Marylyn D Ritchie

List of Publications by Year
in descending order

267 papers	29,281 citations	11651 70 h-index	6300 158 g-index
289 all docs	289 docs citations	289 times ranked	34540 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Multifactor-Dimensionality Reduction Reveals High-Order Interactions among Estrogen-Metabolism Genes in Sporadic Breast Cancer. American Journal of Human Genetics, 2001, 69, 138-147.	6.2	1,745
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
4	Multifactor dimensionality reduction software for detecting geneâ€"gene and geneâ€"environment interactions. Bioinformatics, 2003, 19, 376-382.	4.1	1,067
5	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover geneâ€"disease associations. Bioinformatics, 2010, 26, 1205-1210.	4.1	966
6	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	17.5	846
7	Methods of integrating data to uncover genotypeâ€"phenotype interactions. Nature Reviews Genetics, 2015, 16, 85-97.	16.3	803
8	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	27.0	633
9	The eMERGE Network: A consortium of biorepositories linked to electronic medical records data for conducting genomic studies. BMC Medical Genomics, 2011, 4, 13.	1.5	618
10	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
11	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	21.4	533
12	Genetic Determinants of Response to Warfarin during Initial Anticoagulation. New England Journal of Medicine, 2008, 358, 999-1008.	27.0	516
13	Power of multifactor dimensionality reduction for detecting geneâ€gene interactions in the presence of genotyping error, missing data, phenocopy, and genetic heterogeneity. Genetic Epidemiology, 2003, 24, 150-157.	1.3	515
14	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	12.6	464
15	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 1123-1133.	27.0	411
16	A genome-wide scan for common genetic variants with a large influence on warfarin maintenance dose. Blood, 2008, 112, 1022-1027.	1.4	410
17	Genetic identification of familial hypercholesterolemia within a single U.S. health care system. Science, 2016, 354, .	12.6	349
18	Renin-Angiotensin System Gene Polymorphisms and Atrial Fibrillation. Circulation, 2004, 109, 1640-1646.	1.6	343

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19	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. Genetic Epidemiology, 2007, 31, 306-315.	1.3	337
20	Different contributions of polymorphisms in VKORC1 and CYP2C9 to intra- and inter-population differences in maintenance dose of warfarin in Japanese, Caucasians and African-Americans. Pharmacogenetics and Genomics, 2006, 16, 101-110.	1.5	326
21	Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record. American Journal of Human Genetics, 2010, 86, 560-572.	6.2	302
22	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
23	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
24	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	12.6	269
25	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
26	Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. PLoS Biology, 2013, 11, e1001661.	5.6	235
27	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
28	Machine Learning for Detecting Gene-Gene Interactions. Applied Bioinformatics, 2006, 5, 77-88.	1.6	209
29	Optimizationof neural network architecture using genetic programming improvesdetection and modeling of gene-gene interactions in studies of humandiseases. BMC Bioinformatics, 2003, 4, 28.	2.6	190
30	Visualizing genomic information across chromosomes with PhenoGram. BioData Mining, 2013, 6, 18.	4.0	175
31	Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. PLoS Genetics, 2013, 9, e1003087.	3.5	171
32	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
33	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
34	Exome Sequencingâ€"Based Screening for BRCA1/2 Expected Pathogenic Variants Among Adult Biobank Participants. JAMA Network Open, 2018, 1, e182140.	5.9	163
35	The Next PAGE in Understanding Complex Traits: Design for the Analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. American Journal of Epidemiology, 2011, 174, 849-859.	3.4	161
36	A Large Candidate Gene Survey Identifies the KCNE1 D85N Polymorphism as a Possible Modulator of Drug-Induced Torsades de Pointes. Circulation: Cardiovascular Genetics, 2012, 5, 91-99.	5.1	150

