Daniel E Weeks

List of Publications by Year
in descending order

267 papers	23,105 citations	10986 71 h-index	9103 144 g-index
292 all docs	292 docs citations	292 times ranked	22306 citing authors

#	Article	IF	Citations
1	Decreased DNA Methylation of RGMA is Associated with Intracranial Hypertension After Severe Traumatic Brain Injury: An Exploratory Epigenome-Wide Association Study. Neurocritical Care, 2022, 37, 26-37.	2.4	8
2	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
4	CREBRF missense variant rs373863828 has both direct and indirect effects on type 2 diabetes and fasting glucose in Polynesian peoples living in Samoa and Aotearoa New Zealand. BMJ Open Diabetes Research and Care, 2022, 10, e002275.	2.8	2
5	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
6	A loss-of-function IFNAR1 allele in Polynesia underlies severe viral diseases in homozygotes. Journal of Experimental Medicine, 2022, 219, .	8.5	28
7	The missense variant, rs373863828, in CREBRF plays a role in longitudinal changes in body mass index in Samoans. Obesity Research and Clinical Practice, 2022, 16, 220-227.	1.8	1
8	Post hoc power is not informative. Genetic Epidemiology, 2022, 46, 390-394.	1.3	11
9	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
10	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.	2.3	7
11	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.	3.1	3
12	ECHS1 disease in two unrelated families of Samoan descent: Common variant â€•rare disorder. American Journal of Medical Genetics, Part A, 2021, 185, 157-167.	1.2	13
13	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.	3.4	18
14	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. Translational Vision Science and Technology, 2021, 10, 29.	2.2	14
15	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
16	Robust, flexible, and scalable tests for Hardyâ€"Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
17	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.	2.5	7
18	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17

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19	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.	3.4	29
20	Acute Brain-Derived Neurotrophic Factor 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.	2.9	8
21	CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotypeâ€“genotype interaction. Bioinformatics, 2021, 37, 4764-4770.	4.1	0
22	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.	2.5	3
23	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. Advances in Experimental Medicine and Biology, 2021, 1256, 191-200.	1.6	6
24	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.	1.1	1
25	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration. JAMA Ophthalmology, 2021, 139, 1299.	2.5	29
26	Characterization of cerebrospinal fluid DNA methylation age during the acute recovery period following aneurysmal subarachnoid hemorrhage. , 2021, 1, .		3
27	Iron homeostasis pathway DNA methylation trajectories reveal a role for STEAP3 metalloreductase in patient outcomes after aneurysmal subarachnoid hemorrhage. , 2021, 1, .		13
28	ANGPT1 methylation and delayed cerebral ischemia in aneurysmal subarachnoid hemorrhage patients. , 2021, 1, .		1
29	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.	2.4	10
30	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
31	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.	21.4	146
32	A missense variant in CREBRF is associated with taller stature in Samoans. American Journal of Human Biology, 2020, 32, e23414.	1.6	15
33	Methylation Data Processing Protocol and Comparison of Blood and Cerebral Spinal Fluid Following Aneurysmal Subarachnoid Hemorrhage. Frontiers in Genetics, 2020, 11, 671.	2.3	8
34	Deep-learning-based prediction of late age-related macular degeneration progression. Nature Machine Intelligence, 2020, 2, 141-150.	16.0	79
35	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. Journal of Allergy and Clinical Immunology, 2020, 146, 671-675.	2.9	16
36	Genetic Variability in the Iron Homeostasis Pathway and Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. Neurocritical Care, 2020, 33, 749-758.	2.4	4

