# Daniel E Weeks

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 267 papers | 23,105 citations | 12597 71 h-index | 10679 143 g-index |
| 292 all docs | 292 docs citations | 292 times ranked | 24532 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. | 1.2 | 8 |
| 2 | Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084. | 3.0 | 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. | 2.6 | 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. | 1.2 | 2 |
| 5 | Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579. | 4.7 | 36 |
| 6 | A loss-of-function IFNAR1 allele in Polynesia underlies severe viral diseases in homozygotes. Journal of Experimental Medicine, 2022, 219, . | 4.2 | 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. | 0.8 | 1 |
| 8 | Post hoc power is not informative. Genetic Epidemiology, 2022, 46, 390-394. | 0.6 | 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. | 1.3 | 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. | 1.1 | 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. | 1.8 | 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. | 0.7 | 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. | 1.6 | 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. | 1.1 | 14 |
| 15 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299. | 13.7 | 1,069 |
| 16 | Robust, flexible, and scalable tests for Hardyâ€"Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, . | 1.2 | 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. | 1.1 | 7 |
| 18 | Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182. | 5.8 | 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. | 1.6 | 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. | 1.4 | 8 |
| 21 | CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotypeâ€“genotype interaction. Bioinformatics, 2021, 37, 4764-4770. | 1.8 | 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. | 1.1 | 3 |
| 23 | AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. Advances in Experimental Medicine and Biology, 2021, 1256, 191-200. | 0.8 | 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. | 0.5 | 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. | 1.4 | 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. | 1.2 | 10 |
| 30 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768. | 13.7 | 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. | 9.4 | 146 |
| 32 | A missense variant in CREBRF is associated with taller stature in Samoans. American Journal of Human Biology, 2020, 32, e23414. | 0.8 | 15 |
| 33 | Methylation Data Processing Protocol and Comparison of Blood and Cerebral Spinal Fluid Following Aneurysmal Subarachnoid Hemorrhage. Frontiers in Genetics, 2020, 11, 671. | 1.1 | 8 |
| 34 | Deep-learning-based prediction of late age-related macular degeneration progression. Nature Machine Intelligence, 2020, 2, 141-150. | 8.3 | 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. | 1.5 | 16 |
| 36 | Genetic Variability in the Iron Homeostasis Pathway and Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. Neurocritical Care, 2020, 33, 749-758. | 1.2 | 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. | 3.3 | 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. | 0.5 | 13 |
| 39 | Linear mixed models for association analysis of quantitative traits with nextâ€generation sequencing data. Genetic Epidemiology, 2019, 43, 189-206. | 0.6 | 5 |
| 40 | Spinning convincing stories for both true and false association signals. Genetic Epidemiology, 2019, 43, 356-364. | 0.6 | 7 |
| 41 | Y chromosome mosaicism is associated with age-related macular degeneration. European Journal of Human Genetics, 2019, 27, 36-41. | 1.4 | 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. | 5.2 | 147 |
| 43 | Genome-wide association study of maternal genetic effects and parent-of-origin effects on food allergy. Medicine (United States), 2018, 97, e0043. | 0.4 | 18 |
| 44 | Genome-wide analysis of disease progression in age-related macular degeneration. Human Molecular Genetics, 2018, 27, 929-940. | 1.4 | 67 |
| 45 | Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC Oral Health, 2018, 18, 98. | 0.8 | 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. | 1.6 | 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. | 2.9 | 61 |
| 48 | Statistics for Xâ€chromosome associations. Genetic Epidemiology, 2018, 42, 539-550. | 0.6 | 16 |
| 49 | The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Research, 2018, 7, 1352. | 0.8 | 1 |
| 50 | The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Research, 2018, 7, 1352. | 0.8 | 1 |
| 51 | An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577. | 1.5 | 53 |
| 52 | Genetic risk models: Influence of model size on risk estimates and precision. Genetic Epidemiology, 2017, 41, 282-296. | 0.6 | 4 |
| 53 | Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. Nature Communications, 2017, 8, 15608. | 5.8 | 31 |