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37	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	3.4	150
38	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
39	Multilocus Analysis of Hypertension: A Hierarchical Approach. Human Heredity, 2004, 57, 28-38.	0.8	146
40	A genome- and phenome-wide association study to identify genetic variants influencing platelet count and volume and their pleiotropic effects. Human Genetics, 2014, 133, 95-109.	3.8	135
41	The Challenges of Whole-Genome Approaches to Common Diseases. JAMA - Journal of the American Medical Association, 2004, 291, 1642-1643.	7.4	133
42	Multifactor dimensionality reduction: An analysis strategy for modelling and detecting gene - gene interactions in human genetics and pharmacogenomics studies. Human Genomics, 2006, 2, 318-28.	2.9	132
43	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	2.3	130
44	Mitochondrial haplogroups and peripheral neuropathy during antiretroviral therapy: an adult AIDS clinical trials group study. Aids, 2005, 19, 1341-1349.	2.2	129
45	An application of conditional logistic regression and multifactor dimensionality reduction for detecting gene-gene Interactions on risk of myocardial infarction: The importance of model validation. BMC Bioinformatics, 2004, 5, 49.	2.6	127
46	Identification of Genomic Predictors of Atrioventricular Conduction. Circulation, 2010, 122, 2016-2021.	1.6	117
47	Susceptibility and modifier genes in Portuguese transthyretin V30M amyloid polyneuropathy: complexity in a single-gene disease. Human Molecular Genetics, 2005, 14, 543-553.	2.9	108
48	Reninâ€"angiotensin system gene polymorphisms and coronary artery disease in a large angiographic cohort: Detection of high order geneâ€"gene interaction. Atherosclerosis, 2007, 195, 172-180.	0.8	107
49	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
50	Variation in the 4q25 Chromosomal Locus Predicts Atrial Fibrillation After Coronary Artery Bypass Graft Surgery. Circulation: Cardiovascular Genetics, 2009, 2, 499-506.	5.1	104
51	Single-Nucleotide Polymorphisms for Diagnosis of Salt-Sensitive Hypertension. Clinical Chemistry, 2006, 52, 352-360.	3.2	103
52	Comparison of approaches for machineâ€learning optimization of neural networks for detecting geneâ€gene interactions in genetic epidemiology. Genetic Epidemiology, 2008, 32, 325-340.	1.3	103
53	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. Human Genetics, 2012, 131, 639-652.	3.8	103
54	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99

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55	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. Circulation, 2019, 140, 42-54.	1.6	97
56	Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. Genetics in Medicine, 2010, 12, 648-650.	2.4	94
57	Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records and Genomics (eMERGE) Network. Genetics in Medicine, 2012, 14, 424-431.	2.4	94
58	Polymorphism modulates symptomatic response to antiarrhythmic drug therapy in patients with lone atrial fibrillation. Heart Rhythm, 2007, 4, 743-749.	0.7	92
59	A Phenomics-Based Strategy Identifies Loci on APOC1, BRAP, and PLCG1 Associated with Metabolic Syndrome Phenotype Domains. PLoS Genetics, 2011, 7, e1002322.	3.5	92
60	Drug Transporter and Metabolizing Enzyme Gene Variants and Nonnucleoside Reverse-Transcriptase Inhibitor Hepatotoxicity. Clinical Infectious Diseases, 2006, 43, 779-782.	5.8	91
61	Predicting warfarin dosage in Europeanâ€"Americans and Africanâ€"Americans using DNA samples linked to an electronic health record. Pharmacogenomics, 2012, 13, 407-418.	1.3	90
62	The use of a DNA biobank linked to electronic medical records to characterize pharmacogenomic predictors of tacrolimus dose requirement in kidney transplant recipients. Pharmacogenetics and Genomics, 2012, 22, 32-42.	1.5	89
63	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	6.2	86
64	Chromosome 4q25 Variants Are Genetic Modifiers of Rare Ion Channel Mutations Associated With Familial Atrial Fibrillation. Journal of the American College of Cardiology, 2012, 60, 1173-1181.	2.8	80
65	Relative contribution of CYP2C9 and VKORC1 genotypes and early INR response to the prediction of warfarin sensitivity during initiation of therapy. Blood, 2009, 113, 3925-3930.	1.4	79
66	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	2.3	79
67	Knowledge boosting: a graph-based integration approach with multi-omics data and genomic knowledge for cancer clinical outcome prediction. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 109-120.	4.4	79
68	Biofilter: a knowledge-integration system for the multi-locus analysis of genome-wide association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 368-79.	0.7	79
69	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	16.3	78
70	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	6.2	77
71	GPNN: Power studies and applications of a neural network method for detecting gene-gene interactions in studies of human disease. BMC Bioinformatics, 2006, 7, 39.	2.6	75
72	Facilitating pharmacogenetic studies using electronic health records and natural-language processing: a case study of warfarin. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 387-391.	4.4	74