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37	Evolutionary history of modern Samoans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9458-9465.	7.1	14
38	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.	1.0	13
39	Linear mixed models for association analysis of quantitative traits with nextâ€generation sequencing data. Genetic Epidemiology, 2019, 43, 189-206.	1.3	5
40	Spinning convincing stories for both true and false association signals. Genetic Epidemiology, 2019, 43, 356-364.	1.3	7
41	Y chromosome mosaicism is associated with age-related macular degeneration. European Journal of Human Genetics, 2019, 27, 36-41.	2.8	49
42	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. Lancet Respiratory Medicine,the, 2019, 7, 336-346.	10.7	147
43	Genome-wide association study of maternal genetic effects and parent-of-origin effects on food allergy. Medicine (United States), 2018, 97, e0043.	1.0	18
44	Genome-wide analysis of disease progression in age-related macular degeneration. Human Molecular Genetics, 2018, 27, 929-940.	2.9	67
45	Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC Oral Health, 2018, 18, 98.	2.3	8
46	Re: â€œWidespread prevalence of a CREBRF variant among MÄ•ori and Pacific children is associated with weight and height in early childhoodâ€• International Journal of Obesity, 2018, 42, 1389-1391.	3.4	5
47	Discordant association of the CREBRF rs373863828 A allele with increased BMI and protection from type 2 diabetes in MÄ•ori and Pacific (Polynesian) people living in Aotearoa/New Zealand. Diabetologia, 2018, 61, 1603-1613.	6.3	61
48	Statistics for Xâ€chromosome associations. Genetic Epidemiology, 2018, 42, 539-550.	1.3	16
49	The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Research, 2018, 7, 1352.	1.6	1
50	The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Research, 2018, 7, 1352.	1.6	1
51	An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577.	2.9	53
52	Genetic risk models: Influence of model size on risk estimates and precision. Genetic Epidemiology, 2017, 41, 282-296.	1.3	4
53	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. Nature Communications, 2017, 8, 15608.	12.8	31
54	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. Genetics, 2017, 206, 119-133.	2.9	46

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55	A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for nextâ€generation sequencing. Genetic Epidemiology, 2017, 41, 18-34.	1.3	3
56	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. European Journal of Human Genetics, 2017, 25, 350-359.	2.8	4
57	Genetic pleiotropy between age-related macular degeneration and 16 complex diseases and traits. Genome Medicine, 2017, 9, 29.	8.2	52
58	Joint Analysis of Nuclear and Mitochondrial Variants in Age-Related Macular Degeneration Identifies Novel Loci TRPM1 and ABHD2/RLBP1. , 2017, 58, 4027.		21
59	Enhanced B Cell Alloantigen Presentation and Its Epigenetic Dysregulation in Liver Transplant Rejection. American Journal of Transplantation, 2016, 16, 497-508.	4.7	17
60	Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. Genetic Epidemiology, 2016, 40, 133-143.	1.3	12
61	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.	2.9	51
62	A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. Genetic Epidemiology, 2016, 40, 702-721.	1.3	10
63	A thrifty variant in CREBRF strongly influences body mass index in Samoans. Nature Genetics, 2016, 48, 1049-1054.	21.4	201
64	The impact of genotype calling errors on family-based studies. Scientific Reports, 2016, 6, 28323.	3.3	12
65	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. Genetic Epidemiology, 2016, 40, 161-171.	1.3	3
66	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	21.4	1,167
67	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. Human Heredity, 2015, 80, 126-138.	0.8	9
68	Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. Human Heredity, 2015, 80, 79-89.	0.8	0
69	Identification of epidermal growth factor receptor (EGFR) genetic variants that modify risk for head and neck squamous cell carcinoma. Cancer Letters, 2015, 357, 549-556.	7.2	16
70	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. Nature Communications, 2015, 6, 6304.	12.8	192
71	dbVOR: a database system for importing pedigree, phenotype and genotype data and exporting selected subsets. BMC Bioinformatics, 2015, 16, 91.	2.6	1
72	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. Genetics, 2015, 201, 1329-1339.	2.9	14

