Eleanor Feingold

List of Publications by Year
in descending order

193 papers	9,109 citations	61984 43 h-index	54911 84 g-index
201 all docs	201 docs citations	201 times ranked	14303 citing authors

#	Article	IF	Citations
1	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	21.4	834
2	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
3	Comprehensive literature review and statistical considerations for microarray meta-analysis. Nucleic Acids Research, 2012, 40, 3785-3799.	14.5	427
4	Peripheral Blood Mononuclear Cell Gene Expression Profiles Predict Poor Outcome in Idiopathic Pulmonary Fibrosis. Science Translational Medicine, 2013, 5, 205ra136.	12.4	242
5	Gaussian models for genetic linkage analysis using complete high-resolution maps of identity by descent. American Journal of Human Genetics, 1993, 53, 234-51.	6.2	212
6	Genome-wide association study of Alzheimer's disease. Translational Psychiatry, 2012, 2, e117-e117.	4.8	209
7	Genome-wide mapping of global-to-local genetic effects on human facial shape. Nature Genetics, 2018, 50, 414-423.	21.4	205
8	Decreased expression of miRâ€125b and miRâ€100 in oral cancer cells contributes to malignancy. Genes Chromosomes and Cancer, 2009, 48, 569-582.	2.8	203
9	Characterization of susceptible chiasma configurations that increase the risk for maternal nondisjunction of chromosome 21. Human Molecular Genetics, 1997, 6, 1391-1399.	2.9	185
10	Non-disjunction in human sperm: evidence for an effect of increasing paternal age. Human Molecular Genetics, 1995, 4, 2227-2232.	2.9	183
11	A multi-ethnic genome-wide association study identifies novel loci for non-syndromic cleft lip with or without cleft palate on 2p24.2, 17q23 and 19q13. Human Molecular Genetics, 2016, 25, ddw104.	2.9	163
12	Comprehensive literature review and statistical considerations for GWAS meta-analysis. Nucleic Acids Research, 2012, 40, 3777-3784.	14.5	154
13	New Insights into Human Nondisjunction of Chromosome 21 in Oocytes. PLoS Genetics, 2008, 4, e1000033.	3.5	146
14	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. American Journal of Human Genetics, 2016, 98, 744-754.	6.2	146
15	Genetic Analysis of Variation in Human Meiotic Recombination. PLoS Genetics, 2009, 5, e1000648.	3.5	142
16	GJC2 Missense Mutations Cause Human Lymphedema. American Journal of Human Genetics, 2010, 86, 943-948.	6.2	141
17	Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. PLoS Genetics, 2016, 12, e1006149.	3.5	140
18	The gene, environment association studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. Genetic Epidemiology, 2010, 34, 364-372.	1.3	139

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19	Genome-wide meta-analyses of nonsyndromic orofacial clefts identify novel associations between FOXE1 and all orofacial clefts, and TP63 and cleft lip with or without cleft palate. Human Genetics, 2017, 136, 275-286.	3.8	139
20	Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. Journal of Dental Research, 2011, 90, 1457-1462.	5.2	108
21	Association between Maternal Age and Meiotic Recombination for Trisomy 21. American Journal of Human Genetics, 2005, 76, 91-99.	6.2	107
22	Skeletal muscle fatigue, strength, and quality in the elderly: the Health ABC Study. Journal of Applied Physiology, 2005, 99, 210-216.	2.5	102
23	Mass Spectral Determination of Fasting Tear Glucose Concentrations in Nondiabetic Volunteers. Clinical Chemistry, 2007, 53, 1370-1372.	3.2	101
24	An Excess of Deleterious Variants in VEGF-A Pathway Genes in Down-Syndrome-Associated Atrioventricular Septal Defects. American Journal of Human Genetics, 2012, 91, 646-659.	6.2	99
25	Connexin 47 Mutations Increase Risk for Secondary Lymphedema Following Breast Cancer Treatment. Clinical Cancer Research, 2012, 18, 2382-2390.	7.0	95
26	Insights into the genetic architecture of the human face. Nature Genetics, 2021, 53, 45-53.	21.4	94
27	Genome-wide association analysis of age-at-onset in Alzheimer's disease. Molecular Psychiatry, 2012, 17, 1340-1346.	7.9	89
28	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. PLoS Genetics, 2015, 11, e1005059.	3.5	82
29	GWAS of Dental Caries Patterns in the Permanent Dentition. Journal of Dental Research, 2013, 92, 38-44.	5.2	77
30	Etiology of Down syndrome: Evidence for consistent association among altered meiotic recombination, nondisjunction, and maternal age across populations. American Journal of Medical Genetics, Part A, 2009, 149A, 1415-1420.	1.2	76
31	Regression-Based Quantitative-Traitâ€“Locus Mapping in the 21st Century. American Journal of Human Genetics, 2002, 71, 217-222.	6.2	71
32	Gender-specific association of ATP-binding cassette transporter 1 (ABCA1) polymorphisms with the risk of late-onset Alzheimer's disease. Neurobiology of Aging, 2007, 28, 856-862.	3.1	69
33	Association tests using kernelâ€based measures of multiâ€locus genotype similarity between individuals. Genetic Epidemiology, 2010, 34, 213-221.	1.3	69
34	Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57.	2.3	69
35	Genome-wide association study of facial morphology reveals novel associations with FREM1 and PARK2. PLoS ONE, 2017, 12, e0176566.	2.5	68
36	Variation in folate pathway genes contributes to risk of congenital heart defects among individuals with Down syndrome. Genetic Epidemiology, 2010, 34, 613-623.	1.3	66

