Mariza de Andrade

List of Publications by Year
in descending order

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206 papers	14,609 citations	30070 54 h-index	22832 112 g-index
219 all docs	219 docs citations	219 times ranked	24039 citing authors

#	Article	IF	Citations
1	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
2	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	21.4	834
3	Lower Cancer Incidence in Amsterdam-I Criteria Families Without Mismatch Repair Deficiency. JAMA - Journal of the American Medical Association, 2005, 293, 1979.	7.4	491
4	Survival patterns after oophorectomy in premenopausal women: a population-based cohort study. Lancet Oncology, The, 2006, 7, 821-828.	10.7	482
5	High-Resolution Whole-Genome Association Study of Parkinson Disease. American Journal of Human Genetics, 2005, 77, 685-693.	6.2	479
6	Pancreatic Cancerâ€“Associated Diabetes Mellitus: Prevalence and Temporal Association With Diagnosis of Cancer. Gastroenterology, 2008, 134, 95-101.	1.3	416
7	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
8	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
9	A Genomic Pathway Approach to a Complex Disease: Axon Guidance and Parkinson Disease. PLoS Genetics, 2007, 3, e98.	3.5	342
10	Atrial Natriuretic Peptide Frameshift Mutation in Familial Atrial Fibrillation. New England Journal of Medicine, 2008, 359, 158-165.	27.0	300
11	Mutations in Ribonucleic Acid Binding Protein Gene Cause Familial Dilated Cardiomyopathy. Journal of the American College of Cardiology, 2009, 54, 930-941.	2.8	299
12	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
13	Probability of Pancreatic Cancer Following Diabetes: A Population-Based Study. Gastroenterology, 2005, 129, 504-511.	1.3	234
14	Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. American Journal of Human Genetics, 2011, 89, 529-542.	6.2	232
15	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. Nature Genetics, 2017, 49, 269-273.	21.4	230
16	UCHL1 is a Parkinson's disease susceptibility gene. Annals of Neurology, 2004, 55, 512-521.	5.3	227
17	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
18	Human brain derived neurotrophic factor (BDNF) genes, splicing patterns, and assessments of associations with substance abuse and Parkinson's Disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 134B, 93-103.	1.7	192

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19	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
20	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
21	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
22	Adrenomedullin is Up-regulated in Patients With Pancreatic Cancer and Causes Insulin Resistance in Î² Cells and Mice. Gastroenterology, 2012, 143, 1510-1517.e1.	1.3	145
23	Metaâ€Analysis of Genomeâ€wide Linkage Studies in BMI and Obesity. Obesity, 2007, 15, 2263-2275.	3.0	138
24	Parkin variants in North American Parkinson's disease: Cases and controls. Movement Disorders, 2003, 18, 1306-1311.	3.9	131
25	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	2.3	130
26	Increased prevalence of antimitochondrial antibodies in first-degree relatives of patients with primary biliary cirrhosis. Hepatology, 2007, 46, 785-792.	7.3	125
27	Long-term risk of depressive and anxiety symptoms after early bilateral oophorectomy. Menopause, 2008, 15, 1050-1059.	2.0	124
28	Identifying disease modifying genes in multiple sclerosis. Journal of Neuroimmunology, 2002, 123, 144-159.	2.3	121
29	A new statistic for identifying batch effects in high-throughput genomic data that uses guided principal component analysis. Bioinformatics, 2013, 29, 2877-2883.	4.1	118
30	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
31	Randomâ€effects Cox proportional hazards model: General variance components methods for timeâ€toâ€event data. Genetic Epidemiology, 2005, 28, 97-109.	1.3	105
32	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
33	Temporal Association of Changes in Fasting Blood Glucose and Body Mass Index With Diagnosis of Pancreatic Cancer. American Journal of Gastroenterology, 2009, 104, 2318-2325.	0.4	99
34	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99
35	Brazilian urban population genetic structure reveals a high degree of admixture. European Journal of Human Genetics, 2012, 20, 111-116.	2.8	95
36	Comparison of Multivariate Tests for Genetic Linkage. Human Heredity, 2001, 51, 133-144.	0.8	92

