Daniel E Weeks

List of Publications by Year
in descending order

267 papers	23,105 citations	10956 71 h-index	9311 143 g-index
292 all docs	292 docs citations	292 times ranked	22306 citing authors

#	Article	IF	Citations
1	PedCheck: A Program for Identification of Genotype Incompatibilities in Linkage Analysis. American Journal of Human Genetics, 1998, 63, 259-266.	2.6	1,923
2	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	9.4	1,272
3	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
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
5	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	9.4	687
6	Localization of an ataxia-telangiectasia gene to chromosome 11q22â€“23. Nature, 1988, 336, 577-580.	13.7	677
7	Programs for pedigree analysis: Mendel, Fisher, and dGene. Genetic Epidemiology, 1988, 5, 471-472.	0.6	562
8	Susceptibility Genes for Age-Related Maculopathy on Chromosome 10q26. American Journal of Human Genetics, 2005, 77, 389-407.	2.6	515
9	The VITESSE algorithm for rapid exact multilocus linkage analysis via genotype setâ€“recoding and fuzzy inheritance. Nature Genetics, 1995, 11, 402-408.	9.4	514
10	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, 571-578.	1.4	492
11	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
12	A Genomewide Screen for Autism: Strong Evidence for Linkage to Chromosomes 2q, 7q, and 16p. American Journal of Human Genetics, 2001, 69, 570-581.	2.6	439
13	The affected-pedigree-member method of linkage analysis. American Journal of Human Genetics, 1988, 42, 315-26.	2.6	385
14	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
15	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, 5918-5921.	3.3	364
16	A Quantitative-Trait Locus on Chromosome 6p Influences Different Aspects of Developmental Dyslexia. American Journal of Human Genetics, 1999, 64, 146-156.	2.6	260
17	Similarity of DNA Fingerprints Due to Chance and Relatedness. Human Heredity, 1993, 43, 45-52.	0.4	242
18	A molecular defect in loricrin, the major component of the cornified cell envelope, underlies Vohwinkel's syndrome. Nature Genetics, 1996, 13, 70-77.	9.4	236

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19	Whole-Genome Screening in Ankylosing Spondylitis: Evidence of Non-MHC Genetic-Susceptibility Loci. American Journal of Human Genetics, 2001, 68, 918-926.	2.6	231
20	Meta-analysis of genome scans of age-related macular degeneration. Human Molecular Genetics, 2005, 14, 2257-2264.	1.4	224
21	Polygenic disease: methods for mapping complex disease traits. Trends in Genetics, 1995, 11, 513-519.	2.9	221
22	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
23	Interpretation of Genetic Association Studies: Markers with Replicated Highly Significant Odds Ratios May Be Poor Classifiers. PLoS Genetics, 2009, 5, e1000337.	1.5	211
24	Linkage mapping of dopaâ€“responsive dystonia (DRD) to chromosome 14q. Nature Genetics, 1993, 5, 386-391.	9.4	202
25	A thrifty variant in CREBRF strongly influences body mass index in Samoans. Nature Genetics, 2016, 48, 1049-1054.	9.4	201
26	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
27	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
28	Multipoint Estimation of Identity-by-Descent Probabilities at Arbitrary Positions among Marker Loci on General Pedigrees. Human Heredity, 2001, 52, 121-131.	0.4	188
29	High-Density Genome Scan in Crohn Disease Shows Confirmed Linkage to Chromosome 14q11-12. American Journal of Human Genetics, 2000, 66, 1857-1862.	2.6	182
30	Two-Sex Models: Chaos, Extinction, and Other Dynamic Consequences of Sex. American Naturalist, 1986, 128, 707-735.	1.0	177
31	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
32	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, 2077-2085.	1.4	172
33	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
34	Further characterization of the autism susceptibility locus AUTS1 on chromosome 7q. Human Molecular Genetics, 2001, 10, 973-982.	1.4	159
35	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	9.4	158
36	A gene for Hirschsprung disease (megacolon) in the pericentromeric region of human chromosome 10. Nature Genetics, 1993, 4, 351-356.	9.4	154

