, **2010**, 34, 213-21	2.6	62
164	Interpretation of genetic association studies: markers with replicated highly significant odds ratios may be poor classifiers. *PLoS Genetics*, **2009**, 5, e1000337	6	191
163	CasaresQmap function: no need for a QcorrectedQHaldaneQ map function. *Genetica*, **2009**, 135, 305-7	1.5	2
162	Suggestive linkage detected for blood pressure related traits on 2q and 22q in the population on the Samoan islands. *BMC Medical Genetics*, **2009**, 10, 107	2.1	10
161	A tagging SNP in INSIG2 is associated with obesity-related phenotypes among Samoans. *BMC Medical Genetics*, **2009**, 10, 143	2.1	11
160	Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. *BMC Medical Genetics*, **2009**, 10, 85	2.1	34
159	Susceptibility loci for adiposity phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. *Obesity*, **2009**, 17, 518-24	8	23
158	A whole genome linkage scan identifies multiple chromosomal regions influencing adiposity-related traits among Samoans. *Annals of Human Genetics*, **2008**, 72, 780-92	2.2	26
157	Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. *BMC Bioinformatics*, **2008**, 9, 317	3.6	5

156	Genetic variants in major histocompatibility complex-linked genes associate with pediatric liver transplant rejection. *Gastroenterology*, **2008**, 135, 830-9, 839.e1-10	13.3	20
155	Applying novel genome-wide linkage strategies to search for loci influencing type 2 diabetes and adult height in American Samoa. *Human Biology*, **2008**, 80, 99-123	1.2	3
154	A genome-wide linkage scan identifies multiple chromosomal regions influencing serum lipid levels in the population on the Samoan islands. *Journal of Lipid Research*, **2008**, 49, 2169-78	6.3	23
153	Relationship uncertainty linkage statistics (RULS): affected relative pair statistics that model relationship uncertainty. *Genetic Epidemiology*, **2008**, 32, 313-24	2.6	6
152	Dopaminergic mutations: within-family association and linkage in multiplex alcohol dependence families. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 517-26	3.5	37
151	Robust score statistics for QTL linkage analysis. *American Journal of Human Genetics*, **2008**, 82, 567-82	11	8
150	C2 and CFB genes in age-related maculopathy and joint action with CFH and LOC387715 genes. *PLoS ONE*, **2008**, 3, e2199	3.7	69
149	Two-dimensional linkage analyses of rheumatoid arthritis. *BMC Proceedings*, **2007**, 1 Suppl 1, S68	2.3	4
148	The elusive goal of pedigree weights. *Genetic Epidemiology*, **2007**, 31, 51-65	2.6	11
147	A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. *Genetic Epidemiology*, **2007**, 31, 417-30	2.6	2
146	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. *Nature Genetics*, **2007**, 39, 319-28	36.3	1083
145	Genome-wide scan for adiposity-related phenotypes in adults from American Samoa. *International Journal of Obesity*, **2007**, 31, 1832-42	5.5	32
144	Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13-15. *Human Reproduction*, **2007**, 22, 717-28	5.7	42
143	Estimating prevalence, false-positive rate, and false-negative rate with use of repeated testing when true responses are unknown. *American Journal of Human Genetics*, **2007**, 81, 1111-3	11	1
142	Comparison of methods incorporating quantitative covariates into affected sib pair linkage analysis. *Genetic Epidemiology*, **2006**, 30, 77-93	2.6	6
141	Gene-dropping vs. empirical variance estimation for allele-sharing linkage statistics. *Genetic Epidemiology*, **2006**, 30, 652-65	2.6	9
140	Treatment of uninformative families in mean allele sharing tests for linkage. *Statistical Applications in Genetics and Molecular Biology*, **2006**, 5, Article13	1.2	
139	CFH, ELOVL4, PLEKHA1 and LOC387715 genes and susceptibility to age-related maculopathy: AREDS and CHS cohorts and meta-analyses. *Human Molecular Genetics*, **2006**, 15, 3206-18	5.6	135

138	Ordered genotypes: an extended ITO method and a general formula for genetic covariance. *American Journal of Human Genetics*, **2006**, 78, 1035-45	11	5