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73	Genetic MEâ€“a visualization application for merging and editing pedigrees for genetic studies. BMC Research Notes, 2015, 8, 241.	1.4	0
74	Predisposition to Childhood Otitis Media and Genetic Polymorphisms within the Toll-Like Receptor 4 (TLR4) Locus. PLoS ONE, 2015, 10, e0132551.	2.5	35
75	Endophenotypes for Age-Related Macular Degeneration: Extending Our Reach into the Preclinical Stages of Disease. Journal of Clinical Medicine, 2014, 3, 1335-1356.	2.4	11
76	Mega2: validated data-reformatting for linkage and association analyses. Source Code for Biology and Medicine, 2014, 9, 26.	1.7	11
77	Stratified randomization controls better for batch effects in 450K methylation analysis: a cautionary tale. Frontiers in Genetics, 2014, 5, 354.	2.3	43
78	Genetic-based prediction of disease traits: prediction is very difficult, especially about the futureÃ¢â‚¬Â. Frontiers in Genetics, 2014, 5, 162.	2.3	53
79	Generalized Functional Linear Models for Geneâ€Based Caseâ€Control Association Studies. Genetic Epidemiology, 2014, 38, 622-637.	1.3	22
80	Genome-Wide Association Study of Primary Dentition Pit-and-Fissure and Smooth Surface Caries. Caries Research, 2014, 48, 330-338.	2.0	38
81	Genome-Wide Association Study of Periodontal Health Measured by Probing Depth in Adults Ages 18â€“49 years. G3: Genes, Genomes, Genetics, 2014, 4, 307-314.	1.8	54
82	Prevalence of adiposity and associated cardiometabolic risk factors in the samoan genomeâ€wide association study. American Journal of Human Biology, 2014, 26, 491-501.	1.6	72
83	Rare and common variants in extracellular matrix gene Fibrillin 2 (FBN2) are associated with macular degeneration. Human Molecular Genetics, 2014, 23, 5827-5837.	2.9	52
84	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.	1.8	39
85	Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. Journal of Dental Research, 2013, 92, 32-37.	5.2	31
86	GWAS of Dental Caries Patterns in the Permanent Dentition. Journal of Dental Research, 2013, 92, 38-44.	5.2	77
87	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
88	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	21.4	158
89	ADCYAP1R1 and Asthma in Puerto Rican Children. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 584-588.	5.6	97
90	Genome-wide Association Studies of Pit-and-Fissure- and Smooth-surface Caries in Permanent Dentition. Journal of Dental Research, 2013, 92, 432-437.	5.2	61

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91	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, 364-373.	1.9	22
92	INSIG2 variants, dietary patterns and metabolic risk in Samoa. European Journal of Clinical Nutrition, 2013, 67, 101-107.	2.9	20
93	Abstract 1340: Identification of epidermal growth factor receptor (EGFR) polymorphisms that modify risk for squamous cell carcinoma of the head and neck (HNSCC).. , 2013, , .		0
94	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. International Journal of Epidemiology, 2012, 41, 250-262.	1.9	79
95	Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57.	2.3	69
96	Effects of Smoking and Genotype on the PSR Index of Periodontal Disease in Adults Aged 18â€“49. International Journal of Environmental Research and Public Health, 2012, 9, 2839-2850.	2.6	14
97	ASTN1 and alcohol dependence: Familyâ€based association analysis in multiplex alcohol dependence families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 445-455.	1.7	18
98	Common Variants in FTO Are Not Significantly Associated with Obesityâ€Related Phenotypes among Samoans of Polynesia. Annals of Human Genetics, 2012, 76, 17-24.	0.8	14
99	Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. Journal of Pediatrics, 2012, 160, 19-24.e4.	1.8	21
100	Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. BMC Oral Health, 2012, 12, 7.	2.3	35
101	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.	2.5	34
102	Enhanced genetic maps from family-based disease studies: population-specific comparisons. BMC Medical Genetics, 2011, 12, 15.	2.1	5
103	Evidence of association ofAPOEwith age-related macular degeneration - a pooled analysis of 15 studies. Human Mutation, 2011, 32, 1407-1416.	2.5	130
104	Variations in Apolipoprotein E Frequency With Age in a Pooled Analysis of a Large Group of Older People. American Journal of Epidemiology, 2011, 173, 1357-1364.	3.4	85
105	Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. Journal of Dental Research, 2011, 90, 1457-1462.	5.2	108
106	Coordinated Conditional Simulation with SLINK and SUP of Many Markers Linked or Associated to a Trait in Large Pedigrees. Human Heredity, 2011, 71, 126-134.	0.8	20
107	Role of African Ancestry and Geneâ€“Environment Interactions in Predicting Preterm Birth. Obstetrics and Gynecology, 2011, 118, 1081-1089.	2.4	19
108	Dissection of Chromosome 16p12 Linkage Peak Suggests a Possible Role forCACNG3Variants in Age-Related Macular Degeneration Susceptibility. , 2011, 52, 1748.		10

