

Eleanor Feingold

List of Publications by Year in descending order

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Version: 2024-02-01

193
papers

9,109
citations

61857

43
h-index

54797

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. <i>Cell</i> , 2022, 185, 95-112.e18.	13.5	30
2	Genome-wide Interaction Study Implicates VGLL2 and Alcohol Exposure and PRL and Smoking in Orofacial Cleft Risk. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 621261.	1.8	3
3	Genome-wide association study of multiethnic nonsyndromic orofacial cleft families identifies novel loci specific to family and phenotypic subtypes. <i>Genetic Epidemiology</i> , 2022, , .	0.6	4
4	Genome-Wide Association Study of Incident Dementia in a Community-Based Sample of Older Subjects. <i>Journal of Alzheimer's Disease</i> , 2022, 88, 787-798.	1.2	2
5	Genome-wide association study of brain amyloid deposition as measured by Pittsburgh Compound-B (PiB)-PET imaging. <i>Molecular Psychiatry</i> , 2021, 26, 309-321.	4.1	47
6	Insights into the genetic architecture of the human face. <i>Nature Genetics</i> , 2021, 53, 45-53.	9.4	94
7	Impact of low-frequency coding variants on human facial shape. <i>Scientific Reports</i> , 2021, 11, 748.	1.6	3
8	Analyses stratified by maternal age and recombination further characterize genes associated with maternal nondisjunction of chromosome 21. <i>Prenatal Diagnosis</i> , 2021, 41, 591-609.	1.1	4
9	Detecting Gene-Environment Interaction for Maternal Exposures Using Case-Parent Trios Ascertained Through a Case With Non-Syndromic Orofacial Cleft. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 621018.	1.8	2
10	Genome-Wide Association Study of Non-syndromic Orofacial Clefts in a Multiethnic Sample of Families and Controls Identifies Novel Regions. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 621482.	1.8	16
11	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100025.	1.0	9
12	Assessment of genetic risk of type 2 diabetes among Pakistanis based on GWAS-implicated loci. <i>Gene</i> , 2021, 783, 145563.	1.0	7
13	<i>FAT4</i> identified as a potential modifier of orofacial cleft laterality. <i>Genetic Epidemiology</i> , 2021, 45, 721-735.	0.6	14
14	Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. <i>PLoS Genetics</i> , 2021, 17, e1009695.	1.5	13
15	PRICKLE1 – FOCAD Interaction Revealed by Genome-Wide vQTL Analysis of Human Facial Traits. <i>Frontiers in Genetics</i> , 2021, 12, 674642.	1.1	6
16	Oral health and related risk indicators in north-central Appalachia differ by rurality. <i>Community Dentistry and Oral Epidemiology</i> , 2021, 49, 427-436.	0.9	1
17	The haptoglobin 2-2 genotype is associated with cardiac autonomic neuropathy in type 1 diabetes: the RETRO HDLc study. <i>Acta Diabetologica</i> , 2020, 57, 271-278.	1.2	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. <i>Human Genetics</i> , 2020, 139, 215-226.	1.8	19

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19	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. Development (Cambridge), 2020, 147, .	1.2	25
20	Association of <i>VPREB1</i> Gene Copy Number Variation and Rheumatoid Arthritis Susceptibility. Disease Markers, 2020, 2020, 1-5.	0.6	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.	0.6	6
22	Investigating the GWAS-Implicated Loci for Rheumatoid Arthritis in the Pakistani Population. Disease Markers, 2020, 2020, 1-9.	0.6	11
23	A sequencing study of CTLA4 in Pakistani rheumatoid arthritis cases. PLoS ONE, 2020, 15, e0239426.	1.1	9
24	Whole-Exome Sequencing Analysis of Alzheimer's Disease in Non-APOE*4 Carriers. Journal of Alzheimer's Disease, 2020, 76, 1553-1565.	1.2	18
25	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	2.6	48
26	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	0.6	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.	0.6	5
28	Gene Expression and Cardiometabolic Phenotypes of Vitamin D-Deficient Overweight and Obese Black Children. Nutrients, 2019, 11, 2016.	1.7	3
29	Pilot GWAS of caries in African-Americans shows genetic heterogeneity. BMC Oral Health, 2019, 19, 215.	0.8	9
30	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	0.6	36
31	Predictors of dental care utilization in north-central Appalachia in the USA. Community Dentistry and Oral Epidemiology, 2019, 47, 283-290.	0.9	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.	1.5	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.	1.1	16
34	A candidate gene analysis and GWAS for genes associated with maternal nondisjunction of chromosome 21. PLoS Genetics, 2019, 15, e1008414.	1.5	25
35	Association of low-frequency genetic variants in regulatory regions with nonsyndromic orofacial clefts. American Journal of Medical Genetics, Part A, 2019, 179, 467-474.	0.7	18
36	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	2.8	58