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37	Is there an interchromosomal effect in reciprocal translocation carriers? Sperm FISH studies. Human Genetics, 2000, 106, 517-524.	3.8	64
38	Genetic variation in fatty acid-binding protein-4 and peroxisome proliferator-activated receptor Î³ interactively influence insulin sensitivity and body composition in males. Metabolism: Clinical and Experimental, 2004, 53, 303-309.	3.4	63
39	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
40	Genetic association of ubiquilin with Alzheimer's disease and related quantitative measures. Molecular Psychiatry, 2006, 11, 273-279.	7.9	59
41	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	6.0	58
42	Evaluation of human leukocyte N-formylpeptide receptor (FPR1) SNPs in aggressive periodontitis patients. Genes and Immunity, 2003, 4, 22-29.	4.1	56
43	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
44	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	6.2	48
45	Genome-wide association study of brain amyloid deposition as measured by Pittsburgh Compound-B (PiB)-PET imaging. Molecular Psychiatry, 2021, 26, 309-321.	7.9	47
46	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. PLoS Genetics, 2018, 14, e1007501.	3.5	44
47	Referral to cancer genetic counseling: Are there stages of readiness?. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2006, 142C, 221-231.	1.6	43
48	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, 109, 1030-1038.	1.5	41
49	Local High-Capacity Adenovirus-Mediated mCTLA4Ig and mCD40Ig Expression Prolongs Recombinant Gene Expression in Skeletal Muscle. Molecular Therapy, 2001, 3, 892-900.	8.2	40
50	Methods for Linkage Analysis of Quantitative Trait Loci in Humans. Theoretical Population Biology, 2001, 60, 167-180.	1.1	39
51	Altered patterns of multiple recombinant events are associated with nondisjunction of chromosome 21. Human Genetics, 2012, 131, 1039-1046.	3.8	39
52	Life factors affecting depression and burden in amyotrophic lateral sclerosis caregivers. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2014, 15, 292-297.	1.7	39
53	Telomere length is associated with types of chromosome 21 nondisjunction: a new insight into the maternal age effect on Down syndrome birth. Human Genetics, 2010, 127, 403-409.	3.8	38
54	Pooling-Based Genome-Wide Association Study Implicates Gamma-Glutamyltransferase 1 (GGT1) Gene in Pancreatic Carcinogenesis. Pancreatology, 2010, 10, 194-200.	1.1	38

