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	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
2	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
3	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
4	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
5	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
6	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	5.4	19
7	Genetic Variation and Recurrent Haplotypes on Chromosome 6q23-25 Risk Locus in Familial Lung Cancer. Cancer Research, 2021, 81, 3162-3173.	0.9	5
8	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
9	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
10	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	3.6	24
11	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
12	Identification of Susceptibility Loci for Spontaneous Coronary Artery Dissection. JAMA Cardiology, 2020, 5, 929.	6.1	54
13	A digital health weight-loss intervention in severe obesity. Digital Health, 2020, 6, 205520762091027.	1.8	10
14	A Digital Health Weight Loss Program in 250,000 Individuals. Journal of Obesity, 2020, 2020, 1-8.	2.7	12
15	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
16	Bivariate traits association analysis using generalized estimating equations in family data. Statistical Applications in Genetics and Molecular Biology, 2020, 19, .	0.6	1
17	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
18	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

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19	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
20	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
21	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
22	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
23	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
24	Stress hormones concentrations in the normal microenvironment predict risk for chemically induced cancer in rats. Psychoneuroendocrinology, 2018, 89, 229-238.	2.7	26
25	GAW20: methods and strategies for the new frontiers of epigenetics and pharmacogenomics. BMC Proceedings, 2018, 12, 26.	1.6	2
26	Age-related DNA methylation and hemostatic factors. Blood, 2018, 132, 1736-1736.	1.4	0
27	The challenge of detecting genotype-by-methylation interaction: GAW20. BMC Genetics, 2018, 19, 81.	2.7	2
28	SLCO1B1 genetic variation and hormone therapy in menopausal women. Menopause, 2018, 25, 877-882.	2.0	16
29	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
30	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
31	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
32	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	3.8	46
33	Hepatocyte growth factor demonstrates racial heterogeneity as a biomarker for coronary heart disease. Heart, 2017, 103, 1185-1193.	2.9	23
34	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
35	Elevated Levels of Adhesion Proteins Are Associated With Low Ankleâ€“Brachial Index. Angiology, 2017, 68, 322-329.	1.8	4
36	Familial Lung Cancer: A Brief History from the Earliest Work to the Most Recent Studies. Genes, 2017, 8, 36.	2.4	22

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37	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
38	Identification of Genetic Interaction with Risk Factors Using a Time-To-Event Model. International Journal of Environmental Research and Public Health, 2017, 14, 1228.	2.6	1
39	Identification of unique venous thromboembolism-susceptibility variants in African-Americans. Thrombosis and Haemostasis, 2017, 117, 758-768.	3.4	35
40	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
41	EGFR mediates activation of RET in lung adenocarcinoma with neuroendocrine differentiation characterized by ASCL1 expression. Oncotarget, 2017, 8, 27155-27165.	1.8	11
42	Multiple-level validation identifies PARK2 in the development of lung cancer and chronic obstructive pulmonary disease. Oncotarget, 2016, 7, 44211-44223.	1.8	42
43	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
44	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
45	Sexâ€Specific Genetic Variants are Associated With Coronary Endothelial Dysfunction. Journal of the American Heart Association, 2016, 5, e002544.	3.7	34
46	Parametric Linkage Analysis Identifies Five Novel Genome-Wide Significant Loci for Familial Lung Cancer. Human Heredity, 2016, 82, 64-74.	0.8	13
47	Impact of adiposity on cellular adhesion: The Multiâ€Ethnic Study of atherosclerosis (MESA). Obesity, 2016, 24, 223-230.	3.0	9
48	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
49	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
50	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
51	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
52	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
53	A Recurrent Mutation in PARK2 Is Associated with Familial Lung Cancer. American Journal of Human Genetics, 2015, 96, 301-308.	6.2	61
54	Compound heterozygous NOTCH1 mutations underlie impaired cardiogenesis in a patient with hypoplastic left heart syndrome. Human Genetics, 2015, 134, 1003-1011.	3.8	71