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37	Genome-wide mapping of global-to-local genetic effects on human facial shape. <i>Nature Genetics</i> , 2018, 50, 414-423.	9.4	205
38	SNPs Associated With Testosterone Levels Influence Human Facial Morphology. <i>Frontiers in Genetics</i> , 2018, 9, 497.	1.1	23
39	Associations Between Medical History, Cognition, and Behavior in Youth With Down Syndrome: A Report From the Down Syndrome Cognition Project. <i>American Journal on Intellectual and Developmental Disabilities</i> , 2018, 123, 514-528.	0.8	25
40	Six NSCL/P Loci Show Associations With Normal-Range Craniofacial Variation. <i>Frontiers in Genetics</i> , 2018, 9, 502.	1.1	20
41	Genome-wide interaction studies identify sex-specific risk alleles for nonsyndromic orofacial clefts. <i>Genetic Epidemiology</i> , 2018, 42, 664-672.	0.6	15
42	GWAS reveals loci associated with velopharyngeal dysfunction. <i>Scientific Reports</i> , 2018, 8, 8470.	1.6	8
43	Novel caries loci in children and adults implicated by genome-wide analysis of families. <i>BMC Oral Health</i> , 2018, 18, 98.	0.8	8
44	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. <i>PLoS Genetics</i> , 2018, 14, e1007501.	1.5	44
45	Mapping genetic variants for cranial vault shape in humans. <i>PLoS ONE</i> , 2018, 13, e0196148.	1.1	11
46	The Association between SNPs and a Quantitative Trait: Power Calculation. <i>European Journal of Environment and Public Health</i> , 2018, 2, .	0.9	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. <i>Human Genetics</i> , 2017, 136, 275-286.	1.8	139
48	Variants on chromosome 4q21 near PKD2 and SIBLINGs are associated with dental caries. <i>Journal of Human Genetics</i> , 2017, 62, 491-496.	1.1	11
49	Association studies of low-frequency coding variants in nonsyndromic cleft lip with or without cleft palate. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 1531-1538.	0.7	36
50	Multiple signals at the extended 8p23 locus are associated with susceptibility to systemic lupus erythematosus. <i>Journal of Medical Genetics</i> , 2017, 54, 381-389.	1.5	13
51	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. <i>Birth Defects Research</i> , 2017, 109, 1030-1038.	0.8	41
52	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. <i>American Journal of Human Genetics</i> , 2017, 101, 913-924.	2.6	29
53	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 887-897.	0.6	24
54	A Preliminary Genome-Wide Association Study of Pain-Related Fear: Implications for Orofacial Pain. <i>Pain Research and Management</i> , 2017, 2017, 1-12.	0.7	20