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55	Genome-Wide Association Study of Primary Dentition Pit-and-Fissure and Smooth Surface Caries. Caries Research, 2014, 48, 330-338.	2.0	38
56	Effects of enamel matrix genes on dental caries are moderated by fluoride exposures. Human Genetics, 2015, 134, 159-167.	3.8	38
57	Epidemiology of Down Syndrome: New Insight Into the Multidimensional Interactions Among Genetic and Environmental Risk Factors in the Oocyte. American Journal of Epidemiology, 2011, 174, 1009-1016.	3.4	37
58	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	1.4	37
59	Sex ratio in normal and disomic sperm: evidence that the extra chromosome 21 preferentially segregates with the Y chromosome. American Journal of Human Genetics, 1996, 59, 1108-13.	6.2	37
60	Composite Statistics for QTL Mapping with Moderately Discordant Sibling Pairs. American Journal of Human Genetics, 2000, 66, 1642-1660.	6.2	36
61	A Survey of Affected-Sibship Statistics for Nonparametric Linkage Analysis. American Journal of Human Genetics, 2001, 69, 179-190.	6.2	36
62	Association studies of lowâ€frequency coding variants in nonsyndromic cleft lip with or without cleft palate. American Journal of Medical Genetics, Part A, 2017, 173, 1531-1538.	1.2	36
63	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	1.3	36
64	What's the best statistic for a simple test of genetic association in a caseâ€control study?. Genetic Epidemiology, 2010, 34, 246-253.	1.3	35
65	Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. BMC Oral Health, 2012, 12, 7.	2.3	35
66	Multicolor fluorescence in situ hybridization analysis of the spermatozoa of a male heterozygous for a reciprocal translocation t(11;22)(q23;q11). Human Genetics, 1999, 104, 412-417.	3.8	34
67	Genome-wide variation in recombination in female meiosis: a risk factor for non-disjunction of chromosome 21. Human Molecular Genetics, 2000, 9, 515-523.	2.9	33
68	Genetic variation in uncoupling protein 3 is associated with dietary intake and body composition in females. Metabolism: Clinical and Experimental, 2004, 53, 458-464.	3.4	32
69	Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. Journal of Dental Research, 2013, 92, 32-37.	5.2	31
70	Age of onset in hereditary lymphedema. Journal of Pediatrics, 2003, 142, 704-708.	1.8	30
71	Caries Experience Differs between Females and Males across Age Groups in Northern Appalachia. International Journal of Dentistry, 2015, 2015, 1-8.	1.5	30
72	Identification of a New Susceptibility Locus for Systemic Lupus Erythematosus on Chromosome 12 in Individuals of European Ancestry. Arthritis and Rheumatology, 2016, 68, 174-183.	5.6	30

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73	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	28.9	30
74	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	6.2	29
75	Markov processes for modeling and analyzing a new genetic mapping method. Journal of Applied Probability, 1993, 30, 766-779.	0.7	28
76	The C161â†'T polymorphism in peroxisome proliferatorâ€"activated receptor gamma, but not P12A, is associated with insulin resistance in Hispanic and non-Hispanic white women: evidence for another functional variant in peroxisome proliferatorâ€"activated receptor gamma. Metabolism: Clinical and Experimental, 2005, 54, 1552-1556.	3.4	28
77	The origin of trisomy 22: Evidence for acrocentric chromosomeâ€specific patterns of nondisjunction. American Journal of Medical Genetics, Part A, 2007, 143A, 2249-2255.	1.2	28
78	Genetic Association of MPPED2 and ACTN2 with Dental Caries. Journal of Dental Research, 2014, 93, 626-632.	5.2	28
79	Evaluation of disease burden and response to treatment in adults with type 1 gaucher disease using a validated disease severity scoring system (DS3). Orphanet Journal of Rare Diseases, 2015, 10, 64.	2.7	28
80	Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. G3: Genes, Genomes, Genetics, 2015, 5, 1961-1971.	1.8	28
81	FOOTER: a web tool for finding mammalian DNA regulatory regions using phylogenetic footprinting. Nucleic Acids Research, 2005, 33, W442-W446.	14.5	27
82	Relationship of recombination patterns and maternal age among non-disjoined chromosomes 21. Biochemical Society Transactions, 2006, 34, 578-580.	3.4	27
83	Recent Advances in Human Quantitative-Traitâ€"Locus Mapping: Comparison of Methods for Selected Sibling Pairs. American Journal of Human Genetics, 2003, 73, 863-873.	6.2	26
84	Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. Genome Biology, 2007, 8, R84.	9.6	26
85	Investigation of factors associated with paternal nondisjunction of chromosome 21. American Journal of Medical Genetics, Part A, 2009, 149A, 1685-1690.	1.2	26
86	Increased expression of interferon-inducible genes in macaque lung tissues during simian immunodeficiency virus infection. Microbes and Infection, 2006, 8, 1839-1850.	1.9	25
87	Associations Between Medical History, Cognition, and Behavior in Youth With Down Syndrome: A Report From the Down Syndrome Cognition Project. American Journal on Intellectual and Developmental Disabilities, 2018, 123, 514-528.	1.6	25
88	A candidate gene analysis and GWAS for genes associated with maternal nondisjunction of chromosome 21. PLoS Genetics, 2019, 15, e1008414.	3.5	25
89	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. Development (Cambridge), 2020, 147, .	2.5	25
90	Systemic Delivery of a High-Capacity Adenoviral Vector Expressing Mouse CTLA4Ig Improves Skeletal Muscle Gene Therapy. Molecular Therapy, 2002, 6, 369-376.	8.2	24