137	The Khatri Sikh Diabetes Study (SDS): study design, methodology, sample collection, and initial results. *Human Biology*, **2006**, 78, 43-63	1.2	27
136	No convincing evidence of linkage for restless legs syndrome on chromosome 9p. *American Journal of Human Genetics*, **2005**, 76, 705-7; author reply 707-10	11	15
135	Candidate-gene screening and association analysis at the autism-susceptibility locus on chromosome 16p: evidence of association at GRIN2A and ABAT. *American Journal of Human Genetics*, **2005**, 76, 950-66	11	143
134	Genomewide linkage study in 1,176 affected sister pair families identifies a significant susceptibility locus for endometriosis on chromosome 10q26. *American Journal of Human Genetics*, **2005**, 77, 365-76	11	173
133	Susceptibility genes for age-related maculopathy on chromosome 10q26. *American Journal of Human Genetics*, **2005**, 77, 389-407	11	473
132	Meta-analysis of genome scans of age-related macular degeneration. *Human Molecular Genetics*, **2005**, 14, 2257-64	5.6	197
131	Analysis of alcohol dependence phenotype in the COGA families using covariates to detect linkage. *BMC Genetics*, **2005**, 6 Suppl 1, S143	2.6	18
130	A comparison between microsatellite and single-nucleotide polymorphism markers with respect to two measures of information content. *BMC Genetics*, **2005**, 6 Suppl 1, S27	2.6	5
129	Mega2: data-handling for facilitating genetic linkage and association analyses. *Bioinformatics*, **2005**, 21, 2556-7	7.2	128
128	Analysis of IMGSAC autism susceptibility loci: evidence for sex limited and parent of origin specific effects. *Journal of Medical Genetics*, **2005**, 42, 132-7	5.8	94
127	Candidate gene analysis suggests a role for fatty acid biosynthesis and regulation of the complement system in the etiology of age-related maculopathy. *Human Molecular Genetics*, **2005**, 14, 1991-2002	5.6	128
126	Familial aggregation of endometriosis in a large pedigree of rhesus macaques. *Human Reproduction* , **2004**, 19, 448-55	5.7	75
125	Inflammatory bowel disease susceptibility loci defined by genome scan meta-analysis of 1952 affected relative pairs. *Human Molecular Genetics*, **2004**, 13, 763-70	5.6	198
124	Comparative study of multipoint methods for genotype error detection. *Human Heredity*, **2004**, 58, 175-89	1.1	17
123	Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. *BMC Genetics*, **2004**, 5, 18	2.6	36
122	Efficient simulation of P values for linkage analysis. *Genetic Epidemiology*, **2004**, 26, 88-96	2.6	10
121	No "bias" toward the null hypothesis in most conventional multipoint nonparametric linkage analyses. *American Journal of Human Genetics*, **2004**, 75, 716-8; author reply 723-7	11	6

120	Age-related maculopathy: a genomewide scan with continued evidence of susceptibility loci within the 1q31, 10q26, and 17q25 regions. *American Journal of Human Genetics*, **2004**, 75, 174-89	11	154
119	Distribution of genome-wide linkage disequilibrium based on microsatellite loci in the Samoan population. *Human Genomics*, **2004**, 1, 327-34	6.8	19
118	A genome-wide scan for loci affecting normal adult height in the Framingham Heart Study. *Human Heredity*, **2003**, 55, 191-201	1.1	23
117	Linkage analysis of adult height with parent-of-origin effects in the Framingham Heart Study. *BMC Genetics*, **2003**, 4 Suppl 1, S76	2.6	16
116	Interleukin 10 polymorphisms in ankylosing spondylitis. *Genes and Immunity*, **2003**, 4, 74-6	4.4	27
115	Human leptin locus (LEP) alleles and BMI in Samoans. *International Journal of Obesity*, **2002**, 26, 783-8	5.5	12
114	The genetic epidemiology of spontaneous endometriosis in the rhesus monkey. *Annals of the New York Academy of Sciences*, **2002**, 955, 233-8; discussion 293-5, 396-406	6.5	22
113	A tale of two genotypes: consistency between two high-throughput genotyping centers. *Genome Research*, **2002**, 12, 430-5	9.7	35