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55	Genetic Association of MMP10, MMP14, and MMP16 with Dental Caries. <i>International Journal of Dentistry</i> , 2017, 2017, 1-7.	0.5	12
56	Combined association of Presenilin-1 and Apolipoprotein E polymorphisms with maternal meiosis II error in Down syndrome births. <i>Genetics and Molecular Biology</i> , 2017, 40, 577-585.	0.6	8
57	Genome-wide association study of facial morphology reveals novel associations with <i>FREM1</i> and <i>PARK2</i> . <i>PLoS ONE</i> , 2017, 12, e0176566.	1.1	68
58	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. <i>Birth Defects Research</i> , 2017, , .	0.8	0
59	Variation in the Zinc Finger of <i>PRDM9</i> is Associated with the Absence of Recombination along Nondisjoined Chromosomes 21 of Maternal Origin. <i>Journal of Down Syndrome & Chromosome Abnormalities</i> , 2016, 02, .	0.1	7
60	Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. <i>PLoS Genetics</i> , 2016, 12, e1006149.	1.5	140
61	Regionally Smoothed Meta-Analysis Methods for GWAS Datasets. <i>Genetic Epidemiology</i> , 2016, 40, 154-160.	0.6	6
62	Genome-Wide Association Study of Meiotic Recombination Phenotypes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3995-4007.	0.8	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. <i>Human Molecular Genetics</i> , 2016, 25, ddw104.	1.4	163
64	Identification of a New Susceptibility Locus for Systemic Lupus Erythematosus on Chromosome 12 in Individuals of European Ancestry. <i>Arthritis and Rheumatology</i> , 2016, 68, 174-183.	2.9	30
65	Structural and genomic variation in preterm birth. <i>Pediatric Research</i> , 2016, 80, 829-836.	1.1	22
66	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. <i>Genetic Epidemiology</i> , 2016, 40, 161-171.	0.6	3
67	Maternal Telomere Length and Risk of Down Syndrome: Epidemiological Impact of Smokeless Chewing Tobacco and Oral Contraceptive on Segregation of Chromosome 21. <i>Public Health Genomics</i> , 2016, 19, 11-18.	0.6	14
68	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in <i>GRHL3</i> . <i>American Journal of Human Genetics</i> , 2016, 98, 744-754.	2.6	146
69	Efficient Identification of Null-Allele Single Nucleotide Polymorphism Markers. <i>Human Heredity</i> , 2015, 80, 79-89.	0.4	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). <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, 64.	1.2	28
71	Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1961-1971.	0.8	28
72	Genetic Determinants of Survival in Patients with Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 45, 651-658.	1.2	11

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73	Caries Experience Differs between Females and Males across Age Groups in Northern Appalachia. <i>International Journal of Dentistry</i> , 2015, 2015, 1-8.	0.5	30
74	Effects of enamel matrix genes on dental caries are moderated by fluoride exposures. <i>Human Genetics</i> , 2015, 134, 159-167.	1.8	38
75	Genome-wide copy-number variation study of psychosis in Alzheimer's disease. <i>Translational Psychiatry</i> , 2015, 5, e574-e574.	2.4	24
76	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. <i>PLoS Genetics</i> , 2015, 11, e1005059.	1.5	82
77	A Rare Duplication on Chromosome 16p11.2 Is Identified in Patients with Psychosis in Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e111462.	1.1	16
78	Life factors affecting depression and burden in amyotrophic lateral sclerosis caregivers. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2014, 15, 292-297.	1.1	39
79	Evidence for dysregulation of genome-wide recombination in oocytes with nondisjoined chromosomes 21. <i>Human Molecular Genetics</i> , 2014, 23, 408-417.	1.4	17
80	Genome-Wide Association Study of Primary Dentition Pit-and-Fissure and Smooth Surface Caries. <i>Caries Research</i> , 2014, 48, 330-338.	0.9	38
81	Genome-Wide Association Study of Periodontal Health Measured by Probing Depth in Adults Ages 18-49 years. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 307-314.	0.8	54
82	Genetic Association of <i>MPPED2</i> and <i>ACTN2</i> with Dental Caries. <i>Journal of Dental Research</i> , 2014, 93, 626-632.	2.5	28
83	An Examination of the Relationship between Hotspots and Recombination Associated with Chromosome 21 Nondisjunction. <i>PLoS ONE</i> , 2014, 9, e99560.	1.1	15
84	Allelic Interaction between <i>CRELD1</i> and <i>VEGFA</i> in the Pathogenesis of Cardiac Atrioventricular Septal Defects. <i>AIMS Genetics</i> , 2014, 01, 001-019.	1.9	13
85	Allelic Interaction between <i>ACTN2</i> and <i>VEGFA</i> in the Pathogenesis of Cardiac Atrioventricular Septal Defects. <i>AIMS Genetics</i> , 2014, 1, 1-19.	1.9	7
86	Clustering Tooth Surfaces into Biologically Informative Caries Outcomes. <i>Journal of Dental Research</i> , 2013, 92, 32-37.	2.5	31
87	GWAS of Dental Caries Patterns in the Permanent Dentition. <i>Journal of Dental Research</i> , 2013, 92, 38-44.	2.5	77
88	Genome-wide Association Studies of Pit-and-Fissure- and Smooth-surface Caries in Permanent Dentition. <i>Journal of Dental Research</i> , 2013, 92, 432-437.	2.5	61
89	Peripheral Blood Mononuclear Cell Gene Expression Profiles Predict Poor Outcome in Idiopathic Pulmonary Fibrosis. <i>Science Translational Medicine</i> , 2013, 5, 205ra136.	5.8	242
90	Demographic, socioeconomic, and behavioral factors affecting patterns of tooth decay in the permanent dentition: principal components and factor analyses. <i>Community Dentistry and Oral Epidemiology</i> , 2013, 41, 364-373.	0.9	22

