# 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 | Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18. | 28.9 | 30 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Insights into the genetic architecture of the human face. Nature Genetics, 2021, 53, 45-53. | 21.4 | 94 |
| 7 | Impact of low-frequency coding variants on human facial shape. Scientific Reports, 2021, 11, 748. | 3.3 | 3 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | Assessment of genetic risk of type 2 diabetes among Pakistanis based on GWAS-implicated loci. Gene, 2021, 783, 145563. | 2.2 | 7 |
| 13 | FAT4 identified as a potential modifier of orofacial cleft laterality. Genetic Epidemiology, 2021, 45, 721-735. | 1.3 | 14 |
| 14 | Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. PLoS Genetics, 2021, 17, e1009695. | 3.5 | 13 |
| 15 | PRICKLE1 Ã— FOCAD Interaction Revealed by Genome-Wide vQTL Analysis of Human Facial Traits. Frontiers in Genetics, 2021, 12, 674642. | 2.3 | 6 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|---|---|---|---|
| 19 | FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. Development (Cambridge), 2020, 147, . | 2.5 | 25 |
| 20 | Association of VPREB1 Gene Copy Number Variation and Rheumatoid Arthritis Susceptibility. Disease Markers, 2020, 2020, 1-5. | 1.3 | 5 |
| 21 | 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 |
| 22 | Investigating the GWAS-Implicated Loci for Rheumatoid Arthritis in the Pakistani Population. Disease Markers, 2020, 2020, 1-9. | 1.3 | 11 |
| 23 | A sequencing study of CTLA4 in Pakistani rheumatoid arthritis cases. PLoS ONE, 2020, 15, e0239426. | 2.5 | 9 |
| 24 | 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 |
| 25 | Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136. | 6.2 | 48 |
| 26 | Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237. | 1.4 | 37 |
| 27 | 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 |
| 28 | Gene Expression and Cardiometabolic Phenotypes of Vitamin D-Deficient Overweight and Obese Black Children. Nutrients, 2019, 11, 2016. | 4.1 | 3 |
| 29 | Pilot GWAS of caries in African-Americans shows genetic heterogeneity. BMC Oral Health, 2019, 19, 215. | 2.3 | 9 |
| 30 | A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716. | 1.3 | 36 |
| 31 | Predictors of dental care utilization in northâ€central Appalachia in the USA. Community Dentistry and Oral Epidemiology, 2019, 47, 283-290. | 1.9 | 17 |
| 32 | 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 |
| 33 | 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 |
| 34 | A candidate gene analysis and GWAS for genes associated with maternal nondisjunction of chromosome 21. PLoS Genetics, 2019, 15, e1008414. | 3.5 | 25 |
| 35 | 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 |
| 36 | Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, . | 6.0 | 58 |

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|---|---|---|---|
| 37 | Genome-wide mapping of global-to-local genetic effects on human facial shape. Nature Genetics, 2018, 50, 414-423. | 21.4 | 205 |
| 38 | SNPs Associated With Testosterone Levels Influence Human Facial Morphology. Frontiers in Genetics, 2018, 9, 497. | 2.3 | 23 |
| 39 | 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 |
| 40 | Six NSCL/P Loci Show Associations With Normal-Range Craniofacial Variation. Frontiers in Genetics, 2018, 9, 502. | 2.3 | 20 |
| 41 | Genomeâ€wide interaction studies identify sexâ€specific risk alleles for nonsyndromic orofacial clefts. Genetic Epidemiology, 2018, 42, 664-672. | 1.3 | 15 |
| 42 | GWAS reveals loci associated with velopharyngeal dysfunction. Scientific Reports, 2018, 8, 8470. | 3.3 | 8 |
| 43 | Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC Oral Health, 2018, 18, 98. | 2.3 | 8 |
| 44 | Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. PLoS Genetics, 2018, 14, e1007501. | 3.5 | 44 |
| 45 | Mapping genetic variants for cranial vault shape in humans. PLoS ONE, 2018, 13, e0196148. | 2.5 | 11 |
| 46 | The Association between SNPs and a Quantitative Trait: Power Calculation. European Journal of Environment and Public Health, 2018, 2, . | 2.0 | 11 |
| 47 | 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 |
| 48 | Variants on chromosome 4q21 near PKD2 and SIBLINGs are associated with dental caries. Journal of Human Genetics, 2017, 62, 491-496. | 2.3 | 11 |
| 49 | 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 |
| 50 | 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 |
| 51 | Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, 109, 1030-1038. | 1.5 | 41 |
| 52 | Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924. | 6.2 | 29 |
| 53 | Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. Genetic Epidemiology, 2017, 41, 887-897. | 1.3 | 24 |
| 54 | 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 |