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37	Linkage and Association between Inflammatory Bowel Disease and a Locus on Chromosome 12. American Journal of Human Genetics, 1998, 63, 95-100.	2.6	152
38	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
39	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
40	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
41	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
42	A Juvenile-Onset, Progressive Cataract Locus on Chromosome 3q21-q22 Is Associated with a Missense Mutation in the Beaded Filament Structural Proteinâ€“2. American Journal of Human Genetics, 2000, 66, 1426-1431.	2.6	140
43	Serotonin transporter (5-HTT) and ?-aminobutyric acid receptor subunit ?3 (GABRB3) gene polymorphisms are not associated with autism in the IMGSA families. , 1999, 88, 492-496.		139
44	Mega2: data-handling for facilitating genetic linkage and association analyses. Bioinformatics, 2005, 21, 2556-2557.	1.8	138
45	A pooled case-control study of the apolipoprotein E (APOE) gene in age-related maculopathy. Ophthalmic Genetics, 2002, 23, 209-223.	0.5	136
46	True and False Positive Peaks in Genomewide Scans: Applications of Length-Biased Sampling to Linkage Mapping. American Journal of Human Genetics, 1997, 61, 430-438.	2.6	132
47	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.	1.7	132
48	Evidence of association ofAPOEwith age-related macular degeneration - a pooled analysis of 15 studies. Human Mutation, 2011, 32, 1407-1416.	1.1	130
49	Measuring the inflation of the lod score due to its maximization over model parameter values in human linkage analysis. Genetic Epidemiology, 1990, 7, 237-243.	0.6	127
50	A full genome scan for age-related maculopathy. Human Molecular Genetics, 2000, 9, 1329-1349.	1.4	123
51	Computer programs for multilocus haplotyping of general pedigrees. American Journal of Human Genetics, 1995, 56, 1506-7.	2.6	120
52	A genome-wide screen for susceptibility loci in ankylosing spondylitis. Arthritis and Rheumatism, 2004, 41, 588-595.	6.7	117
53	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
54	Mapping of a gene determining tuberous sclerosis to human chromosome 11q14î—¸11q23. Genomics, 1990, 6, 105-114.	1.3	109

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55	Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. Journal of Dental Research, 2011, 90, 1457-1462.	2.5	108
56	Linkage and association studies of the relationship between endometriosis and genes encoding the detoxification enzymes GSTM1, GSTT1 and CYP1A1. Molecular Human Reproduction, 2001, 7, 1073-1078.	1.3	99
57	ADCYAP1R1 and Asthma in Puerto Rican Children. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 584-588.	2.5	97
58	Nonparametric simulation-based statistics for detecting linkage in general pedigrees. American Journal of Human Genetics, 1996, 58, 867-80.	2.6	97
59	Comparison of Nonparametric Statistics for Detection of Linkage in Nuclear Families: Single-Marker Evaluation. American Journal of Human Genetics, 1997, 61, 1431-1444.	2.6	94
60	Type 2 Diabetes and Three Calpain-10 Gene Polymorphisms in Samoans: No Evidence of Association. American Journal of Human Genetics, 2001, 69, 1236-1244.	2.6	92
61	Mitochondrial Neurogastrointestinal Encephalomyopathy Syndrome Maps to Chromosome 22q13.32-qter. American Journal of Human Genetics, 1998, 63, 526-533.	2.6	91
62	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, 124-131.	2.8	89
63	Familial aggregation of endometriosis in a large pedigree of rhesus macaques. Human Reproduction, 2004, 19, 448-455.	0.4	88
64	The IBD2 Locus Shows Linkage Heterogeneity between Ulcerative Colitis and Crohn Disease. American Journal of Human Genetics, 2000, 67, 1605-1610.	2.6	85
65	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
66	C2 and CFB Genes in Age-Related Maculopathy and Joint Action with CFH and LOC387715 Genes. PLoS ONE, 2008, 3, e2199.	1.1	85
67	Polymorphisms of the CYP2D6 gene increase susceptibility to ankylosing spondylitis. Human Molecular Genetics, 2000, 9, 1563-1566.	1.4	79
68	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
69	Deep-learning-based prediction of late age-related macular degeneration progression. Nature Machine Intelligence, 2020, 2, 141-150.	8.3	79
70	GWAS of Dental Caries Patterns in the Permanent Dentition. Journal of Dental Research, 2013, 92, 38-44.	2.5	77
71	A multilocus extension of the affected-pedigree-member method of linkage analysis. American Journal of Human Genetics, 1992, 50, 859-68.	2.6	77
72	Assessment of Chronic Î³ Radiosensitivity as an in Vitro Assay for Heterozygote Identification of Ataxia-Telangiectasia. Radiation Research, 1991, 128, 90.	0.7	74