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73	Multifactor dimensionality reduction for detecting geneâ€"gene and geneâ€"environment interactions in pharmacogenomics studies. Pharmacogenomics, 2005, 6, 823-834.	1.3	72
74	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. Genetic Epidemiology, 2011, 35, 887-898.	1.3	71
75	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
76	Phenome-wide association study (PheWAS) in EMR-linked pediatric cohorts, genetically links PLCL1 to speech language development and IL5-IL13 to Eosinophilic Esophagitis. Frontiers in Genetics, 2014, 5, 401.	2.3	70
77	Model-Based Multifactor Dimensionality Reduction for detecting epistasis in case-control data in the presence of noise. Annals of Human Genetics, 2011, 75, 78-89.	0.8	69
78	The search for gene-gene interactions in genome-wide association studies: challenges in abundance of methods, practical considerations, and biological interpretation. Annals of Translational Medicine, 2018, 6, 157-157.	1.7	69
79	Genetic risk factors for BMI and obesity in an ethnically diverse population: Results from the population architecture using genomics and epidemiology (PAGE) study. Obesity, 2013, 21, 835-846.	3.0	68
80	Parallel multifactor dimensionality reduction: a tool for the large-scale analysis of gene-gene interactions. Bioinformatics, 2006, 22, 2173-2174.	4.1	67
81	Using Biological Knowledge to Uncover the Mystery in the Search for Epistasis in Genome-Wide Association Studies. Annals of Human Genetics, 2011, 75, 172-182.	0.8	66
82	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	2.3	66
83	PheWAS and Beyond: The Landscape of Associations with Medical Diagnoses and Clinical Measures across 38,662 Individuals from Geisinger. American Journal of Human Genetics, 2018, 102, 592-608.	6.2	66
84	Immunogenetics of CD4 Lymphocyte Count Recovery during Antiretroviral Therapy: An AIDS Clinical Trials Group Study. Journal of Infectious Diseases, 2006, 194, 1098-1107.	4.0	65
85	The success of pharmacogenomics in moving genetic association studies from bench to bedside: study design and implementation of precision medicine in the post-GWAS era. Human Genetics, 2012, 131, 1615-1626.	3.8	65
86	A simulation study investigating power estimates in phenome-wide association studies. BMC Bioinformatics, 2018, 19, 120.	2.6	65
87	Pharmacogenomics Clinical Annotation Tool (Pharm<scp>CAT</scp>). Clinical Pharmacology and Therapeutics, 2020, 107, 203-210.	4.7	65
88	ATHENA: Identifying interactions between different levels of genomic data associated with cancer clinical outcomes using grammatical evolution neural network. BioData Mining, 2013, 6, 23.	4.0	64
89	Detection of Pleiotropy through a Phenome-Wide Association Study (PheWAS) of Epidemiologic Data as Part of the Environmental Architecture for Genes Linked to Environment (EAGLE) Study. PLoS Genetics, 2014, 10, e1004678.	3.5	64
90	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

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91	Novel methods for detecting epistasis in pharmacogenomics studies. Pharmacogenomics, 2007, 8, 1229-1241.	1.3	61
92	Genetic programming neural networks: A powerful bioinformatics tool for human genetics. Applied Soft Computing Journal, 2007, 7, 471-479.	7.2	60
93	Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. PLoS ONE, 2011, 6, e19586.	2.5	60
94	Multilocus genetic interactions and response to efavirenz-containing regimens: an Adult AIDS Clinical Trials Group study. Pharmacogenetics and Genomics, 2006, 16, 837-845.	1.5	59
95	Association of the FTO Obesity Risk Variant rs8050136 With Percentage of Energy Intake From Fat in Multiple Racial/Ethnic Populations. American Journal of Epidemiology, 2013, 178, 780-790.	3.4	59
96	Genetic Determinants of Age-Related Macular Degeneration in Diverse Populations From the PAGE Study. Investigative Ophthalmology and Visual Science, 2014, 55, 6839-6850.	3.3	59
97	Alternative contingency table measures improve the power and detection of multifactor dimensionality reduction. BMC Bioinformatics, 2008, 9, 238.	2.6	57
98	Analysis pipeline for the epistasis search Ã¢â‚¬â€œ statistical versus biological filtering. Frontiers in Genetics, 2014, 5, 106.	2.3	57
99	Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes. PLoS ONE, 2013, 8, e78511.	2.5	57
100	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	2.9	56
101	Complement Receptor 1 Gene Variants Are Associated with Erythrocyte Sedimentation Rate. American Journal of Human Genetics, 2011, 89, 131-138.	6.2	55
102	Human-Disease Phenotype Map Derived from PheWAS across 38,682 Individuals. American Journal of Human Genetics, 2019, 104, 55-64.	6.2	54
103	Hemochromatosis (HFE) gene mutations and peripheral neuropathy during antiretroviral therapy. Aids, 2006, 20, 1503-1513.	2.2	53
104	BIOFILTER: A KNOWLEDGE-INTEGRATION SYSTEM FOR THE MULTI-LOCUS ANALYSIS OF GENOME-WIDE ASSOCIATION STUDIES. , 2008, , .		53
105	The effect of reduction in crossâ€validation intervals on the performance of multifactor dimensionality reduction. Genetic Epidemiology, 2006, 30, 546-555.	1.3	52
106	Routine discovery of complex genetic models using genetic algorithms. Applied Soft Computing Journal, 2004, 4, 79-86.	7.2	51
107	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003288.	8.4	51
108	Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. BioData Mining, 2013, 6, 25.	4.0	50