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|---|---|---|---|
| 55 | Genetic Association ofMMP10,MMP14, andMMP16with Dental Caries. International Journal of Dentistry, 2017, 2017, 1-7. | 1.5 | 12 |
| 56 | 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 |
| 57 | Genome-wide association study of facial morphology reveals novel associations with FREM1 and PARK2. PLoS ONE, 2017, 12, e0176566. | 2.5 | 68 |
| 58 | Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, , . | 1.5 | 0 |
| 59 | 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 |
| 60 | Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. PLoS Genetics, 2016, 12, e1006149. | 3.5 | 140 |
| 61 | Regionally Smoothed Meta-Analysis Methods for GWAS Datasets. Genetic Epidemiology, 2016, 40, 154-160. | 1.3 | 6 |
| 62 | Genome-Wide Association Study of Meiotic Recombination Phenotypes. G3: Genes, Genomes, Genetics, 2016, 6, 3995-4007. | 1.8 | 9 |
| 63 | 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 |
| 64 | 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 |
| 65 | Structural and genomic variation in preterm birth. Pediatric Research, 2016, 80, 829-836. | 2.3 | 22 |
| 66 | A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. Genetic Epidemiology, 2016, 40, 161-171. | 1.3 | 3 |
| 67 | 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 |
| 68 | 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 |
| 69 | Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. Human Heredity, 2015, 80, 79-89. | 0.8 | 0 |
| 70 | 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 |
| 71 | Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. G3: Genes, Genomes, Genetics, 2015, 5, 1961-1971. | 1.8 | 28 |
| 72 | Genetic Determinants of Survival in Patients with Alzheimer's Disease. Journal of Alzheimer's Disease, 2015, 45, 651-658. | 2.6 | 11 |

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| 73 | Caries Experience Differs between Females and Males across Age Groups in Northern Appalachia. International Journal of Dentistry, 2015, 2015, 1-8. | 1.5 | 30 |
| 74 | Effects of enamel matrix genes on dental caries are moderated by fluoride exposures. Human Genetics, 2015, 134, 159-167. | 3.8 | 38 |
| 75 | Genome-wide copy-number variation study of psychosis in Alzheimerâ€™s disease. Translational Psychiatry, 2015, 5, e574-e574. | 4.8 | 24 |
| 76 | 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 |
| 77 | 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 |
| 78 | Life factors affecting depression and burden in amyotrophic lateral sclerosis caregivers. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2014, 15, 292-297. | 1.7 | 39 |
| 79 | Evidence for dysregulation of genome-wide recombination in oocytes with nondisjoined chromosomes 21. Human Molecular Genetics, 2014, 23, 408-417. | 2.9 | 17 |
| 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 | Genetic Association of MPPED2 and ACTN2 with Dental Caries. Journal of Dental Research, 2014, 93, 626-632. | 5.2 | 28 |
| 83 | An Examination of the Relationship between Hotspots and Recombination Associated with Chromosome 21 Nondisjunction. PLoS ONE, 2014, 9, e99560. | 2.5 | 15 |
| 84 | Allelic Interaction between CRELD1 and VEGFA in the Pathogenesis of Cardiac Atrioventricular Septal Defects. AIMS Genetics, 2014, 01, 001-019. | 1.9 | 13 |
| 85 | Allelic Interaction between and in the Pathogenesis of Cardiac Atrioventricular Septal Defects. AIMS Genetics, 2014, 1, 1-19. | 1.9 | 7 |
| 86 | Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. Journal of Dental Research, 2013, 92, 32-37. | 5.2 | 31 |
| 87 | GWAS of Dental Caries Patterns in the Permanent Dentition. Journal of Dental Research, 2013, 92, 38-44. | 5.2 | 77 |
| 88 | 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 |
| 89 | Peripheral Blood Mononuclear Cell Gene Expression Profiles Predict Poor Outcome in Idiopathic Pulmonary Fibrosis. Science Translational Medicine, 2013, 5, 205ra136. | 12.4 | 242 |
| 90 | 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 |