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91	Association Signals Unveiled by a Comprehensive Gene Set Enrichment Analysis of Dental Caries Genome-Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e72653.	1.1	15
92	Association of maternal CNVs in GSTT1/GSTT2 with smoking, preterm delivery, and low birth weight. <i>Frontiers in Genetics</i> , 2013, 4, 196.	1.1	17
93	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. <i>PLoS ONE</i> , 2013, 8, e76666.	1.1	24
94	Genome-wide Association Studies. <i>Journal of Dental Research</i> , 2012, 91, 637-641.	2.5	12
95	Connexin 47 Mutations Increase Risk for Secondary Lymphedema Following Breast Cancer Treatment. <i>Clinical Cancer Research</i> , 2012, 18, 2382-2390.	3.2	95
96	Genome-wide association analysis of age-at-onset in Alzheimer's disease. <i>Molecular Psychiatry</i> , 2012, 17, 1340-1346.	4.1	89
97	Comprehensive literature review and statistical considerations for microarray meta-analysis. <i>Nucleic Acids Research</i> , 2012, 40, 3785-3799.	6.5	427
98	No observed association for mitochondrial SNPs with preterm delivery and related outcomes. <i>Pediatric Research</i> , 2012, 72, 539-544.	1.1	22
99	Polymorphic haplotypes of <i>CRELD1</i> differentially predispose Down syndrome and euploids individuals to atrioventricular septal defect. <i>American Journal of Medical Genetics, Part A</i> , 2012, 158A, 2843-2848.	0.7	13
100	Genome-wide association study of Alzheimer's disease. <i>Translational Psychiatry</i> , 2012, 2, e117-e117.	2.4	209
101	An Excess of Deleterious Variants in VEGF-A Pathway Genes in Down-Syndrome-Associated Atrioventricular Septal Defects. <i>American Journal of Human Genetics</i> , 2012, 91, 646-659.	2.6	99
102	Genome-wide association Scan of dental caries in the permanent dentition. <i>BMC Oral Health</i> , 2012, 12, 57.	0.8	69
103	Effects of Smoking and Genotype on the PSR Index of Periodontal Disease in Adults Aged 18-49. <i>International Journal of Environmental Research and Public Health</i> , 2012, 9, 2839-2850.	1.2	14
104	Detectable clonal mosaicism from birth to old age and its relationship to cancer. <i>Nature Genetics</i> , 2012, 44, 642-650.	9.4	511
105	Using Family Data as a Verification Standard to Evaluate Copy Number Variation Calling Strategies for Genetic Association Studies. <i>Genetic Epidemiology</i> , 2012, 36, 253-262.	0.6	19
106	Comprehensive literature review and statistical considerations for GWAS meta-analysis. <i>Nucleic Acids Research</i> , 2012, 40, 3777-3784.	6.5	154
107	Altered patterns of multiple recombinant events are associated with nondisjunction of chromosome 21. <i>Human Genetics</i> , 2012, 131, 1039-1046.	1.8	39
108	Replication of a Genome-Wide Association Study of Birth Weight in Preterm Neonates. <i>Journal of Pediatrics</i> , 2012, 160, 19-24.e4.	0.9	21