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109	NOD2 Gene Polymorphism rs2066844 Associates With Need for Combined Liverâ€“Intestine Transplantation in Children With Short-Gut Syndrome. American Journal of Gastroenterology, 2011, 106, 157-165.	0.4	44
110	Association tests using kernelâ€based measures of multiâ€locus genotype similarity between individuals. Genetic Epidemiology, 2010, 34, 213-221.	1.3	69
111	Genetic variants near TIMP3 and high-density lipoproteinâ€“associated loci influence susceptibility to age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7401-7406.	7.1	475
112	Interpretation of Genetic Association Studies: Markers with Replicated Highly Significant Odds Ratios May Be Poor Classifiers. PLoS Genetics, 2009, 5, e1000337.	3.5	211
113	Casaresâ€™ map function: no need for a â€˜correctedâ€™ Haldaneâ€™s map function. Genetica, 2009, 135, 305-307.	1.1	3
114	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	13
115	A tagging SNP in INSIG2 is associated with obesity-related phenotypes among Samoans. BMC Medical Genetics, 2009, 10, 143.	2.1	14
116	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	37
117	Susceptibility Loci for Adiposity Phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. Obesity, 2009, 17, 518-524.	3.0	28
118	Relationship uncertainty linkage statistics (RULS): affected relative pair statistics that model relationship uncertainty. Genetic Epidemiology, 2008, 32, 313-324.	1.3	6
119	Dopaminergic mutations: Withinâ€family association and linkage in multiplex alcohol dependence families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 517-526.	1.7	42
120	Robust Score Statistics for QTL Linkage Analysis. American Journal of Human Genetics, 2008, 82, 567-582.	6.2	9
121	A Whole Genome Linkage Scan Identifies Multiple Chromosomal Regions Influencing Adiposityâ€Related Traits among Samoans. Annals of Human Genetics, 2008, 72, 780-792.	0.8	33
122	Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. BMC Bioinformatics, 2008, 9, 317.	2.6	5
123	Genetic Variants in Major Histocompatibility Complex-Linked Genes Associate With Pediatric Liver Transplant Rejection. Gastroenterology, 2008, 135, 830-839.e10.	1.3	28
124	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.	0.2	4
125	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, 2169-2178.	4.2	29
126	C2 and CFB Genes in Age-Related Maculopathy and Joint Action with CFH and LOC387715 Genes. PLoS ONE, 2008, 3, e2199.	2.5	85

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127	Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13â€“15. Human Reproduction, 2007, 22, 717-728.	0.9	54
128	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, 1111-1113.	6.2	1
129	Two-dimensional linkage analyses of rheumatoid arthritis. BMC Proceedings, 2007, 1, S68.	1.6	4
130	The elusive goal of pedigree weights. Genetic Epidemiology, 2007, 31, 51-65.	1.3	17
131	A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. Genetic Epidemiology, 2007, 31, 417-430.	1.3	2
132	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	21.4	1,272
133	Genome-wide scan for adiposity-related phenotypes in adults from American Samoa. International Journal of Obesity, 2007, 31, 1832-1842.	3.4	41
134	CFH, ELOVL4, PLEKHA1 and LOC387715 genes and susceptibility to age-related maculopathy: AREDS and CHS cohorts and meta-analyses. Human Molecular Genetics, 2006, 15, 3206-3218.	2.9	152
135	Ordered Genotypes: An Extended ITO Method and a General Formula for Genetic Covariance. American Journal of Human Genetics, 2006, 78, 1035-1045.	6.2	7
136	The Khatri Sikh Diabetes Study (SDS): Study Design, Methodology, Sample Collection, and Initial Results. Human Biology, 2006, 78, 43-63.	0.2	33
137	Comparison of methods incorporating quantitative covariates into affected sib pair linkage analysis. Genetic Epidemiology, 2006, 30, 77-93.	1.3	6
138	Geneâ€dropping vs. empirical variance estimation for alleleâ€sharing linkage statistics. Genetic Epidemiology, 2006, 30, 652-665.	1.3	10
139	Treatment of Uninformative Families in Mean Allele Sharing Tests for Linkage. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article13.	0.6	0
140	Analysis of alcohol dependence phenotype in the COGA families using covariates to detect linkage. BMC Genetics, 2005, 6, S143.	2.7	18
141	A comparison between microsatellite and single-nucleotide polymorphism markers with respect to two measures of information content. BMC Genetics, 2005, 6, S27.	2.7	8
142	Mega2: data-handling for facilitating genetic linkage and association analyses. Bioinformatics, 2005, 21, 2556-2557.	4.1	138
143	Analysis of IMGSAC autism susceptibility loci: evidence for sex limited and parent of origin specific effects. Journal of Medical Genetics, 2005, 42, 132-137.	3.2	114
144	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.	2.9	143