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55	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
56	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
57	Global Individual Ancestry Using Principal Components for Family Data. Human Heredity, 2015, 80, 1-11.	0.8	6
58	Genetics of cardiovascular disease: Importance of sex and ethnicity. Atherosclerosis, 2015, 241, 219-228.	0.8	92
59	P-selectin and subclinical and clinical atherosclerosis: The Multi-Ethnic Study of Atherosclerosis (MESA). Atherosclerosis, 2015, 240, 3-9.	0.8	47
60	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
61	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
62	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
63	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. Genome Medicine, 2015, 7, 67.	8.2	23
64	The association of copy number variation and percent mammographic density. BMC Research Notes, 2015, 8, 297.	1.4	2
65	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
66	Abstract LB-189: Genetic Epidemiology of Lung Cancer Consortium: genome-wide association study of familial lung cancer cases. , 2015, , .		0
67	Abstract 2757: Evaluation ofEYA4as a candidate risk locus in familial lung cancer families linked to 6q. , 2015, , .		0
68	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
69	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
70	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	2.3	130
71	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
72	Using Item Response Theory to Model Multiple Phenotypes and Their Joint Heritability in Family Data. Genetic Epidemiology, 2014, 38, 152-161.	1.3	4

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73	Using the theory of added-variable plot for linear mixed models to decompose genetic effects in family data. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 359-78.	0.6	1
74	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
75	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
76	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
77	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
78	Nutrients from Fruit and Vegetable Consumption Reduce the Risk of Pancreatic Cancer. Journal of Gastrointestinal Cancer, 2013, 44, 152-161.	1.3	72
79	630 Coffee Consumption Is Associated With Reduced Risk of Primary Sclerosing Cholangitis but Not Primary Biliary Cirrhosis. Gastroenterology, 2013, 144, S-956.	1.3	0
80	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
81	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
82	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
83	Abstract 330: Ethnic Variability in the Association of Pulse Pressure with Adhesion Pathway Proteins: The Multi-Ethnic Study of Atherosclerosis (MESA) Study. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, .	2.4	0
84	Genome-Wide Association Study (GWAS) Of Venous Thromboembolism (VTE) In African-Americans From The Electronic Medical Records & Genomics (eMERGE) Networkm. Blood, 2013, 122, 458-458.	1.4	0
85	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Record-Linked Genome-Wide Association Study: A Case Series. Journal of Investigative Medicine, 2013, 1, .	1.6	0
86	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
87	Brazilian urban population genetic structure reveals a high degree of admixture. European Journal of Human Genetics, 2012, 20, 111-116.	2.8	95
88	SNP interaction detection with Random Forests in high-dimensional genetic data. BMC Bioinformatics, 2012, 13, 164.	2.6	83
89	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
90	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

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91	Association of mitogen activated protein kinase genetic polymorphism with carotid intima medial thickness (CIMT) in women enrolled in the Kronos Early Estrogen Prevention Study (KEEPS). FASEB Journal, 2012, 26, 1134.6.	0.5	0
92	Single Nucleotide Polymorphisms (SNPs) Associated with Pulmonary Embolism (PE): A Genome-Wide Association Study (GWAS). Blood, 2012, 120, 1148-1148.	1.4	0
93	Association of TNFSF8 Polymorphisms With Peripheral Neutrophil Count. Mayo Clinic Proceedings, 2011, 86, 1075-1081.	3.0	2
94	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
95	Software comparison for evaluating genomic copy number variation for Affymetrix 6.0 SNP array platform. BMC Bioinformatics, 2011, 12, 220.	2.6	51
96	Leukocyte DNA Methylation Signature Differentiates Pancreatic Cancer Patients from Healthy Controls. PLoS ONE, 2011, 6, e18223.	2.5	73
97	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	21.4	834
98	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
99	Fruit and vegetable consumption is inversely associated with having pancreatic cancer. Cancer Causes and Control, 2011, 22, 1613-1625.	1.8	75
100	Heritability of physical activity traits in Brazilian families: the Baependi Heart Study. BMC Medical Genetics, 2011, 12, 155.	2.1	19
101	Entropy Based Genetic Association Tests and Gene-Gene Interaction Tests. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	6
102	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
103	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. Blood, 2011, 118, 2295-2295.	1.4	1
104	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. Blood, 2011, 118, 1242-1242.	1.4	0
105	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. Blood, 2011, 118, 709-709.	1.4	0
106	Replication of Candidate Gene Single Nucleotide Polymorphisms (SNPs) Previously Reported As Associated with Venous Thromboembolism (VTE). Blood, 2011, 118, 1238-1238.	1.4	0
107	Clinical Features of Bronchioloalveolar Carcinoma with New Histologic and Staging Definitions. Journal of Thoracic Oncology, 2010, 5, 1213-1220.	1.1	16
108	Obesity adversely affects survival in pancreatic cancer patients. Cancer, 2010, 116, 5054-5062.	4.1	81