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109	Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. <i>BMC Oral Health</i> , 2012, 12, 7.	0.8	35
110	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011, 43, 519-525.	9.4	834
111	Long-term outcomes, branch-specific expressivity, and disease-related mortality in von Hippel-Lindau type 2A. <i>Familial Cancer</i> , 2011, 10, 701-707.	0.9	5
112	Genotype-phenotype correlations of pheochromocytoma in two large von Hippel-Lindau (VHL) type 2A kindreds with different missense mutations. <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 168-173.	0.7	18
113	Association Between NEDD4L Gene and Sodium Lithium Countertransport. <i>American Journal of Hypertension</i> , 2011, 24, 145-148.	1.0	6
114	Epidemiology of Down Syndrome: New Insight Into the Multidimensional Interactions Among Genetic and Environmental Risk Factors in the Oocyte. <i>American Journal of Epidemiology</i> , 2011, 174, 1009-1016.	1.6	37
115	Genome-wide Association Scan for Childhood Caries Implicates Novel Genes. <i>Journal of Dental Research</i> , 2011, 90, 1457-1462.	2.5	108
116	Association tests using kernel-based measures of multi-locus genotype similarity between individuals. <i>Genetic Epidemiology</i> , 2010, 34, 213-221.	0.6	69
117	What's the best statistic for a simple test of genetic association in a case-control study?. <i>Genetic Epidemiology</i> , 2010, 34, 246-253.	0.6	35
118	292 A Genome-Wide Association Study of Spontaneous Preterm Delivery. <i>Pediatric Research</i> , 2010, 68, 150-150.	1.1	1
119	CJC2 Missense Mutations Cause Human Lymphedema. <i>American Journal of Human Genetics</i> , 2010, 86, 943-948.	2.6	141
120	Telomere length is associated with types of chromosome 21 nondisjunction: a new insight into the maternal age effect on Down syndrome birth. <i>Human Genetics</i> , 2010, 127, 403-409.	1.8	38
121	The gene, environment association studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. <i>Genetic Epidemiology</i> , 2010, 34, 364-372.	0.6	139
122	Variation in folate pathway genes contributes to risk of congenital heart defects among individuals with Down syndrome. <i>Genetic Epidemiology</i> , 2010, 34, 613-623.	0.6	66
123	A Likelihood-Based Approach for Missing Genotype Data. <i>Human Heredity</i> , 2010, 69, 171-183.	0.4	2
124	Genetic Control of Hotspots. <i>Science</i> , 2010, 327, 791-792.	6.0	24
125	Pooling-Based Genome-Wide Association Study Implicates Gamma-Glutamyltransferase 1 (GGT1) Gene in Pancreatic Carcinogenesis. <i>Pancreatology</i> , 2010, 10, 194-200.	0.5	38
126	Host Genetics, Steatosis and Insulin Resistance among African Americans and Caucasian Americans with Hepatitis C Virus Genotype-1 Infection. <i>Intervirology</i> , 2009, 52, 49-56.	1.2	8