112	Evidence for an inflammatory bowel disease locus on chromosome 3p26: linkage, transmission/disequilibrium and partitioning of linkage. *Human Molecular Genetics*, **2002**, 11, 2599-606	5.6	23
111	A pooled case-control study of the apolipoprotein E (APOE) gene in age-related maculopathy. *Ophthalmic Genetics*, **2002**, 23, 209-23	1.2	116
110	Statistics for nonparametric linkage analysis of X-linked traits in general pedigrees. *American Journal of Human Genetics*, **2002**, 70, 181-91	11	4
109	The complexity of linkage analysis with neural networks. *Human Heredity*, **2001**, 51, 169-76	1.1	20
108	Multipoint estimation of identity-by-descent probabilities at arbitrary positions among marker loci on general pedigrees. *Human Heredity*, **2001**, 52, 121-31	1.1	184
107	Toward developing a genome-wide microsatellite marker set for linkage analysis in the rhesus macaque (Macaca mulatta): identification of 76 polymorphic markers. *American Journal of Primatology*, **2001**, 54, 223-31	2.5	19
106	Further characterization of the autism susceptibility locus AUTS1 on chromosome 7q. *Human Molecular Genetics*, **2001**, 10, 973-82	5.6	132
105	Ulcerative colitis is more strongly linked to chromosome 12 than Crohn's disease. *Gut*, **2001**, 49, 311	19.2	3
104	Affected sib-pair analysis in endometriosis. *Human Reproduction Update*, **2001**, 7, 411-8	15.8	38
103	Association between endometriosis and N-acetyl transferase 2 polymorphisms in a UK population. *Molecular Human Reproduction*, **2001**, 7, 1079-83	4.4	48

102	Linkage and association studies of the relationship between endometriosis and genes encoding the detoxification enzymes GSTM1, GSTT1 and CYP1A1. *Molecular Human Reproduction*, **2001**, 7, 1073-8	4.4	83
101	Newton Morton's influence on genetics: the Morton number. *Advances in Genetics*, **2001**, 42, 7-10	3.3	1
100	Pedigree selection and information content. *Current Protocols in Human Genetics*, **2001**, Chapter 1, Unit 1.2	3.2	
99	Age-related maculopathy: an expanded genome-wide scan with evidence of susceptibility loci within the 1q31 and 17q25 regions. *American Journal of Ophthalmology*, **2001**, 132, 682-92	4.9	113
98	Whole-genome screening in ankylosing spondylitis: evidence of non-MHC genetic-susceptibility loci. *American Journal of Human Genetics*, **2001**, 68, 918-26	11	200
97	A survey of affected-sibship statistics for nonparametric linkage analysis. *American Journal of Human Genetics*, **2001**, 69, 179-90	11	33
96	A genomewide screen for autism: strong evidence for linkage to chromosomes 2q, 7q, and 16p. *American Journal of Human Genetics*, **2001**, 69, 570-81	11	403
95	Type 2 diabetes and three calpain-10 gene polymorphisms in Samoans: no evidence of association. *American Journal of Human Genetics*, **2001**, 69, 1236-44	11	89
94	The IBD4 locus shows linkage heterogeneity between Crohn's disease and ulcerative colitis. *Gastroenterology*, **2001**, 120, A455	13.3	2
93	Comparison of allele-sharing statistics for general pedigrees. *Genetic Epidemiology*, **2000**, 19 Suppl 1, S92-8	2.6	8
92	Polymorphisms of the CYP2D6 gene increase susceptibility to ankylosing spondylitis. *Human Molecular Genetics*, **2000**, 9, 1563-6	5.6	59
91	A juvenile-onset, progressive cataract locus on chromosome 3q21-q22 is associated with a missense mutation in the beaded filament structural protein-2. *American Journal of Human Genetics*, **2000**, 66, 1426-31	11	131
90	High-density genome scan in Crohn disease shows confirmed linkage to chromosome 14q11-12. *American Journal of Human Genetics*, **2000**, 66, 1857-62	11	162
89	The IBD2 locus shows linkage heterogeneity between ulcerative colitis and Crohn disease. *American Journal of Human Genetics*, **2000**, 67, 1605-10	11	73
88	A full genome scan for age-related maculopathy. *Human Molecular Genetics*, **2000**, 9, 1329-49	5.6	94
87	A genome scan at 751 microsatellite loci reveals linkage between Crohn's disease and chromosome 14q11–12, the IBD4 locus. *Gastroenterology*, **2000**, 118, A708	13.3	2