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|---|---|---|---|
| 91 | 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 |
| 92 | Association of maternal CNVs in GSTT1/GSTT2 with smoking, preterm delivery, and low birth weight. Frontiers in Genetics, 2013, 4, 196. | 2.3 | 17 |
| 93 | Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666. | 2.5 | 24 |
| 94 | Genome-wide Association Studies. Journal of Dental Research, 2012, 91, 637-641. | 5.2 | 12 |
| 95 | Connexin 47 Mutations Increase Risk for Secondary Lymphedema Following Breast Cancer Treatment. Clinical Cancer Research, 2012, 18, 2382-2390. | 7.0 | 95 |
| 96 | Genome-wide association analysis of age-at-onset in Alzheimer's disease. Molecular Psychiatry, 2012, 17, 1340-1346. | 7.9 | 89 |
| 97 | Comprehensive literature review and statistical considerations for microarray meta-analysis. Nucleic Acids Research, 2012, 40, 3785-3799. | 14.5 | 427 |
| 98 | No observed association for mitochondrial SNPs with preterm delivery and related outcomes. Pediatric Research, 2012, 72, 539-544. | 2.3 | 22 |
| 99 | 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 |
| 100 | Genome-wide association study of Alzheimer's disease. Translational Psychiatry, 2012, 2, e117-e117. | 4.8 | 209 |
| 101 | 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 |
| 102 | Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57. | 2.3 | 69 |
| 103 | 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 |
| 104 | Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650. | 21.4 | 511 |
| 105 | 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 |
| 106 | Comprehensive literature review and statistical considerations for GWAS meta-analysis. Nucleic Acids Research, 2012, 40, 3777-3784. | 14.5 | 154 |
| 107 | Altered patterns of multiple recombinant events are associated with nondisjunction of chromosome 21. Human Genetics, 2012, 131, 1039-1046. | 3.8 | 39 |
| 108 | Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. Journal of Pediatrics, 2012, 160, 19-24.e4. | 1.8 | 21 |

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|---|---|---|---|
| 109 | Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. BMC Oral Health, 2012, 12, 7. | 2.3 | 35 |
| 110 | Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525. | 21.4 | 834 |
| 111 | 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 |
| 112 | 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 |
| 113 | Association Between NEDD4L Gene and Sodium Lithium Countertransport. American Journal of Hypertension, 2011, 24, 145-148. | 2.0 | 6 |
| 114 | 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 |
| 115 | Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. Journal of Dental Research, 2011, 90, 1457-1462. | 5.2 | 108 |
| 116 | Association tests using kernelâ€based measures of multiâ€locus genotype similarity between individuals. Genetic Epidemiology, 2010, 34, 213-221. | 1.3 | 69 |
| 117 | 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 |
| 118 | 292 A Genome-Wide Association Study of Spontaneous Preterm Delivery. Pediatric Research, 2010, 68, 150-150. | 2.3 | 1 |
| 119 | GJC2 Missense Mutations Cause Human Lymphedema. American Journal of Human Genetics, 2010, 86, 943-948. | 6.2 | 141 |
| 120 | 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 |
| 121 | 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 |
| 122 | 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 |
| 123 | A Likelihood-Based Approach for Missing Genotype Data. Human Heredity, 2010, 69, 171-183. | 0.8 | 2 |
| 124 | Genetic Control of Hotspots. Science, 2010, 327, 791-792. | 12.6 | 24 |
| 125 | Pooling-Based Genome-Wide Association Study Implicates Gamma-Glutamyltransferase 1 (GGT1) Gene in Pancreatic Carcinogenesis. Pancreatology, 2010, 10, 194-200. | 1.1 | 38 |
| 126 | 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 |