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109	Evaluating gene by sex and age interactions on cardiovascular risk factors in Brazilian families. BMC Medical Genetics, 2010, 11, 132.	2.1	10
110	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
111	Familial Aggregation of Irritable Bowel Syndrome: A Family Caseâ€“Control Study. American Journal of Gastroenterology, 2010, 105, 833-841.	0.4	91
112	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
113	T1385 Adrenomedullin: A Biomarker of Pancreatic Cancer-Associated Diabetes?. Gastroenterology, 2010, 138, S-551.	1.3	1
114	GPC5 rs2352028 variant and risk of lung cancer in never smokers â€“ Authors' reply. Lancet Oncology, The, 2010, 11, 716.	10.7	0
115	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study. Blood, 2010, 116, 480-480.	1.4	0
116	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
117	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
118	Genetic Analysis of Age-at-Onset for Cardiovascular Risk Factors in a Brazilian Family Study. Human Heredity, 2009, 68, 131-138.	0.8	5
119	Adjusting for HLA-DRÎ²1 in a genome-wide association analysis of rheumatoid arthritis and related biomarkers. BMC Proceedings, 2009, 3, S12.	1.6	2
120	Assessment of genotype imputation methods. BMC Proceedings, 2009, 3, S5.	1.6	29
121	Identification of gene-gene interaction using principal components. BMC Proceedings, 2009, 3, S78.	1.6	13
122	Identification of genes and haplotypes that predict rheumatoid arthritis using random forests. BMC Proceedings, 2009, 3, S68.	1.6	30
123	Î±-Synuclein, alcohol use disorders, and Parkinson disease: A caseâ€“control study. Parkinsonism and Related Disorders, 2009, 15, 430-434.	2.2	30
124	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
125	Genomic Susceptibility Loci for Brain Atrophy, Ventricular Volume, and Leukoaraiosis in Hypertensive Sibships. Archives of Neurology, 2009, 66, 847-57.	4.5	23
126	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Pathway-Directed Candidate-Gene Case-Control Study.. Blood, 2009, 114, 150-150.	1.4	1