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127	Genetic Analysis of Variation in Human Meiotic Recombination. <i>PLoS Genetics</i> , 2009, 5, e1000648.	1.5	142
128	Etiology of Down syndrome: Evidence for consistent association among altered meiotic recombination, nondisjunction, and maternal age across populations. <i>American Journal of Medical Genetics, Part A</i> , 2009, 149A, 1415-1420.	0.7	76
129	A comparison of principal component analysis and factor analysis strategies for uncovering pleiotropic factors. <i>Genetic Epidemiology</i> , 2009, 33, 325-331.	0.6	19
130	Decreased expression of miR-125b and miR-100 in oral cancer cells contributes to malignancy. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 569-582.	1.5	203
131	Investigation of factors associated with paternal nondisjunction of chromosome 21. <i>American Journal of Medical Genetics, Part A</i> , 2009, 149A, 1685-1690.	0.7	26
132	Robust Score Statistics for QTL Linkage Analysis. <i>American Journal of Human Genetics</i> , 2008, 82, 567-582.	2.6	9
133	New Insights into Human Nondisjunction of Chromosome 21 in Oocytes. <i>PLoS Genetics</i> , 2008, 4, e1000033.	1.5	146
134	Smarter clustering methods for SNP genotype calling. <i>Bioinformatics</i> , 2008, 24, 2665-2671.	1.8	18
135	Inverted duplication pattern in anaphase bridges confirms the breakage-fusion-bridge (BFB) cycle model for 11q13 amplification. <i>Cytogenetic and Genome Research</i> , 2007, 116, 46-52.	0.6	22
136	Mass Spectral Determination of Fasting Tear Glucose Concentrations in Nondiabetic Volunteers. <i>Clinical Chemistry</i> , 2007, 53, 1370-1372.	1.5	101
137	Gender-specific association of ATP-binding cassette transporter 1 (ABCA1) polymorphisms with the risk of late-onset Alzheimer's disease. <i>Neurobiology of Aging</i> , 2007, 28, 856-862.	1.5	69
138	Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. <i>Genome Biology</i> , 2007, 8, R84.	13.9	26
139	The origin of trisomy 22: Evidence for acrocentric chromosome-specific patterns of nondisjunction. <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 2249-2255.	0.7	28
140	The elusive goal of pedigree weights. <i>Genetic Epidemiology</i> , 2007, 31, 51-65.	0.6	17
141	A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. <i>Genetic Epidemiology</i> , 2007, 31, 417-430.	0.6	2
142	Web-Based Identification of Evolutionary Conserved DNA cis-Regulatory Elements. <i>Methods in Molecular Biology</i> , 2007, 395, 425-436.	0.4	2
143	Relationship of recombination patterns and maternal age among non-disjoined chromosomes 21. <i>Biochemical Society Transactions</i> , 2006, 34, 578-580.	1.6	27
144	Genetic association of ubiquilin with Alzheimer's disease and related quantitative measures. <i>Molecular Psychiatry</i> , 2006, 11, 273-279.	4.1	59

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145	Increased expression of interferon-inducible genes in macaque lung tissues during simian immunodeficiency virus infection. <i>Microbes and Infection</i> , 2006, 8, 1839-1850.	1.0	25
146	Gene-dropping vs. empirical variance estimation for allele-sharing linkage statistics. <i>Genetic Epidemiology</i> , 2006, 30, 652-665.	0.6	10
147	Referral to cancer genetic counseling: Are there stages of readiness?. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2006, 142C, 221-231.	0.7	43
148	Treatment of Uninformative Families in Mean Allele Sharing Tests for Linkage. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2006, 5, Article13.	0.2	0
149	Skeletal muscle fatigue, strength, and quality in the elderly: the Health ABC Study. <i>Journal of Applied Physiology</i> , 2005, 99, 210-216.	1.2	102
150	QTL mapping with discordant and concordant sibling pairs: new statistics and new design strategies. <i>Genetic Epidemiology</i> , 2005, 28, 326-340.	0.6	4
151	Footer: A quantitative comparative genomics method for efficient recognition of cis-regulatory elements. <i>Genome Research</i> , 2005, 15, 840-847.	2.4	23
152	FOOTER: a web tool for finding mammalian DNA regulatory regions using phylogenetic footprinting. <i>Nucleic Acids Research</i> , 2005, 33, W442-W446.	6.5	27
153	Association between Maternal Age and Meiotic Recombination for Trisomy 21. <i>American Journal of Human Genetics</i> , 2005, 76, 91-99.	2.6	107
154	The C161T polymorphism in peroxisome proliferator-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 proliferator-activated receptor gamma. <i>Metabolism: Clinical and Experimental</i> , 2005, 54, 1552-1556.	1.5	28
155	Efficient Simulation of P Values for Linkage Analysis. <i>Genetic Epidemiology</i> , 2004, 26, 88-96.	0.6	10
156	A trisomic transmission disequilibrium test. <i>Genetic Epidemiology</i> , 2004, 26, 125-131.	0.6	7
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