86	Absence of a relationship between endometriosis and the N314D polymorphism of galactose-1-phosphate uridyl transferase in a UK population. *Molecular Human Reproduction*, **1999**, 5, 990-3	4.4	28
85	Serotonin transporter (5-HTT) and gamma-aminobutyric acid receptor subunit beta3 (GABRB3) gene polymorphisms are not associated with autism in the IMGSA families. The International Molecular Genetic Study of Autism Consortium. *American Journal of Medical Genetics Part A*, **1999**, 88, 492-6		122

84	A quantitative-trait locus on chromosome 6p influences different aspects of developmental dyslexia. *American Journal of Human Genetics*, **1999**, 64, 146-56	11	233
83	An optimal algorithm for automatic genotype elimination. *American Journal of Human Genetics*, **1999**, 65, 1733-40	11	39
82	A comparison of two algorithms, MultiMap and gene mapping system, for automated construction of genetic linkage maps. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S649-54	2.6	3
81	Discovery of cancer susceptibility genes: study designs, analytic approaches, and trends in technology. *Journal of the National Cancer Institute Monographs*, **1999**, 1-16	4.8	15
80	Molecular genetic investigations of autism. *Journal of Autism and Developmental Disorders*, **1998**, 28, 427-37	4.6	14
79	. . . and linguistic diversity. *Nature*, **1998**, 391, 118	50.4	
78	Magnetic resonance imaging to assess familial risk in relatives of women with endometriosis. *Lancet, The*, **1998**, 352, 1440-1	40	45
77	Consanguinity and relative-pair methods for linkage analysis. *American Journal of Human Genetics*, **1998**, 62, 728-36	11	6
76	Mutational mechanisms for generating microsatellite allele-frequency distributions: an analysis of 4,558 markers. *American Journal of Human Genetics*, **1998**, 62, 1260-2	11	20
75	PedCheck: a program for identification of genotype incompatibilities in linkage analysis. *American Journal of Human Genetics*, **1998**, 63, 259-66	11	1856
74	Linkage and association between inflammatory bowel disease and a locus on chromosome 12. *American Journal of Human Genetics*, **1998**, 63, 95-100	11	131
73	Autosomal recessive juvenile parkinsonism maps to 6q25.2-q27 in four ethnic groups: detailed genetic mapping of the linked region. *American Journal of Human Genetics*, **1998**, 63, 80-7	11	56
72	Mitochondrial neurogastrointestinal encephalomyopathy syndrome maps to chromosome 22q13.32-qter. *American Journal of Human Genetics*, **1998**, 63, 526-33	11	81
71	A genome-wide screen for susceptibility loci in ankylosing spondylitis. *Arthritis and Rheumatism*, **1998**, 41, 588-95		73
70	A full genome screen for autism with evidence for linkage to a region on chromosome 7q. International Molecular Genetic Study of Autism Consortium. *Human Molecular Genetics*, **1998**, 7, 571-8	5.6	397
69	A genome-wide screen for susceptibility loci in ankylosing spondylitis **1998**, 41, 588		65
68	Molecular genetic analysis of Lubag. *Advances in Neurology*, **1998**, 78, 341-8		3
67	Genetic susceptibility for human familial essential hypertension in a region of homology with blood pressure linkage on rat chromosome 10. *Human Molecular Genetics*, **1997**, 6, 2077-85	5.6	162

66	Comparison of nonparametric statistics for detection of linkage in nuclear families: single-marker evaluation. *American Journal of Human Genetics*, **1997**, 61, 1431-44	11	84
65	True and false positive peaks in genomewide scans: applications of length-biased sampling to linkage mapping. *American Journal of Human Genetics*, **1997**, 61, 430-8	11	123
64	A linkage study across the T cell receptor A and T cell receptor B loci in families with rheumatoid arthritis. *Arthritis and Rheumatism*, **1997**, 40, 1798-802		11
63	Use of MRI in genetic studies of endometriosis **1997**, 71, 371-372		14
62	Analysis of bipolar disorder using affected relatives. *Genetic Epidemiology*, **1997**, 14, 605-10	2.6	1