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127	Heritability of cardiovascular risk factors in a Brazilian population: Baependi Heart Study. BMC Medical Genetics, 2008, 9, 32.	2.1	76
128	Coffee, caffeineâ€related genes, and Parkinson's disease: A caseâ€“control study. Movement Disorders, 2008, 23, 2033-2040.	3.9	38
129	Missing phenotype data imputation in pedigree data analysis. Genetic Epidemiology, 2008, 32, 52-60.	1.3	5
130	Human Leukocyte Antigen Class II Alleles Are Associated with Risk of Alopecia Areata. Journal of Investigative Dermatology, 2008, 128, 240-243.	0.7	26
131	179 Clinical Characteristics of Familial Irritable Bowel Syndrome (IBS) Differ from Sporadic IBS. Gastroenterology, 2008, 134, A-30.	1.3	2
132	643 Temporal Association of Changes in Fasting Blood Glucose and Body Mass Index to Diagnosis of Pancreatic Cancer. Gastroenterology, 2008, 134, A-92.	1.3	0
133	Pancreatic Cancerâ€“Associated Diabetes Mellitus: Prevalence and Temporal Association With Diagnosis of Cancer. Gastroenterology, 2008, 134, 95-101.	1.3	416
134	Long-Term Survival and Prognostic Indicators in Small (â‰2 cm) Pancreatic Cancer. Pancreatology, 2008, 8, 587-592.	1.1	32
135	Atrial Natriuretic Peptide Frameshift Mutation in Familial Atrial Fibrillation. New England Journal of Medicine, 2008, 359, 158-165.	27.0	300
136	Interferon Gamma Allelic Variants. Archives of Neurology, 2008, 65, 349-57.	4.5	33
137	Long-term risk of depressive and anxiety symptoms after early bilateral oophorectomy. Menopause, 2008, 15, 1050-1059.	2.0	124
138	A Genomic Pathway Approach to a Complex Disease: Axon Guidance and Parkinson Disease. PLoS Genetics, 2007, 3, e98.	3.5	342
139	Linkage analysis of chromosome 4 in families with familial pancreatic cancer. Cancer Biology and Therapy, 2007, 6, 320-323.	3.4	20
140	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
141	Comparison of tagging single-nucleotide polymorphism methods in association analyses. BMC Proceedings, 2007, 1, S6.	1.6	5
142	Comparison of variable and model selection methods for genetic association studies using the GAW15 simulated data. BMC Proceedings, 2007, 1, S34.	1.6	1
143	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
144	The genetics of gene expression: comparison of linkage scans using two phenotype normalization methods. BMC Proceedings, 2007, 1, S151.	1.6	2

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145	Linkage analysis using principal components of gene expression data. BMC Proceedings, 2007, 1, S79.	1.6	1
146	Summary of contributions to GAW15 Group 13: candidate gene association studies. Genetic Epidemiology, 2007, 31, S110-S117.	1.3	2
147	Increased prevalence of antimitochondrial antibodies in first-degree relatives of patients with primary biliary cirrhosis. Hepatology, 2007, 46, 785-792.	7.3	125
148	Number of children and risk of Parkinson's disease. Movement Disorders, 2007, 22, 632-639.	3.9	12
149	Metaâ€Analysis of Genomeâ€wide Linkage Studies in BMI and Obesity. Obesity, 2007, 15, 2263-2275.	3.0	138
150	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
151	Response from Maraganore et al.. American Journal of Human Genetics, 2006, 78, 1092-1094.	6.2	28
152	Survival patterns after oophorectomy in premenopausal women: a population-based cohort study. Lancet Oncology, The, 2006, 7, 821-828.	10.7	482
153	Genomic loci with pleiotropic effects on coronary artery calcification. Atherosclerosis, 2006, 185, 340-346.	0.8	26
154	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
155	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
156	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
157	Chemical exposures and Parkinson's disease: A population-based caseâ€“control study. Movement Disorders, 2006, 21, 1688-1692.	3.9	85
158	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
159	Novel Genomic Loci Influencing Plasma Homocysteine Levels. Stroke, 2006, 37, 1703-1709.	2.0	22
160	Quantitative trait loci influencing low density lipoprotein particle size in African Americans. Journal of Lipid Research, 2006, 47, 1457-1462.	4.2	10
161	Case-Control Genetic Association Studies in Gastrointestinal Disease: Review and Recommendations. American Journal of Gastroenterology, 2006, 101, 1379-1389.	0.4	24
162	Statistical Approaches to Analysis of Polymorphisms in Multifactorial Conditions. , 2006, , 47-60.		0

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163	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
164	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
165	Randomâ€effects Cox proportional hazards model: General variance components methods for timeâ€toâ€event data. Genetic Epidemiology, 2005, 28, 97-109.	1.3	105
166	Summary of contributions to GAW Group 12: Multivariate Methods. Genetic Epidemiology, 2005, 29, S91-S95.	1.3	1
167	Risk of malignancy in firstâ€degree relatives of patients with pancreatic carcinoma. Cancer, 2005, 104, 388-394.	4.1	78
168	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
169	Interaction of Î±â€synuclein and tau genotypes in Parkinson's disease. Annals of Neurology, 2005, 57, 439-443.	5.3	49
170	Identification of genes involved in alcohol consumption and cigarettes smoking. BMC Genetics, 2005, 6, S112.	2.7	7
171	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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