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109	FAM-MDR: A Flexible Family-Based Multifactor Dimensionality Reduction Technique to Detect Epistasis Using Related Individuals. PLoS ONE, 2010, 5, e10304.	2.5	48
110	A comparison of analytical methods for genetic association studies. Genetic Epidemiology, 2008, 32, 767-778.	1.3	47
111	Early cancer diagnoses through BRCA1/2 screening of unselected adult biobank participants. Genetics in Medicine, 2018, 20, 554-558.	2.4	46
112	ATHENA: the analysis tool for heritable and environmental network associations. Bioinformatics, 2014, 30, 698-705.	4.1	45
113	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
114	Finding unique filter sets in PLATO: a precursor to efficient interaction analysis in GWAS data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2010, , 315-26.	0.7	45
115	Integrating heterogeneous high-throughput data for meta-dimensional pharmacogenomics and disease-related studies. Pharmacogenomics, 2012, 13, 213-222.	1.3	44
116	Exome-wide evaluation of rare coding variants using electronic health records identifies new geneâ€"phenotype associations. Nature Medicine, 2021, 27, 66-72.	30.7	44
117	ATHENA: A knowledge-based hybrid backpropagation-grammatical evolution neural network algorithm for discovering epistasis among quantitative trait Loci. BioData Mining, 2010, 3, 5.	4.0	43
118	Genetic Loci Implicated in Erythroid Differentiation and Cell Cycle Regulation Are Associated With Red Blood Cell Traits. Mayo Clinic Proceedings, 2012, 87, 461-474.	3.0	43
119	Electronic health record phenotype in subjects with genetic variants associated with arrhythmogenic right ventricular cardiomyopathy: a study of 30,716 subjects with exome sequencing. Genetics in Medicine, 2017, 19, 1245-1252.	2.4	43
120	Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. BioData Mining, 2010, 3, 10.	4.0	42
121	High Density GWAS for LDL Cholesterol in African Americans Using Electronic Medical Records Reveals a Strong Protective Variant in APOE. Clinical and Translational Science, 2012, 5, 394-399.	3.1	42
122	Visually integrating and exploring high throughput Phenome-Wide Association Study (PheWAS) results using PheWAS-View. BioData Mining, 2012, 5, 5.	4.0	42
123	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
124	A genome-first approach to aggregating rare genetic variants in LMNA for association with electronic health record phenotypes. Genetics in Medicine, 2020, 22, 102-111.	2.4	42
125	Using knowledge-driven genomic interactions for multi-omics data analysis: metadimensional models for predicting clinical outcomes in ovarian carcinoma. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 577-587.	4.4	41
126	European mitochondrial DNA haplogroups and metabolic changes during antiretroviral therapy in AIDS Clinical Trials Group Study A5142*. Aids, 2011, 25, 37-47.	2.2	40