| 54 | Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. Genetics, 2017, 206, 119-133. | 1.2 | 46 |

| # | Article | IF | Citations |
|---|---|---|---|
| 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. | 0.6 | 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. | 1.4 | 4 |
| 57 | Genetic pleiotropy between age-related macular degeneration and 16 complex diseases and traits. Genome Medicine, 2017, 9, 29. | 3.6 | 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. | 2.6 | 17 |
| 60 | Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. Genetic Epidemiology, 2016, 40, 133-143. | 0.6 | 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. | 1.5 | 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. | 0.6 | 10 |
| 63 | A thrifty variant in CREBRF strongly influences body mass index in Samoans. Nature Genetics, 2016, 48, 1049-1054. | 9.4 | 201 |
| 64 | The impact of genotype calling errors on family-based studies. Scientific Reports, 2016, 6, 28323. | 1.6 | 12 |
| 65 | A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. Genetic Epidemiology, 2016, 40, 161-171. | 0.6 | 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. | 9.4 | 1,167 |
| 67 | Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. Human Heredity, 2015, 80, 126-138. | 0.4 | 9 |
| 68 | Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. Human Heredity, 2015, 80, 79-89. | 0.4 | 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. | 3.2 | 16 |
| 70 | Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. Nature Communications, 2015, 6, 6304. | 5.8 | 192 |
| 71 | dbVOR: a database system for importing pedigree, phenotype and genotype data and exporting selected subsets. BMC Bioinformatics, 2015, 16, 91. | 1.2 | 1 |
| 72 | Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. Genetics, 2015, 201, 1329-1339. | 1.2 | 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. | 0.6 | 0 |
| 74 | Predisposition to Childhood Otitis Media and Genetic Polymorphisms within the Toll-Like Receptor 4 (TLR4) Locus. PLoS ONE, 2015, 10, e0132551. | 1.1 | 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. | 1.0 | 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. | 1.1 | 43 |
| 78 | Genetic-based prediction of disease traits: prediction is very difficult, especially about the futureÃ¢â‚¬Â. Frontiers in Genetics, 2014, 5, 162. | 1.1 | 53 |
| 79 | Generalized Functional Linear Models for Geneâ€Based Caseâ€Control Association Studies. Genetic Epidemiology, 2014, 38, 622-637. | 0.6 | 22 |
| 80 | Genome-Wide Association Study of Primary Dentition Pit-and-Fissure and Smooth Surface Caries. Caries Research, 2014, 48, 330-338. | 0.9 | 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. | 0.8 | 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. | 0.8 | 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. | 1.4 | 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. | 0.9 | 39 |
| 85 | Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. Journal of Dental Research, 2013, 92, 32-37. | 2.5 | 31 |
| 86 | GWAS of Dental Caries Patterns in the Permanent Dentition. Journal of Dental Research, 2013, 92, 38-44. | 2.5 | 77 |
| 87 | Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439. | 9.4 | 687 |
| 88 | Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379. | 9.4 | 158 |
| 89 | ADCYAP1R1 and Asthma in Puerto Rican Children. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 584-588. | 2.5 | 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. | 2.5 | 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. | 0.9 | 22 |
| 92 | INSIG2 variants, dietary patterns and metabolic risk in Samoa. European Journal of Clinical Nutrition, 2013, 67, 101-107. | 1.3 | 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. | 0.9 | 79 |
| 95 | Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57. | 0.8 | 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. | 1.2 | 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. | 1.1 | 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. | 0.3 | 14 |
| 99 | Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. Journal of Pediatrics, 2012, 160, 19-24.e4. | 0.9 | 21 |
| 100 | Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. BMC Oral Health, 2012, 12, 7. | 0.8 | 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. | 1.1 | 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. | 1.1 | 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. | 1.6 | 85 |
| 105 | Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. Journal of Dental Research, 2011, 90, 1457-1462. | 2.5 | 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. | 0.4 | 20 |
| 107 | Role of African Ancestry and Geneâ€“Environment Interactions in Predicting Preterm Birth. Obstetrics and Gynecology, 2011, 118, 1081-1089. | 1.2 | 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. | 0.2 | 44 |