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91	Genetic Control of Hotspots. Science, 2010, 327, 791-792.	12.6	24
92	Genome-wide copy-number variation study of psychosis in Alzheimerâ€™s disease. Translational Psychiatry, 2015, 5, e574-e574.	4.8	24
93	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. Genetic Epidemiology, 2017, 41, 887-897.	1.3	24
94	Estimating Meiotic Exchange Patterns From Recombination Data: An Application to Humans. Genetics, 1997, 146, 1011-1017.	2.9	24
95	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	2.5	24
96	Footer: A quantitative comparative genomics method for efficient recognition of cis-regulatory elements. Genome Research, 2005, 15, 840-847.	5.5	23
97	SNPs Associated With Testosterone Levels Influence Human Facial Morphology. Frontiers in Genetics, 2018, 9, 497.	2.3	23
98	Inverted duplication pattern in anaphase bridges confirms the breakage-fusion-bridge (BFB) cycle model for 11q13 amplification. Cytogenetic and Genome Research, 2007, 116, 46-52.	1.1	22
99	No observed association for mitochondrial SNPs with preterm delivery and related outcomes. Pediatric Research, 2012, 72, 539-544.	2.3	22
100	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
101	Structural and genomic variation in preterm birth. Pediatric Research, 2016, 80, 829-836.	2.3	22
102	A variant of the glucocorticoid receptor gene is not associated with adrenal androgen excess in women with polycystic ovary syndrome. Fertility and Sterility, 2000, 74, 1237-1240.	1.0	21
103	Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. Journal of Pediatrics, 2012, 160, 19-24.e4.	1.8	21
104	Population-based genome-wide association study of cognitive decline in older adults free of dementia: identification of a novel locus for the attention domain. Neurobiology of Aging, 2019, 84, 239.e15-239.e24.	3.1	21
105	Strategies for mapping heterogeneous recessive traits by allele-sharing methods. American Journal of Human Genetics, 1997, 60, 965-78.	6.2	21
106	A Preliminary Genome-Wide Association Study of Pain-Related Fear: Implications for Orofacial Pain. Pain Research and Management, 2017, 2017, 1-12.	1.8	20
107	Six NSCL/P Loci Show Associations With Normal-Range Craniofacial Variation. Frontiers in Genetics, 2018, 9, 502.	2.3	20
108	A comparison of principal component analysis and factor analysis strategies for uncovering pleiotropic factors. Genetic Epidemiology, 2009, 33, 325-331.	1.3	19