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37	Heritability of Longitudinal Measures of Body Mass Index and Lipid and Lipoprotein Levels in Aging Twins. Twin Research and Human Genetics, 2007, 10, 703-711.	0.6	92
38	Genetics of cardiovascular disease: Importance of sex and ethnicity. Atherosclerosis, 2015, 241, 219-228.	0.8	92
39	Familial Aggregation of Irritable Bowel Syndrome: A Family Caseâ€“Control Study. American Journal of Gastroenterology, 2010, 105, 833-841.	0.4	91
40	Chemical exposures and Parkinson's disease: A population-based caseâ€“control study. Movement Disorders, 2006, 21, 1688-1692.	3.9	85
41	SNP interaction detection with Random Forests in high-dimensional genetic data. BMC Bioinformatics, 2012, 13, 164.	2.6	83
42	Obesity adversely affects survival in pancreatic cancer patients. Cancer, 2010, 116, 5054-5062.	4.1	81
43	Alopecia Areata in Families: Association with the HLA Locus. Journal of Investigative Dermatology Symposium Proceedings, 1999, 4, 220-223.	0.8	80
44	Fine Mapping of Chromosome 6q23-25 Region in Familial Lung Cancer Families Reveals RGS17 as a Likely Candidate Gene. Clinical Cancer Research, 2009, 15, 2666-2674.	7.0	80
45	Risk of malignancy in firstâ€degree relatives of patients with pancreatic carcinoma. Cancer, 2005, 104, 388-394.	4.1	78
46	Heritability of cardiovascular risk factors in a Brazilian population: Baependi Heart Study. BMC Medical Genetics, 2008, 9, 32.	2.1	76
47	Fruit and vegetable consumption is inversely associated with having pancreatic cancer. Cancer Causes and Control, 2011, 22, 1613-1625.	1.8	75
48	Immune Cell Infiltration May Be a Key Determinant of Long-Term Survival in Small Cell Lung Cancer. Journal of Thoracic Oncology, 2019, 14, 1286-1295.	1.1	75
49	CTLA4 is associated with susceptibility to multiple sclerosis. Journal of Neuroimmunology, 2003, 134, 133-141.	2.3	73
50	Leukocyte DNA Methylation Signature Differentiates Pancreatic Cancer Patients from Healthy Controls. PLoS ONE, 2011, 6, e18223.	2.5	73
51	Nutrients from Fruit and Vegetable Consumption Reduce the Risk of Pancreatic Cancer. Journal of Gastrointestinal Cancer, 2013, 44, 152-161.	1.3	72
52	Compound heterozygous NOTCH1 mutations underlie impaired cardiogenesis in a patient with hypoplastic left heart syndrome. Human Genetics, 2015, 134, 1003-1011.	3.8	71
53	Analysis of aromatic DNA adducts and 7,8-dihydro-8-oxo- 2â€²-deoxyguanosine in lymphocyte DNA from a caseâ€“control study of lung cancer involving minority populations. , 2000, 27, 34-46.		65
54	Mayo Genome Consortia: A Genotype-Phenotype Resource for Genome-Wide Association Studies With an Application to the Analysis of Circulating Bilirubin Levels. Mayo Clinic Proceedings, 2011, 86, 606-614.	3.0	63