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73	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
74	A genome-wide screen for susceptibility loci in ankylosing spondylitis. , 1998, 41, 588.		71
75	Influence of the HLA-DRB1 locus on susceptibility and severity in rheumatoid arthritis. QJM - Monthly Journal of the Association of Physicians, 1996, 89, 821-830.	0.2	70
76	Association tests using kernelâ€based measures of multiâ€locus genotype similarity between individuals. Genetic Epidemiology, 2010, 34, 213-221.	0.6	69
77	Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57.	0.8	69
78	Genome-wide analysis of disease progression in age-related macular degeneration. Human Molecular Genetics, 2018, 27, 929-940.	1.4	67
79	Two-locus models of disease: comparison of likelihood and nonparametric linkage methods. American Journal of Human Genetics, 1993, 53, 908-15.	2.6	65
80	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, 80-87.	2.6	64
81	Preliminary ranking procedures for multilocus ordering. Genomics, 1987, 1, 236-242.	1.3	63
82	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
83	Discordant association of the CREBRF rs373863828 A allele with increased BMI and protection from type 2 diabetes in MÄori and Pacific (Polynesian) people living in Aotearoa/New Zealand. Diabetologia, 2018, 61, 1603-1613.	2.9	61
84	Association between endometriosis and N-acetyl transferase 2 polymorphisms in a UK population. Molecular Human Reproduction, 2001, 7, 1079-1083.	1.3	54
85	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
86	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
87	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
88	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
89	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
90	Genetic pleiotropy between age-related macular degeneration and 16 complex diseases and traits. Genome Medicine, 2017, 9, 29.	3.6	52

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91	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
92	Y chromosome mosaicism is associated with age-related macular degeneration. European Journal of Human Genetics, 2019, 27, 36-41.	1.4	49
93	Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. BMC Genetics, 2004, 5, 18.	2.7	48
94	An Optimal Algorithm for Automatic Genotype Elimination. American Journal of Human Genetics, 1999, 65, 1733-1740.	2.6	47
95	Magnetic resonance imaging to assess familial risk in relatives of women with endometriosis. Lancet, The, 1998, 352, 1440-1441.	6.3	46
96	Affected sib-pair analysis in endometriosis. Human Reproduction Update, 2001, 7, 411-418.	5.2	46
97	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. Genetics, 2017, 206, 119-133.	1.2	46
98	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
99	Stratified randomization controls better for batch effects in 450K methylation analysis: a cautionary tale. Frontiers in Genetics, 2014, 5, 354.	1.1	43
100	Dopaminergic mutations: Within‐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
101	Genome-wide scan for adiposity-related phenotypes in adults from American Samoa. International Journal of Obesity, 2007, 31, 1832-1842.	1.6	41
102	A Tale of Two Genotypes: Consistency between Two High-Throughput Genotyping Centers. Genome Research, 2002, 12, 430-435.	2.4	40
103	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
104	Multipoint Mapping under Genetic Interference. Human Heredity, 1993, 43, 86-97.	0.4	38
105	Genome-Wide Association Study of Primary Dentition Pit-and-Fissure and Smooth Surface Caries. Caries Research, 2014, 48, 330-338.	0.9	38
106	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
107	A Survey of Affected-Sibship Statistics for Nonparametric Linkage Analysis. American Journal of Human Genetics, 2001, 69, 179-190.	2.6	36
108	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36

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109	Efficient computation of lod scores: genotype elimination, genotype redefinition, and hybrid maximum likelihood algorithms. Annals of Human Genetics, 1989, 53, 67-83.	0.3	35
110	Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. BMC Oral Health, 2012, 12, 7.	0.8	35
111	Predisposition to Childhood Otitis Media and Genetic Polymorphisms within the Toll-Like Receptor 4 (TLR4) Locus. PLoS ONE, 2015, 10, e0132551.	1.1	35
112	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
113	A primary linkage map of the human chromosome 11q22â€“23 region. Genomics, 1990, 6, 316-323.	1.3	33
114	The gene for hereditary progressive dystonia with marked diurnal fluctuation maps to chromosome 14q. Annals of Neurology, 1995, 37, 405-408.	2.8	33
115	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, 990-993.	1.3	33
116	The Khatri Sikh Diabetes Study (SDS): Study Design, Methodology, Sample Collection, and Initial Results. Human Biology, 2006, 78, 43-63.	0.4	33
117	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
118	Evidence for an inflammatory bowel disease locus on chromosome 3p26: linkage, transmission/disequilibrium and partitioning of linkage. Human Molecular Genetics, 2002, 11, 2599-2606.	1.4	32
119	Interleukin 10 polymorphisms in ankylosing spondylitis. Genes and Immunity, 2003, 4, 74-76.	2.2	32
120	Efficient strategies for genomic searching using the affected-pedigree-member method of linkage analysis. American Journal of Human Genetics, 1994, 54, 544-52.	2.6	32
121	Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. Journal of Dental Research, 2013, 92, 32-37.	2.5	31
122	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. Nature Communications, 2017, 8, 15608.	5.8	31
123	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
124	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
125	Haplotyping Algorithms. , 1996, , 89-110.		29
126	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