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109	Using Family Data as a Verification Standard to Evaluate Copy Number Variation Calling Strategies for Genetic Association Studies. Genetic Epidemiology, 2012, 36, 253-262.	1.3	19
110	Whole genome sequencing of orofacial cleft trios from the Gabriella Miller Kids First Pediatric Research Consortium identifies a new locus on chromosome 21. Human Genetics, 2020, 139, 215-226.	3.8	19
111	Linkage disequilibrium mapping in trisomic populations: Analytical approaches and an application to congenital heart defects in Down syndrome. Genetic Epidemiology, 2004, 27, 240-251.	1.3	18
112	Smarter clustering methods for SNP genotype calling. Bioinformatics, 2008, 24, 2665-2671.	4.1	18
113	Genotypeâ€“phenotype correlations of pheochromocytoma in two large von Hippelâ€“Lindau (VHL) type 2A kindreds with different missense mutations. American Journal of Medical Genetics, Part A, 2011, 155, 168-173.	1.2	18
114	Association of lowâ€frequency genetic variants in regulatory regions with nonsyndromic orofacial clefts. American Journal of Medical Genetics, Part A, 2019, 179, 467-474.	1.2	18
115	Whole-Exome Sequencing Analysis of Alzheimerâ€™s Disease in Non-APOE*4 Carriers. Journal of Alzheimer's Disease, 2020, 76, 1553-1565.	2.6	18
116	The elusive goal of pedigree weights. Genetic Epidemiology, 2007, 31, 51-65.	1.3	17
117	Association of maternal CNVs in GSTT1/GSTT2 with smoking, preterm delivery, and low birth weight. Frontiers in Genetics, 2013, 4, 196.	2.3	17
118	Evidence for dysregulation of genome-wide recombination in oocytes with nondisjoined chromosomes 21. Human Molecular Genetics, 2014, 23, 408-417.	2.9	17
119	Predictors of dental care utilization in northâ€central Appalachia in the USA. Community Dentistry and Oral Epidemiology, 2019, 47, 283-290.	1.9	17
120	Multipoint Estimation of Genetic Maps for Human Trisomies with One Parent or Other Partial Data. American Journal of Human Genetics, 2000, 66, 958-968.	6.2	16
121	A Rare Duplication on Chromosome 16p11.2 Is Identified in Patients with Psychosis in Alzheimer's Disease. PLoS ONE, 2014, 9, e111462.	2.5	16
122	Apolipoprotein E-C1-C4-C2 gene cluster region and inter-individual variation in plasma lipoprotein levels: a comprehensive genetic association study in two ethnic groups. PLoS ONE, 2019, 14, e0214060.	2.5	16
123	Genome-Wide Association Study of Non-syndromic Orofacial Clefts in a Multiethnic Sample of Families and Controls Identifies Novel Regions. Frontiers in Cell and Developmental Biology, 2021, 9, 621482.	3.7	16
124	Recent Advances in Human Quantitative-Traitâ€“Locus Mapping: Comparison of Methods for Discordant Sibling Pairs. American Journal of Human Genetics, 2003, 73, 874-885.	6.2	15
125	Association Signals Unveiled by a Comprehensive Gene Set Enrichment Analysis of Dental Caries Genome-Wide Association Studies. PLoS ONE, 2013, 8, e72653.	2.5	15
126	Genomeâ€wide interaction studies identify sexâ€specific risk alleles for nonsyndromic orofacial clefts. Genetic Epidemiology, 2018, 42, 664-672.	1.3	15

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127	An Examination of the Relationship between Hotspots and Recombination Associated with Chromosome 21 Nondisjunction. PLoS ONE, 2014, 9, e99560.	2.5	15
128	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
129	Maternal Telomere Length and Risk of Down Syndrome: Epidemiological Impact of Smokeless Chewing Tobacco and Oral Contraceptive on Segregation of Chromosome 21. Public Health Genomics, 2016, 19, 11-18.	1.0	14
130	FAT4 identified as a potential modifier of orofacial cleft laterality. Genetic Epidemiology, 2021, 45, 721-735.	1.3	14
131	Estimating the Frequency Distribution of Crossovers during Meiosis from Recombination Data. Biometrics, 2001, 57, 427-434.	1.4	13
132	Polymorphic haplotypes of CRELD1 differentially predispose Down syndrome and euploids individuals to atrioventricular septal defect. American Journal of Medical Genetics, Part A, 2012, 158A, 2843-2848.	1.2	13
133	Multiple signals at the extended 8p23 locus are associated with susceptibility to systemic lupus erythematosus. Journal of Medical Genetics, 2017, 54, 381-389.	3.2	13
134	Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. PLoS Genetics, 2021, 17, e1009695.	3.5	13
135	Allelic Interaction between CRELD1 and VEGFA in the Pathogenesis of Cardiac Atrioventricular Septal Defects. AIMS Genetics, 2014, 01, 001-019.	1.9	13
136	Methods for genetic linkage analysis using trisomies. American Journal of Human Genetics, 1995, 56, 475-83.	6.2	13
137	Genome-wide Association Studies. Journal of Dental Research, 2012, 91, 637-641.	5.2	12
138	Genetic Association ofMMP10,MMP14, andMMP16with Dental Caries. International Journal of Dentistry, 2017, 2017, 1-7.	1.5	12
139	Genetic Determinants of Survival in Patients with Alzheimer's Disease. Journal of Alzheimer's Disease, 2015, 45, 651-658.	2.6	11
140	Variants on chromosome 4q21 near PKD2 and SIBLINGs are associated with dental caries. Journal of Human Genetics, 2017, 62, 491-496.	2.3	11
141	Mapping genetic variants for cranial vault shape in humans. PLoS ONE, 2018, 13, e0196148.	2.5	11
142	Investigating the GWAS-Implicated Loci for Rheumatoid Arthritis in the Pakistani Population. Disease Markers, 2020, 2020, 1-9.	1.3	11
143	The Association between SNPs and a Quantitative Trait: Power Calculation. European Journal of Environment and Public Health, 2018, 2, .	2.0	11
144	Efficient Simulation ofP Values for Linkage Analysis. Genetic Epidemiology, 2004, 26, 88-96.	1.3	10