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145	No Convincing Evidence of Linkage for Restless Legs Syndrome on Chromosome 9p. American Journal of Human Genetics, 2005, 76, 705-707.	6.2	15
146	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, 950-966.	6.2	165
147	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, 365-376.	6.2	200
148	Susceptibility Genes for Age-Related Maculopathy on Chromosome 10q26. American Journal of Human Genetics, 2005, 77, 389-407.	6.2	515
149	Meta-analysis of genome scans of age-related macular degeneration. Human Molecular Genetics, 2005, 14, 2257-2264.	2.9	224
150	Familial aggregation of endometriosis in a large pedigree of rhesus macaques. Human Reproduction, 2004, 19, 448-455.	0.9	88
151	Inflammatory bowel disease susceptibility loci defined by genome scan meta-analysis of 1952 affected relative pairs. Human Molecular Genetics, 2004, 13, 763-770.	2.9	219
152	Comparative Study of Multipoint Methods for Genotype Error Detection. Human Heredity, 2004, 58, 175-189.	0.8	17
153	Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. BMC Genetics, 2004, 5, 18.	2.7	48
154	A genome-wide screen for susceptibility loci in ankylosing spondylitis. Arthritis and Rheumatism, 2004, 41, 588-595.	6.7	117
155	Efficient Simulation ofP Values for Linkage Analysis. Genetic Epidemiology, 2004, 26, 88-96.	1.3	10
156	No â€œBiasâ€•Toward the Null Hypothesis in Most Conventional Multipoint Nonparametric Linkage Analyses. American Journal of Human Genetics, 2004, 75, 716-718.	6.2	6
157	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, 174-189.	6.2	174
158	Distribution of genome-wide linkage disequilibrium based on microsatellite loci in the Samoan population. Human Genomics, 2004, 1, 327.	2.9	23
159	Linkage analysis of adult height with parent-of-origin effects in the Framingham Heart Study. BMC Genetics, 2003, 4, S76.	2.7	18
160	Interleukin 10 polymorphisms in ankylosing spondylitis. Genes and Immunity, 2003, 4, 74-76.	4.1	32
161	A Genome-Wide Scan for Loci Affecting Normal Adult Height in the Framingham Heart Study. Human Heredity, 2003, 55, 191-201.	0.8	25
162	A Tale of Two Genotypes: Consistency between Two High-Throughput Genotyping Centers. Genome Research, 2002, 12, 430-435.	5.5	40

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163	Evidence for an inflammatory bowel disease locus on chromosome 3p26: linkage, transmission/disequilibrium and partitioning of linkage. Human Molecular Genetics, 2002, 11, 2599-2606.	2.9	32
164	A pooled case-control study of the apolipoprotein E (APOE) gene in age-related maculopathy. Ophthalmic Genetics, 2002, 23, 209-223.	1.2	136
165	Statistics for Nonparametric Linkage Analysis of X-Linked Traits in General Pedigrees. American Journal of Human Genetics, 2002, 70, 181-191.	6.2	4
166	Human leptin locus (LEP) alleles and BMI in Samoans. International Journal of Obesity, 2002, 26, 783-788.	3.4	13
167	The Genetic Epidemiology of Spontaneous Endometriosis in the Rhesus Monkey. Annals of the New York Academy of Sciences, 2002, 955, 233-238.	3.8	23
168	Pedigree Selection and Information Content. Current Protocols in Human Genetics, 2001, 29, Unit 1.2.	3.5	1
169	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, 682-692.	3.3	132
170	Whole-Genome Screening in Ankylosing Spondylitis: Evidence of Non-MHC Genetic-Susceptibility Loci. American Journal of Human Genetics, 2001, 68, 918-926.	6.2	231
171	A Survey of Affected-Sibship Statistics for Nonparametric Linkage Analysis. American Journal of Human Genetics, 2001, 69, 179-190.	6.2	36
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