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|---|---|---|---|
| 127 | Genetic Analysis of Variation in Human Meiotic Recombination. PLoS Genetics, 2009, 5, e1000648. | 3.5 | 142 |
| 128 | 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 |
| 129 | A comparison of principal component analysis and factor analysis strategies for uncovering pleiotropic factors. Genetic Epidemiology, 2009, 33, 325-331. | 1.3 | 19 |
| 130 | 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 |
| 131 | Investigation of factors associated with paternal nondisjunction of chromosome 21. American Journal of Medical Genetics, Part A, 2009, 149A, 1685-1690. | 1.2 | 26 |
| 132 | Robust Score Statistics for QTL Linkage Analysis. American Journal of Human Genetics, 2008, 82, 567-582. | 6.2 | 9 |
| 133 | New Insights into Human Nondisjunction of Chromosome 21 in Oocytes. PLoS Genetics, 2008, 4, e1000033. | 3.5 | 146 |
| 134 | Smarter clustering methods for SNP genotype calling. Bioinformatics, 2008, 24, 2665-2671. | 4.1 | 18 |
| 135 | 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 |
| 136 | Mass Spectral Determination of Fasting Tear Glucose Concentrations in Nondiabetic Volunteers. Clinical Chemistry, 2007, 53, 1370-1372. | 3.2 | 101 |
| 137 | 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 |
| 138 | Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. Genome Biology, 2007, 8, R84. | 9.6 | 26 |
| 139 | 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 |
| 140 | The elusive goal of pedigree weights. Genetic Epidemiology, 2007, 31, 51-65. | 1.3 | 17 |
| 141 | A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. Genetic Epidemiology, 2007, 31, 417-430. | 1.3 | 2 |
| 142 | Web-Based Identification of Evolutionary Conserved DNA cis-Regulatory Elements. Methods in Molecular Biology, 2007, 395, 425-436. | 0.9 | 2 |
| 143 | Relationship of recombination patterns and maternal age among non-disjoined chromosomes 21. Biochemical Society Transactions, 2006, 34, 578-580. | 3.4 | 27 |
| 144 | Genetic association of ubiquilin with Alzheimer's disease and related quantitative measures. Molecular Psychiatry, 2006, 11, 273-279. | 7.9 | 59 |

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| 145 | 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 |
| 146 | Geneâ€dropping vs. empirical variance estimation for alleleâ€sharing linkage statistics. Genetic Epidemiology, 2006, 30, 652-665. | 1.3 | 10 |
| 147 | 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 |
| 148 | Treatment of Uninformative Families in Mean Allele Sharing Tests for Linkage. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article13. | 0.6 | 0 |
| 149 | Skeletal muscle fatigue, strength, and quality in the elderly: the Health ABC Study. Journal of Applied Physiology, 2005, 99, 210-216. | 2.5 | 102 |
| 150 | QTL mapping with discordant and concordant sibling pairs: new statistics and new design strategies. Genetic Epidemiology, 2005, 28, 326-340. | 1.3 | 4 |
| 151 | Footer: A quantitative comparative genomics method for efficient recognition of cis-regulatory elements. Genome Research, 2005, 15, 840-847. | 5.5 | 23 |
| 152 | FOOTER: a web tool for finding mammalian DNA regulatory regions using phylogenetic footprinting. Nucleic Acids Research, 2005, 33, W442-W446. | 14.5 | 27 |
| 153 | Association between Maternal Age and Meiotic Recombination for Trisomy 21. American Journal of Human Genetics, 2005, 76, 91-99. | 6.2 | 107 |
| 154 | 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 |
| 155 | Efficient Simulation ofP Values for Linkage Analysis. Genetic Epidemiology, 2004, 26, 88-96. | 1.3 | 10 |
| 156 | A trisomic transmission disequilibrium test. Genetic Epidemiology, 2004, 26, 125-131. | 1.3 | 7 |
| 157 | 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 |
| 158 | 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 |
| 159 | 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 |
| 160 | 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 |
| 161 | A Powerful and Robust New Linkage Statistic for Discordant Sibling Pairs. American Journal of Human Genetics, 2004, 75, 906-909. | 6.2 | 5 |
| 162 | Evaluation of human leukocyte N-formylpeptide receptor (FPR1) SNPs in aggressive periodontitis patients. Genes and Immunity, 2003, 4, 22-29. | 4.1 | 56 |

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| 163 | Age of onset in hereditary lymphedema. Journal of Pediatrics, 2003, 142, 704-708. | 1.8 | 30 |
| 164 | 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 |
| 165 | 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 |
| 166 | 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 |
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