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145	Geneâ€dropping vs. empirical variance estimation for alleleâ€sharing linkage statistics. Genetic Epidemiology, 2006, 30, 652-665.	1.3	10
146	Comparison of allele-sharing statistics for general pedigrees. Genetic Epidemiology, 2000, 19, S92-S98.	1.3	9
147	Robust Score Statistics for QTL Linkage Analysis. American Journal of Human Genetics, 2008, 82, 567-582.	6.2	9
148	Genome-Wide Association Study of Meiotic Recombination Phenotypes. G3: Genes, Genomes, Genetics, 2016, 6, 3995-4007.	1.8	9
149	Pilot GWAS of caries in African-Americans shows genetic heterogeneity. BMC Oral Health, 2019, 19, 215.	2.3	9
150	A sequencing study of CTLA4 in Pakistani rheumatoid arthritis cases. PLoS ONE, 2020, 15, e0239426.	2.5	9
151	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. Human Genetics and Genomics Advances, 2021, 2, 100025.	1.7	9
152	An Empirical Bayesian Method for Differential Expression Studies Using One-Channel Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article8.	0.6	8
153	Host Genetics, Steatosis and Insulin Resistance among African Americans and Caucasian Americans with Hepatitis C Virus Genotype-1 Infection. Intervirology, 2009, 52, 49-56.	2.8	8
154	Combined association of Presenilin-1 and Apolipoprotein E polymorphisms with maternal meiosis II error in Down syndrome births. Genetics and Molecular Biology, 2017, 40, 577-585.	1.3	8
155	GWAS reveals loci associated with velopharyngeal dysfunction. Scientific Reports, 2018, 8, 8470.	3.3	8
156	Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC Oral Health, 2018, 18, 98.	2.3	8
157	A trisomic transmission disequilibrium test. Genetic Epidemiology, 2004, 26, 125-131.	1.3	7
158	Variation in the Zinc Finger of PRDM9 is Associated with the Absence of Recombination along Nondisjoined Chromosomes 21 of Maternal Origin. Journal of Down Syndrome & Chromosome Abnormalities, 2016, 02, .	0.1	7
159	Assessment of genetic risk of type 2 diabetes among Pakistanis based on GWAS-implicated loci. Gene, 2021, 783, 145563.	2.2	7
160	Allelic Interaction between and in the Pathogenesis of Cardiac Atrioventricular Septal Defects. AIMS Genetics, 2014, 1, 1-19.	1.9	7
161	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
162	Association Between NEDD4L Gene and Sodium Lithium Countertransport. American Journal of Hypertension, 2011, 24, 145-148.	2.0	6