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55	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
56	An international genome-wide meta-analysis of primary biliary cholangitis: Novel risk loci and candidate drugs. Journal of Hepatology, 2021, 75, 572-581.	3.7	62
57	A Recurrent Mutation in PARK2 Is Associated with Familial Lung Cancer. American Journal of Human Genetics, 2015, 96, 301-308.	6.2	61
58	Clinical outcomes and changes in lung function after segmentectomy versus lobectomy for lung cancer cases. Journal of Thoracic and Cardiovascular Surgery, 2014, 148, 1186-1192.e3.	0.8	58
59	Segregation analysis of cancer in families of glioma patients. Genetic Epidemiology, 2001, 20, 258-270.	1.3	56
60	The endothelial protein C receptor (PROCR) Ser219Gly variant and risk of common thrombotic disorders: a HuGE review and meta-analysis of evidence from observational studies. Blood, 2012, 119, 2392-2400.	1.4	56
61	Identification of Susceptibility Loci for Spontaneous Coronary Artery Dissection. JAMA Cardiology, 2020, 5, 929.	6.1	54
62	Software comparison for evaluating genomic copy number variation for Affymetrix 6.0 SNP array platform. BMC Bioinformatics, 2011, 12, 220.	2.6	51
63	Interaction of Î±â€synuclein and tau genotypes in Parkinson's disease. Annals of Neurology, 2005, 57, 439-443.	5.3	49
64	A genome-wide linkage scan for ankleâ€“brachial index in African American and non-Hispanic white subjects participating in the GENOA study. Atherosclerosis, 2006, 187, 433-438.	0.8	48
65	P-selectin and subclinical and clinical atherosclerosis: The Multi-Ethnic Study of Atherosclerosis (MESA). Atherosclerosis, 2015, 240, 3-9.	0.8	47
66	Penetrance of Hemochromatosis in HFE Genotypes Resulting in p.Cys282Tyr and p.[Cys282Tyr];[His63Asp] in the eMERGE Network. American Journal of Human Genetics, 2015, 97, 512-520.	6.2	47
67	Segregation analysis of idiopathic talipes equinovarus in a Texan population. , 1998, 79, 97-102.		46
68	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	3.8	46
69	A Robust e-Epidemiology Tool in Phenotyping Heart Failure with Differentiation for Preserved and Reduced Ejection Fraction: the Electronic Medical Records and Genomics (eMERGE) Network. Journal of Cardiovascular Translational Research, 2015, 8, 475-483.	2.4	44
70	Thrombomodulin gene polymorphisms or haplotypes as potential risk factors for venous thromboembolism: a population-based case-control study. Journal of Thrombosis and Haemostasis, 2005, 3, 710-717.	3.8	43
71	Ascertainment issues in variance components models. Genetic Epidemiology, 2000, 19, 333-344.	1.3	42
72	Genomic Susceptibility Loci for Brain Atrophy in Hypertensive Sibships From the GENOA Study. Hypertension, 2005, 45, 793-798.	2.7	42

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73	Multiple-level validation identifies PARK2 in the development of lung cancer and chronic obstructive pulmonary disease. Oncotarget, 2016, 7, 44211-44223.	1.8	42
74	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
75	Methods to estimate genetic components of variance for quantitative traits in family studies. Genetic Epidemiology, 1999, 17, 64-76.	1.3	40
76	Extension of variance components approach to incorporate temporal trends and longitudinal pedigree data analysis. Genetic Epidemiology, 2002, 22, 221-232.	1.3	40
77	Major Histocompatibility Complex Class I Chain-Related Gene A Polymorphisms and Extended Haplotypes Are Associated with Familial Alopecia Areata. Journal of Investigative Dermatology, 2006, 126, 74-78.	0.7	40
78	The ATXN2-SH2B3 locus is associated with peripheral arterial disease: an electronic medical record-based genome-wide association study. Frontiers in Genetics, 2014, 5, 166.	2.3	40
79	Adenocarcinoma in situ, minimally invasive adenocarcinoma, and invasive pulmonary adenocarcinomaâ€"analysis of interobserver agreement, survival, radiographic characteristics, and gross pathology in 296 nodules. Human Pathology, 2016, 51, 41-50.	2.0	39
80	Coffee, caffeineâ€related genes, and Parkinson's disease: A caseâ€"control study. Movement Disorders, 2008, 23, 2033-2040.	3.9	38
81	Reduced Coffee Consumption Among Individuals With Primary Sclerosing Cholangitis but Not Primary Biliary Cirrhosis. Clinical Gastroenterology and Hepatology, 2014, 12, 1562-1568.	4.4	38
82	Family-based association study of matrix metalloproteinase-3 and -9 haplotypes with susceptibility to ischemic white matter injury. Human Genetics, 2007, 120, 671-680.	3.8	36
83	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
84	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
85	CCR5Î"32 polymorphism effects on CCR5 expression, patterns of immunopathology and disease course in multiple sclerosis. Journal of Neuroimmunology, 2005, 169, 137-143.	2.3	35
86	Biochemical response to ursodeoxycholic acid predicts survival in a North American cohort of primary biliary cirrhosis patients. Journal of Gastroenterology, 2014, 49, 1414-1420.	5.1	35
87	Identification of unique venous thromboembolism-susceptibility variants in African-Americans. Thrombosis and Haemostasis, 2017, 117, 758-768.	3.4	35
88	Genetic Variants Associated with Serum Thyroid Stimulating Hormone (TSH) Levels in European Americans and African Americans from the eMERGE Network. PLoS ONE, 2014, 9, e111301.	2.5	34
89	Sexâ€Specific Genetic Variants are Associated With Coronary Endothelial Dysfunction. Journal of the American Heart Association, 2016, 5, e002544.	3.7	34
90	Interferon Gamma Allelic Variants. Archives of Neurology, 2008, 65, 349-57.	4.5	33