61	Analysis of a complex oligogenic disease. *Genetic Epidemiology*, **1997**, 14, 861-6	2.6	1
60	Advances in Statistical Methods for Linkage Analysis **1997**, 153-160		
59	Nonparametric simulation based linkage statistics for general pedigrees. *Journal of Rheumatology*, **1997**, 24, 206-7	4.1	
58	Influence of the HLA-DRB1 locus on susceptibility and severity in rheumatoid arthritis. *QJM - Monthly Journal of the Association of Physicians*, **1996**, 89, 821-9	2.7	66
57	A molecular defect in loricrin, the major component of the cornified cell envelope, underlies Vohwinkel® syndrome. *Nature Genetics*, **1996**, 13, 70-7	36.3	214
56	Nonparametric simulation-based statistics for detecting linkage in general pedigrees. *American Journal of Human Genetics*, **1996**, 58, 867-80	11	90
55	Haplotyping Algorithms **1996**, 89-110		24
54	The VITESSE algorithm for rapid exact multilocus linkage analysis via genotype set-recoding and fuzzy inheritance. *Nature Genetics*, **1995**, 11, 402-8	36.3	465
53	The Gene for Hereditary Progressive Dystonia with Marked Diurnal Fluctuation Maps to Chromosome 14q. *Frontiers of Neurology and Neuroscience*, **1995**, 14, 120-125	1.1	1
52	The affected-pedigree-member method: power to detect linkage. *Human Heredity*, **1995**, 45, 13-24	1.1	13
51	An incremental algorithm for efficient multipoint linkage analysis. *Human Heredity*, **1995**, 45, 323-36	1.1	2
50	Parallel computation of genetic likelihoods using CRI-MAP, PVM, and a network of distributed workstations. *Human Heredity*, **1995**, 45, 103-16	1.1	10
49	An X-linked version of the affected-pedigree-member method of linkage analysis. *Human Heredity*, **1995**, 45, 25-33	1.1	6

48	A high-resolution genetic linkage map of the pericentromeric region of the human X chromosome. *Genomics*, **1995**, 26, 39-46	4.3	11
47	DNA profile match probabilities in a subdivided population: when can subdivision be ignored?. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 12031-5	11.5	1
46	Polygenic disease: methods for mapping complex disease traits. *Trends in Genetics*, **1995**, 11, 513-9	8.5	198
45	The gene for hereditary progressive dystonia with marked diurnal fluctuation maps to chromosome 14q. *Annals of Neurology*, **1995**, 37, 405-8	9.4	32
44	Computer programs for multilocus haplotyping of general pedigrees. *American Journal of Human Genetics*, **1995**, 56, 1506-7	11	109
43	Invalidity of the Rao map function for three loci. *Human Heredity*, **1994**, 44, 178-80	1.1	7
42	Improved programs for the affected-pedigree-member method of linkage analysis. *Genetic Epidemiology*, **1994**, 11, 69-74	2.6	8
41	Chromosome 18 DNA markers and manic-depressive illness: evidence for a susceptibility gene. *Proceedings of the National Academy of Sciences of the United States of America*, **1994**, 91, 5918-21	11.5	330
40	Efficient strategies for genomic searching using the affected-pedigree-member method of linkage analysis. *American Journal of Human Genetics*, **1994**, 54, 544-52	11	31
39	Detection of tandem duplications and implications for linkage analysis. *American Journal of Human Genetics*, **1994**, 54, 1110-21	11	15
38	Detection of genetic interference: simulation studies and mouse data. *Genetics*, **1994**, 136, 1217-26	4	20
37	Similarity of DNA fingerprints due to chance and relatedness. *Human Heredity*, **1993**, 43, 45-52	1.1	203
36	Multipoint mapping under genetic interference. *Human Heredity*, **1993**, 43, 86-97	1.1	29
35	Detecting heterogeneity with the affected-pedigree-member (APM) method. *Genetic Epidemiology*, **1993**, 10, 401-6	2.6	5
34	A gene for Hirschsprung disease (megacolon) in the pericentromeric region of human chromosome 10. *Nature Genetics*, **1993**, 4, 351-6	36.3	136
33	Linkage mapping of dopa-responsive dystonia (DRD) to chromosome 14q. *Nature Genetics*, **1993**, 5, 386-91	36.3	175
32	Two-locus models of disease: comparison of likelihood and nonparametric linkage methods. *American Journal of Human Genetics*, **1993**, 53, 908-15	11	56