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163	Regionally Smoothed Meta-Analysis Methods for GWAS Datasets. Genetic Epidemiology, 2016, 40, 154-160.	1.3	6
164	Association Study of Coronary Artery Disease-Associated Genome-Wide Significant SNPs with Coronary Stenosis in Pakistani Population. Disease Markers, 2020, 2020, 1-7.	1.3	6
165	PRICKLE1 Ã— FOCAD Interaction Revealed by Genome-Wide vQTL Analysis of Human Facial Traits. Frontiers in Genetics, 2021, 12, 674642.	2.3	6
166	A Powerful and Robust New Linkage Statistic for Discordant Sibling Pairs. American Journal of Human Genetics, 2004, 75, 906-909.	6.2	5
167	Long-term outcomes, branch-specific expressivity, and disease-related mortality in von Hippel-Lindau type 2A. Familial Cancer, 2011, 10, 701-707.	1.9	5
168	Exploration of shared genetic susceptibility loci between type 1 diabetes and rheumatoid arthritis in the Pakistani population. BMC Research Notes, 2019, 12, 544.	1.4	5
169	Association of VPREB1 Gene Copy Number Variation and Rheumatoid Arthritis Susceptibility. Disease Markers, 2020, 2020, 1-5.	1.3	5
170	Testing for contributions of mitochondrial DNA mutations to complex diseases. , 1998, 15, 451-469.		4
171	Statistics for Nonparametric Linkage Analysis of X-Linked Traits in General Pedigrees. American Journal of Human Genetics, 2002, 70, 181-191.	6.2	4
172	QTL mapping with discordant and concordant sibling pairs: new statistics and new design strategies. Genetic Epidemiology, 2005, 28, 326-340.	1.3	4
173	Analyses stratified by maternal age and recombination further characterize genes associated with maternal nondisjunction of chromosome 21. Prenatal Diagnosis, 2021, 41, 591-609.	2.3	4
174	Genomeâ€wide association study of multiethnic nonsyndromic orofacial cleft families identifies novel loci specific to family and phenotypic subtypes. Genetic Epidemiology, 2022, , .	1.3	4
175	Methods for Analyzing the Spatial Distribution of Chiasmata During Meiosis Based on Recombination Data. Biometrics, 2002, 58, 369-377.	1.4	3
176	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. Genetic Epidemiology, 2016, 40, 161-171.	1.3	3
177	Gene Expression and Cardiometabolic Phenotypes of Vitamin D-Deficient Overweight and Obese Black Children. Nutrients, 2019, 11, 2016.	4.1	3
178	Impact of low-frequency coding variants on human facial shape. Scientific Reports, 2021, 11, 748.	3.3	3
179	Statistical models for trisomic phenotypes. American Journal of Human Genetics, 1996, 58, 201-12.	6.2	3
180	Genome-wide Interaction Study Implicates VGLL2 and Alcohol Exposure and PRL and Smoking in Orofacial Cleft Risk. Frontiers in Cell and Developmental Biology, 2022, 10, 621261.	3.7	3

#	Article	IF	Citations
181	A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. Genetic Epidemiology, 2007, 31, 417-430.	1.3	2
182	A Likelihood-Based Approach for Missing Genotype Data. Human Heredity, 2010, 69, 171-183.	0.8	2
183	The haptoglobin 2-2 genotype is associated with cardiac autonomic neuropathy in type 1 diabetes: the RETRO HDLc study. Acta Diabetologica, 2020, 57, 271-278.	2.5	2
184	Detecting Gene-Environment Interaction for Maternal Exposures Using Case-Parent Trios Ascertained Through a Case With Non-Syndromic Orofacial Cleft. Frontiers in Cell and Developmental Biology, 2021, 9, 621018.	3.7	2
185	Web-Based Identification of Evolutionary Conserved DNA cis-Regulatory Elements. Methods in Molecular Biology, 2007, 395, 425-436.	0.9	2
186	Genome-Wide Association Study of Incident Dementia in a Community-Based Sample of Older Subjects. Journal of Alzheimer's Disease, 2022, 88, 787-798.	2.6	2
187	A simple allele sharing statistic for multiple locus systems. Genetic Epidemiology, 1999, 17, S497-501.	1.3	1
188	292 A Genome-Wide Association Study of Spontaneous Preterm Delivery. Pediatric Research, 2010, 68, 150-150.	2.3	1
189	Oral health and related risk indicators in northâ€central Appalachia differ by rurality. Community Dentistry and Oral Epidemiology, 2021, 49, 427-436.	1.9	1
190	Treatment of Uninformative Families in Mean Allele Sharing Tests for Linkage. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article13.	0.6	0
191	Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. Human Heredity, 2015, 80, 79-89.	0.8	0
192	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, , .	1.5	0
193	Web-Based Identification of Evolutionary Conserved DNA <i>cis</i>-Regulatory Elements. , 0, , 425-436.		0