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91	Multivariate linkage analysis of blood pressure and body mass index. Genetic Epidemiology, 2004, 27, 64-73.	1.3	32
92	Long-Term Survival and Prognostic Indicators in Small (â‰¤2 cm) Pancreatic Cancer. Pancreatology, 2008, 8, 587-592.	1.1	32
93	Cohort profile: the Baependi Heart Studyâ€"a family-based, highly admixed cohort study in a rural Brazilian town. BMJ Open, 2016, 6, e011598.	1.9	32
94	Complex interactions in Parkinson's disease: A two-phased approach. Movement Disorders, 2003, 18, 631-636.	3.9	30
95	CD95 polymorphisms are associated with susceptibility to MS in women. Journal of Neuroimmunology, 2004, 146, 162-170.	2.3	30
96	Identification of genes and haplotypes that predict rheumatoid arthritis using random forests. BMC Proceedings, 2009, 3, S68.	1.6	30
97	Î±-Synuclein, alcohol use disorders, and Parkinson disease: A caseâ€"control study. Parkinsonism and Related Disorders, 2009, 15, 430-434.	2.2	30
98	Interleukin-1 Receptor Antagonist Allele 2 and Familial Alopecia Areata. Journal of Investigative Dermatology, 2002, 118, 335-337.	0.7	29
99	Assessment of genotype imputation methods. BMC Proceedings, 2009, 3, S5.	1.6	29
100	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
101	Response from Maraganore et al.. American Journal of Human Genetics, 2006, 78, 1092-1094.	6.2	28
102	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. Journal of Thoracic Oncology, 2016, 11, 52-61.	1.1	27
103	Genomic loci with pleiotropic effects on coronary artery calcification. Atherosclerosis, 2006, 185, 340-346.	0.8	26
104	Human Leukocyte Antigen Class II Alleles Are Associated with Risk of Alopecia Areata. Journal of Investigative Dermatology, 2008, 128, 240-243.	0.7	26
105	Stress hormones concentrations in the normal microenvironment predict risk for chemically induced cancer in rats. Psychoneuroendocrinology, 2018, 89, 229-238.	2.7	26
106	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
107	Case-Control Genetic Association Studies in Gastrointestinal Disease: Review and Recommendations. American Journal of Gastroenterology, 2006, 101, 1379-1389.	0.4	24
108	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	3.6	24

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109	Genomic Susceptibility Loci for Brain Atrophy, Ventricular Volume, and Leukoaraiosis in Hypertensive Sibships. Archives of Neurology, 2009, 66, 847-57.	4.5	23
110	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. Genome Medicine, 2015, 7, 67.	8.2	23
111	Pharmacogenomics of estrogens on changes in carotid artery intima-medial thickness and coronary arterial calcification: Kronos Early Estrogen Prevention Study. Physiological Genomics, 2016, 48, 33-41.	2.3	23
112	Hepatocyte growth factor demonstrates racial heterogeneity as a biomarker for coronary heart disease. Heart, 2017, 103, 1185-1193.	2.9	23
113	Association of Family History of Specific Cancers With a Younger Age of Onset of Pancreatic Adenocarcinoma. Clinical Gastroenterology and Hepatology, 2006, 4, 1143-1147.	4.4	22
114	Novel Genomic Loci Influencing Plasma Homocysteine Levels. Stroke, 2006, 37, 1703-1709.	2.0	22
115	Familial Lung Cancer: A Brief History from the Earliest Work to the Most Recent Studies. Genes, 2017, 8, 36.	2.4	22
116	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. Journal of Thoracic Oncology, 2018, 13, 1483-1495.	1.1	22
117	The foundation of precision medicine: integration of electronic health records with genomics through basic, clinical, and translational research. Frontiers in Genetics, 2015, 6, 104.	2.3	21
118	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. Circulation Genomic and Precision Medicine, 2021, 14, e003354.	3.6	21
119	Linkage analysis of chromosome 4 in families with familial pancreatic cancer. Cancer Biology and Therapy, 2007, 6, 320-323.	3.4	20
120	Heritability of physical activity traits in Brazilian families: the Baependi Heart Study. BMC Medical Genetics, 2011, 12, 155.	2.1	19
121	Genetic analyses of smoking initiation, persistence, quantity, and age-at-onset of regular cigarette use in Brazilian families: the Baependi Heart Study. BMC Medical Genetics, 2012, 13, 9.	2.1	19
122	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	2.4	19
123	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	5.4	19
124	Localization of genes involved in the metabolic syndrome using multivariate linkage analysis. BMC Genetics, 2003, 4, S57.	2.7	16
125	A Novel Quantitative Trait Locus on Chromosome 1 with Pleiotropic Effects on HDL-Cholesterol and LDL Particle Size in Hypertensive Sibships. American Journal of Hypertension, 2005, 18, 1084-1090.	2.0	16
126	Clinical Features of Bronchioloalveolar Carcinoma with New Histologic and Staging Definitions. Journal of Thoracic Oncology, 2010, 5, 1213-1220.	1.1	16