31	Further concerns about the genetics of pre-eclampsia. *American Journal of Human Genetics*, **1993**, 53, 963-4	11	

30	The Genetics of Age-Related Maculopathy **1993**, 35-47		
29	Preliminary ranking procedures for multilocus ordering based on radiation hybrid data. *Cytogenetic and Genome Research*, **1992**, 59, 125-7	1.9	9
28	A multilocus extension of the affected-pedigree-member method of linkage analysis. *American Journal of Human Genetics*, **1992**, 50, 859-68	11	68
27	Genetic mapping of "Lubag" (X-linked dystonia-parkinsonism) in a Filipino kindred to the pericentromeric region of the X chromosome. *Annals of Neurology*, **1991**, 29, 124-31	9.4	77
26	Assessment of Chronic Radiosensitivity as an in Vitro Assay for Heterozygote Identification of Ataxia-Telangiectasia. *Radiation Research*, **1991**, 128, 90	3.1	59
25	Assessment of chronic gamma radiosensitivity as an in vitro assay for heterozygote identification of ataxia-telangiectasia. *Radiation Research*, **1991**, 128, 90-9	3.1	13
24	Genetic epidemiology of bilateral breast cancer: a linkage analysis using the affected-pedigree-member method. *Genetic Epidemiology*, **1990**, 7, 47-55	2.6	3
23	Measuring the inflation of the lod score due to its maximization over model parameter values in human linkage analysis. *Genetic Epidemiology*, **1990**, 7, 237-43	2.6	103
22	Linkage methods for identifying genetic risk factors. *World Review of Nutrition and Dietetics*, **1990**, 63, 236-49	0.2	9
21	A primary linkage map of the human chromosome 11q22-23 region. *Genomics*, **1990**, 6, 316-23	4.3	32
20	Mapping of a gene determining tuberous sclerosis to human chromosome 11q14-11q23. *Genomics*, **1990**, 6, 105-14	4.3	92
19	A likelihood-based analysis of consistent linkage of a disease locus to two nonsyntenic marker loci: osteogenesis imperfecta versus COL1A1 and COL1A2. *American Journal of Human Genetics*, **1990**, 47, 592-4	11	4
18	Trials, tribulations, and triumphs of the EM algorithm in pedigree analysis. *Mathematical Medicine and Biology*, **1989**, 6, 209-32	1.3	19
17	Efficient computation of lod scores: genotype elimination, genotype redefinition, and hybrid maximum likelihood algorithms. *Annals of Human Genetics*, **1989**, 53, 67-83	2.2	35
16	Comparison of the affected-pedigree-member and lod-score methods. *Progress in Clinical and Biological Research*, **1989**, 329, 135-40		
15	Risk calculations under heterogeneity. *American Journal of Human Genetics*, **1989**, 45, 819-21	11	13
14	Programs for Pedigree Analysis: MENDEL, FISHER, and dGENE. *Genetic Epidemiology*, **1988**, 5, 471-2	2.6	480
13	Localization of an ataxia-telangiectasia gene to chromosome 11q22-23. *Nature*, **1988**, 336, 577-80	50.4	605

12	The affected-pedigree-member method of linkage analysis. *American Journal of Human Genetics*, **1988**, 42, 315-26	11	350
11	Preliminary ranking procedures for multilocus ordering. *Genomics*, **1987**, 1, 236-42	4.3	57
10	Genetic linkage studies of ataxia-telangiectasia: phenotypic blood markers. *Disease Markers*, **1987**, 5, 207-13	3.2	1
9	Two-Sex Models: Chaos, Extinction, and Other Dynamic Consequences of Sex. *American Naturalist*, **1986**, 128, 707-735	3.7	147
8	A missense variant in CREBRF is associated with taller stature in Samoans		1
7	GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk		2
6	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression		1
5	Utilization of Epigenome-wide DNA Methylation for Longitudinal Comparison of White Blood Cell Proportions Across Preeclamptic and Normotensive Pregnancy by Self-Reported Race		1
4	Rare coding variants in 35 genes associate with circulating lipid levels a multi-ancestry analysis of 170,000 exomes		2
3	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
2	Inherited Causes of Clonal Hematopoiesis of Indeterminate Potential in TOPMed Whole Genomes		11
1	The association of CREBRF variant rs373863828 with body composition in adult Samoans		1