| 110 | Association tests using kernelâ€based measures of multiâ€locus genotype similarity between individuals. Genetic Epidemiology, 2010, 34, 213-221. | 0.6 | 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. | 3.3 | 475 |
| 112 | Interpretation of Genetic Association Studies: Markers with Replicated Highly Significant Odds Ratios May Be Poor Classifiers. PLoS Genetics, 2009, 5, e1000337. | 1.5 | 211 |
| 113 | Casaresâ€™ map function: no need for a â€˜correctedâ€™ Haldaneâ€™s map function. Genetica, 2009, 135, 305-307. | 3.0 | 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. | 1.5 | 28 |
| 118 | Relationship uncertainty linkage statistics (RULS): affected relative pair statistics that model relationship uncertainty. Genetic Epidemiology, 2008, 32, 313-324. | 0.6 | 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. | 1.1 | 42 |
| 120 | Robust Score Statistics for QTL Linkage Analysis. American Journal of Human Genetics, 2008, 82, 567-582. | 2.6 | 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. | 0.3 | 33 |
| 122 | Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. BMC Bioinformatics, 2008, 9, 317. | 1.2 | 5 |
| 123 | Genetic Variants in Major Histocompatibility Complex-Linked Genes Associate With Pediatric Liver Transplant Rejection. Gastroenterology, 2008, 135, 830-839.e10. | 0.6 | 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. | 0.4 | 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. | 2.0 | 29 |
| 126 | C2 and CFB Genes in Age-Related Maculopathy and Joint Action with CFH and LOC387715 Genes. PLoS ONE, 2008, 3, e2199. | 1.1 | 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. | 0.4 | 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. | 2.6 | 1 |
| 129 | Two-dimensional linkage analyses of rheumatoid arthritis. BMC Proceedings, 2007, 1, S68. | 1.8 | 4 |
| 130 | The elusive goal of pedigree weights. Genetic Epidemiology, 2007, 31, 51-65. | 0.6 | 17 |
| 131 | A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. Genetic Epidemiology, 2007, 31, 417-430. | 0.6 | 2 |
| 132 | Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328. | 9.4 | 1,272 |
| 133 | Genome-wide scan for adiposity-related phenotypes in adults from American Samoa. International Journal of Obesity, 2007, 31, 1832-1842. | 1.6 | 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. | 1.4 | 152 |
| 135 | Ordered Genotypes: An Extended ITO Method and a General Formula for Genetic Covariance. American Journal of Human Genetics, 2006, 78, 1035-1045. | 2.6 | 7 |
| 136 | The Khatri Sikh Diabetes Study (SDS): Study Design, Methodology, Sample Collection, and Initial Results. Human Biology, 2006, 78, 43-63. | 0.4 | 33 |
| 137 | Comparison of methods incorporating quantitative covariates into affected sib pair linkage analysis. Genetic Epidemiology, 2006, 30, 77-93. | 0.6 | 6 |
| 138 | Gene-dropping vs. empirical variance estimation for allele-sharing linkage statistics. Genetic Epidemiology, 2006, 30, 652-665. | 0.6 | 10 |
| 139 | Treatment of Uninformative Families in Mean Allele Sharing Tests for Linkage. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article13. | 0.2 | 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. | 1.8 | 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. | 1.5 | 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. | 1.4 | 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. | 2.6 | 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. | 2.6 | 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. | 2.6 | 200 |
| 148 | Susceptibility Genes for Age-Related Maculopathy on Chromosome 10q26. American Journal of Human Genetics, 2005, 77, 389-407. | 2.6 | 515 |
| 149 | Meta-analysis of genome scans of age-related macular degeneration. Human Molecular Genetics, 2005, 14, 2257-2264. | 1.4 | 224 |
| 150 | Familial aggregation of endometriosis in a large pedigree of rhesus macaques. Human Reproduction, 2004, 19, 448-455. | 0.4 | 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. | 1.4 | 219 |
| 152 | Comparative Study of Multipoint Methods for Genotype Error Detection. Human Heredity, 2004, 58, 175-189. | 0.4 | 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. | 0.6 | 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. | 2.6 | 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. | 2.6 | 174 |
| 158 | Distribution of genome-wide linkage disequilibrium based on microsatellite loci in the Samoan population. Human Genomics, 2004, 1, 327. | 1.4 | 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. | 2.2 | 32 |
| 161 | A Genome-Wide Scan for Loci Affecting Normal Adult Height in the Framingham Heart Study. Human Heredity, 2003, 55, 191-201. | 0.4 | 25 |
| 162 | A Tale of Two Genotypes: Consistency between Two High-Throughput Genotyping Centers. Genome Research, 2002, 12, 430-435. | 2.4 | 40 |

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|---|---|---|---|
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