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127	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	12.8	40
128	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
129	Phenome-Wide Association Studies: Leveraging Comprehensive Phenotypic and Genotypic Data for Discovery. Current Genetic Medicine Reports, 2015, 3, 92-100.	1.9	39
130	Genetic Variation and Reproductive Timing: African American Women from the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2013, 8, e55258.	2.5	39
131	African Mitochondrial DNA Subhaplogroups and Peripheral Neuropathy during Antiretroviral Therapy. Journal of Infectious Diseases, 2010, 201, 1703-1707.	4.0	38
132	The joint effect of air pollution exposure and copy number variation on risk for autism. Autism Research, 2017, 10, 1470-1480.	3.8	38
133	Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. PLoS Genetics, 2016, 12, e1006186.	3.5	38
134	Estrogens, Enzyme Variants, and Breast Cancer: A Risk Model. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1620-1629.	2.5	37
135	Generalization of Variants Identified by Genomeâ€Wide Association Studies for Electrocardiographic Traits in African Americans. Annals of Human Genetics, 2013, 77, 321-332.	0.8	37
136	Phenome-wide Association Study Relating Pretreatment Laboratory Parameters With Human Genetic Variants in AIDS Clinical Trials Group Protocols. Open Forum Infectious Diseases, 2015, 2, ofu113.	0.9	37
137	Disrupting upstream translation in mRNAs is associated with human disease. Nature Communications, 2021, 12, 1515.	12.8	37
138	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
139	Complex geneâ€"gene interactions in multiple sclerosis: a multifactorial approach reveals associations with inflammatory genes. Neurogenetics, 2007, 8, 11-20.	1.4	35
140	Identification of unique venous thromboembolism-susceptibility variants in African-Americans. Thrombosis and Haemostasis, 2017, 117, 758-768.	3.4	35
141	An association analysis of Alzheimer disease candidate genes detects an ancestral risk haplotype clade in ACE and putative multilocus association between ACE, A2M, and LRRTM3. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 721-735.	1.7	34
142	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
143	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. Human Heredity, 2015, 79, 137-146.	0.8	34
144	Genetic variation in the mitochondrial enzyme carbamyl-phosphate synthetase I predisposes children to increased pulmonary artery pressure following surgical repair of congenital heart defects: A validated genetic association study. Mitochondrion, 2007, 7, 204-210.	3.4	33

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145	Lack of associations of ten candidate coronary heart disease risk genetic variants and subclinical atherosclerosis in four U.S. populations: The Population Architecture using Genomics and Epidemiology (PAGE) study. Atherosclerosis, 2013, 228, 390-399.	0.8	33
146	Exploring the Performance of Multifactor Dimensionality Reduction in Large Scale SNP Studies and in the Presence of Genetic Heterogeneity among Epistatic Disease Models. Human Heredity, 2009, 67, 183-192.	0.8	32
147	Genetic Variants That Confer Resistance to Malaria Are Associated with Red Blood Cell Traits in African-Americans: An Electronic Medical Record-based Genome-Wide Association Study. G3: Genes, Genomes, Genetics, 2013, 3, 1061-1068.	1.8	32
148	Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. Journal of Biomedical Informatics, 2015, 56, 220-228.	4.3	32
149	Genomewide Association Study of Platelet Reactivity and Cardiovascular Response in Patients Treated With Clopidogrel: A Study by the International Clopidogrel Pharmacogenomics Consortium. Clinical Pharmacology and Therapeutics, 2020, 108, 1067-1077.	4.7	32
150	Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. Trends in Genetics, 2016, 32, 470-484.	6.7	31
151	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
152	Incorporating inter-relationships between different levels of genomic data into cancer clinical outcome prediction. Methods, 2014, 67, 344-353.	3.8	30
153	Identifying the genotype behind the phenotype: a role model found inVKORC1and its association with warfarin dosing. Pharmacogenomics, 2007, 8, 487-496.	1.3	29
154	Diverse convergent evidence in the genetic analysis of complex disease: coordinating omic, informatic, and experimental evidence to better identify and validate risk factors. BioData Mining, 2014, 7, 10.	4.0	28
155	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. Personalized Medicine, 2019, 16, 247-257.	1.5	28
156	Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. Molecular Vision, 2014, 20, 1281-95.	1.1	27
157	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. BMC Medical Genomics, 2016, 9, 32.	1.5	26
158	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
159	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. Biological Psychiatry, 2021, 89, 236-245.	1.3	26
160	Comparison of Neural Network Optimization Approaches for Studies of Human Genetics. Lecture Notes in Computer Science, 2006, , 103-114.	1.3	25
161	Genetic Programming Neural Networks as a Bioinformatics Tool for Human Genetics. Lecture Notes in Computer Science, 2004, , 438-448.	1.3	25
162	Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 200-11.	0.7	25

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163	Mitochondrial DNA variation and HIV-associated sensory neuropathy in CHARTER. Journal of NeuroVirology, 2012, 18, 511-520.	2.1	24
164	Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. Pharmacogenomics, 2013, 14, 735-744.	1.3	24
165	Enhancing the Power of Genetic Association Studies through the Use of Silver Standard Cases Derived from Electronic Medical Records. PLoS ONE, 2013, 8, e63481.	2.5	23
166	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. Genome Medicine, 2015, 7, 67.	8.2	23
167	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	3.4	23
168	Phenome-Wide Association Study to Explore Relationships between Immune System Related Genetic Loci and Complex Traits and Diseases. PLoS ONE, 2016, 11, e0160573.	2.5	23
169	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
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