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127	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
128	Genetic Variants in Major Histocompatibility Complex-Linked Genes Associate With Pediatric Liver Transplant Rejection. Gastroenterology, 2008, 135, 830-839.e10.	0.6	28
129	Susceptibility Loci for Adiposity Phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. Obesity, 2009, 17, 518-524.	1.5	28
130	A loss-of-function IFNAR1 allele in Polynesia underlies severe viral diseases in homozygotes. Journal of Experimental Medicine, 2022, 219, .	4.2	28
131	Detection of genetic interference: simulation studies and mouse data.. Genetics, 1994, 136, 1217-1226.	1.2	27
132	The Complexity of Linkage Analysis with Neural Networks. Human Heredity, 2001, 51, 169-176.	0.4	26
133	A Genome-Wide Scan for Loci Affecting Normal Adult Height in the Framingham Heart Study. Human Heredity, 2003, 55, 191-201.	0.4	25
134	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
135	The Genetic Epidemiology of Spontaneous Endometriosis in the Rhesus Monkey. Annals of the New York Academy of Sciences, 2002, 955, 233-238.	1.8	23
136	Distribution of genome-wide linkage disequilibrium based on microsatellite loci in the Samoan population. Human Genomics, 2004, 1, 327.	1.4	23
137	Trials, Tribulations, and Triumphs of the EM Algorithm in Pedigree Analysis. Mathematical Medicine and Biology, 1989, 6, 209-232.	0.8	22
138	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
139	Generalized Functional Linear Models for Geneâ€Based Caseâ€Control Association Studies. Genetic Epidemiology, 2014, 38, 622-637.	0.6	22
140	Mutational Mechanisms for Generating Microsatellite Allele-Frequency Distributions: An Analysis of 4,558 Markers. American Journal of Human Genetics, 1998, 62, 1260-1262.	2.6	21
141	Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. Journal of Pediatrics, 2012, 160, 19-24.e4.	0.9	21
142	Joint Analysis of Nuclear and Mitochondrial Variants in Age-Related Macular Degeneration Identifies Novel Loci TRPM1 and ABHD2/RLBP1. , 2017, 58, 4027.		21
143	Discovery of Cancer Susceptibility Genes: Study Designs, Analytic Approaches, and Trends in Technology. Journal of the National Cancer Institute Monographs, 1999, 1999, 1-16.	0.9	20
144	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, 223-231.	0.8	20

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145	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
146	INSIG2 variants, dietary patterns and metabolic risk in Samoa. European Journal of Clinical Nutrition, 2013, 67, 101-107.	1.3	20
147	Role of African Ancestry and Geneâ€"Environment Interactions in Predicting Preterm Birth. Obstetrics and Gynecology, 2011, 118, 1081-1089.	1.2	19
148	Linkage analysis of adult height with parent-of-origin effects in the Framingham Heart Study. BMC Genetics, 2003, 4, S76.	2.7	18
149	Analysis of alcohol dependence phenotype in the COGA families using covariates to detect linkage. BMC Genetics, 2005, 6, S143.	2.7	18
150	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
151	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
152	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
153	The Affected-Pedigree-Member Method: Power to Detect Linkage. Human Heredity, 1995, 45, 13-24.	0.4	17
154	Use of MRI in genetic studies of endometriosis. , 1997, 71, 371-372.		17
155	Comparative Study of Multipoint Methods for Genotype Error Detection. Human Heredity, 2004, 58, 175-189.	0.4	17
156	The elusive goal of pedigree weights. Genetic Epidemiology, 2007, 31, 51-65.	0.6	17
157	Enhanced B Cell Alloantigen Presentation and Its Epigenetic Dysregulation in Liver Transplant Rejection. American Journal of Transplantation, 2016, 16, 497-508.	2.6	17
158	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
159	Molecular genetic investigations of autism. Journal of Autism and Developmental Disorders, 1998, 28, 427-437.	1.7	16
160	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
161	Statistics for Xâ€chromosome associations. Genetic Epidemiology, 2018, 42, 539-550.	0.6	16
162	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

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163	Detection of tandem duplications and implications for linkage analysis. American Journal of Human Genetics, 1994, 54, 1110-21.	2.6	16
164	No Convincing Evidence of Linkage for Restless Legs Syndrome on Chromosome 9p. American Journal of Human Genetics, 2005, 76, 705-707.	2.6	15
165	A missense variant in CREBRF is associated with taller stature in Samoans. American Journal of Human Biology, 2020, 32, e23414.	0.8	15
166	A tagging SNP in INSIG2 is associated with obesity-related phenotypes among Samoans. BMC Medical Genetics, 2009, 10, 143.	2.1	14
167	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
168	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
169	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
170	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
171	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
172	Assessment of chronic gamma radiosensitivity as an in vitro assay for heterozygote identification of ataxia-telangiectasia. Radiation Research, 1991, 128, 90-9.	0.7	14
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