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127	SLCO1B1 genetic variation and hormone therapy in menopausal women. Menopause, 2018, 25, 877-882.	2.0	16
128	Controlling for population structure and genotyping platform bias in the eMERGE multi-institutional biobank linked to electronic health records. Frontiers in Genetics, 2014, 5, 352.	2.3	14
129	Risk assessment for developing gliomas: a comparison of two cytogenetic approaches. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2001, 490, 35-44.	1.7	13
130	Case-control study of the ?-synuclein interacting protein gene and Parkinson's disease. Movement Disorders, 2003, 18, 1233-1239.	3.9	13
131	Identification of gene-gene interaction using principal components. BMC Proceedings, 2009, 3, S78.	1.6	13
132	Transâ€Ethnic Metaâ€Analysis Identifies Common and Rare Variants Associated with Hepatocyte Growth Factor Levels in the Multiâ€Ethnic Study of Atherosclerosis (MESA). Annals of Human Genetics, 2015, 79, 264-274.	0.8	13
133	Parametric Linkage Analysis Identifies Five Novel Genome-Wide Significant Loci for Familial Lung Cancer. Human Heredity, 2016, 82, 64-74.	0.8	13
134	Number of children and risk of Parkinson's disease. Movement Disorders, 2007, 22, 632-639.	3.9	12
135	Perceptions of Lung Cancer Risk and Beliefs in Screening Accuracy of Spiral Computed Tomography among High-Risk Lung Cancer Family Members. Academic Radiology, 2010, 17, 1012-1025.	2.5	12
136	A Digital Health Weight Loss Program in 250,000 Individuals. Journal of Obesity, 2020, 2020, 1-8.	2.7	12
137	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
138	Diagnostic tools in linkage analysis for quantitative traits. Genetic Epidemiology, 2003, 24, 302-308.	1.3	11
139	Analysis of variation in NF-Î°B genes and expression levels of NF-Î°B-regulated molecules. BMC Proceedings, 2007, 1, S126.	1.6	11
140	Whole Exome Sequencing of Highly Aggregated Lung Cancer Families Reveals Linked Loci for Increased Cancer Risk on Chromosomes 12q, 7p, and 4q. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 434-442.	2.5	11
141	EGFR mediates activation of RET in lung adenocarcinoma with neuroendocrine differentiation characterized by ASCL1 expression. Oncotarget, 2017, 8, 27155-27165.	1.8	11
142	Analysis of aromatic DNA adducts and 7,8-dihydro-8-oxo-2? deoxyguanosine in lymphocyte DNA from a case-control study of lung cancer involving minority populations. , 2000, 27, 330-330.		10
143	Group 6: Pleiotropy and multivariate analysis. Genetic Epidemiology, 2003, 25, S50-S56.	1.3	10
144	Imputation methods for missing data for polygenic models. BMC Genetics, 2003, 4, S42.	2.7	10

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145	Quantitative trait loci influencing low density lipoprotein particle size in African Americans. Journal of Lipid Research, 2006, 47, 1457-1462.	4.2	10
146	Evaluating gene by sex and age interactions on cardiovascular risk factors in Brazilian families. BMC Medical Genetics, 2010, 11, 132.	2.1	10
147	Linkage analysis of obesity phenotypes in pre- and post-menopausal women from a United States mid-western population. BMC Medical Genetics, 2010, 11, 156.	2.1	10
148	Plasma and serum L-selectin and clinical and subclinical cardiovascular disease: the Multi-Ethnic Study of Atherosclerosis (MESA). Translational Research, 2014, 163, 585-592.	5.0	10
149	Multi-ethnic analysis reveals soluble l-selectin may be post-transcriptionally regulated by 3â€²UTR polymorphism: the Multi-Ethnic Study of Atherosclerosis (MESA). Human Genetics, 2015, 134, 393-403.	3.8	10
150	A digital health weight-loss intervention in severe obesity. Digital Health, 2020, 6, 205520762091027.	1.8	10
151	Impact of adiposity on cellular adhesion: The Multiâ€Ethnic Study of atherosclerosis (MESA). Obesity, 2016, 24, 223-230.	3.0	9
152	Identification of genes involved in alcohol consumption and cigarettes smoking. BMC Genetics, 2005, 6, S112.	2.7	7
153	The Mayo Clinic Cohort Study of Personality and Aging: Design and Sampling, Reliability and Validity of Instruments, and Baseline Description. Neuroepidemiology, 2006, 26, 119-129.	2.3	7
154	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
155	Comparison of longitudinal variance components and regression-based approaches for linkage detection on chromosome 17 for systolic blood pressure. BMC Genetics, 2003, 4, S17.	2.7	6
156	Entropy Based Genetic Association Tests and Gene-Gene Interaction Tests. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	6
157	Global Individual Ancestry Using Principal Components for Family Data. Human Heredity, 2015, 80, 1-11.	0.8	6
158	Comparison of tagging single-nucleotide polymorphism methods in association analyses. BMC Proceedings, 2007, 1, S6.	1.6	5
159	Missing phenotype data imputation in pedigree data analysis. Genetic Epidemiology, 2008, 32, 52-60.	1.3	5
160	Genetic Analysis of Age-at-Onset for Cardiovascular Risk Factors in a Brazilian Family Study. Human Heredity, 2009, 68, 131-138.	0.8	5
161	Evaluating the Influence of Quality Control Decisions and Software Algorithms on SNP Calling for the Affymetrix 6.0 SNP Array Platform. Human Heredity, 2011, 71, 221-233.	0.8	5
162	An Efficient Test for Gene-Environment Interaction in Generalized Linear Mixed Models with Family Data. International Journal of Environmental Research and Public Health, 2017, 14, 1134.	2.6	5

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163	Genetic Variation and Recurrent Haplotypes on Chromosome 6q23-25 Risk Locus in Familial Lung Cancer. Cancer Research, 2021, 81, 3162-3173.	0.9	5
164	Screening the genome to detect an association with hypertension. BMC Genetics, 2003, 4, S63.	2.7	4
165	Using Item Response Theory to Model Multiple Phenotypes and Their Joint Heritability in Family Data. Genetic Epidemiology, 2014, 38, 152-161.	1.3	4
166	Elevated Levels of Adhesion Proteins Are Associated With Low Ankleâ€“Brachial Index. Angiology, 2017, 68, 322-329.	1.8	4
167	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Recordâ€“Linked Genome-Wide Association Study. Journal of Investigative Medicine High Impact Case Reports, 2013, 1, 232470961350893.	0.6	3
168	Estimation of quantitative genetic parameters under non-normal models. Annals of Human Genetics, 1995, 59, 107-122.	0.8	2
169	The genetics of gene expression: comparison of linkage scans using two phenotype normalization methods. BMC Proceedings, 2007, 1, S151.	1.6	2
170	Summary of contributions to GAW15 Group 13: candidate gene association studies. Genetic Epidemiology, 2007, 31, S110-S117.	1.3	2
171	179 Clinical Characteristics of Familial Irritable Bowel Syndrome (IBS) Differ from Sporadic IBS. Gastroenterology, 2008, 134, A-30.	1.3	2
172	Adjusting for HLA-DRÎ²1 in a genome-wide association analysis of rheumatoid arthritis and related biomarkers. BMC Proceedings, 2009, 3, S12.	1.6	2
173	Association of TNFSF8 Polymorphisms With Peripheral Neutrophil Count. Mayo Clinic Proceedings, 2011, 86, 1075-1081.	3.0	2
174	The association of copy number variation and percent mammographic density. BMC Research Notes, 2015, 8, 297.	1.4	2
175	GAW20: methods and strategies for the new frontiers of epigenetics and pharmacogenomics. BMC Proceedings, 2018, 12, 26.	1.6	2
176	The challenge of detecting genotype-by-methylation interaction: GAW20. BMC Genetics, 2018, 19, 81.	2.7	2
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