Marylyn Ritchie

List of Publications by Year
in descending order

178	19,587	38720 50	14736 127
papers	citations	h-index	g-index

202	202	202	29793
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
3	Multifactor-Dimensionality Reduction Reveals High-Order Interactions among Estrogen-Metabolism Genes in Sporadic Breast Cancer. American Journal of Human Genetics, 2001, 69, 138-147.	2.6	1,745
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
5	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover geneâ€“disease associations. Bioinformatics, 2010, 26, 1205-1210.	1.8	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.	9.4	846
7	Methods of integrating data to uncover genotypeâ€“phenotype interactions. Nature Reviews Genetics, 2015, 16, 85-97.	7.7	803
8	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	13.9	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.	0.7	618
10	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	1.1	611
11	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	9.4	533
12	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	6.0	464
13	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 1123-1133.	13.9	411
14	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
15	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
16	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
17	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	6.0	269
18	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	9.4	211

#	Article	IF	Citations
19	Visualizing genomic information across chromosomes with PhenoGram. BioData Mining, 2013, 6, 18.	2.2	175
20	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
21	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
22	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	1.1	130
23	Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. Clinical Pharmacology and Therapeutics, 2018, 103, 778-786.	2.3	110
24	GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. BMC Medicine, 2019, 17, 135.	2.3	110
25	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	0.5	107
26	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
27	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. Circulation, 2019, 140, 42-54.	1.6	97
28	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. Nature Genetics, 2022, 54, 382-392.	9.4	97
29	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 2191.	3.8	93
30	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.	2.6	86
31	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	1.1	79
32	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.	2.2	79
33	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
34	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
35	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	7.7	78
36	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	2.6	72

#	Article	IF	Citations
37	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.	0.6	71
38	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
39	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nature Genetics, 2022, 54, 950-962.	9.4	71
40	Pharmacogenomic polygenic response score predicts ischaemic events and cardiovascular mortality in clopidogrel-treated patients. European Heart Journal - Cardiovascular Pharmacotherapy, 2020, 6, 203-210.	1.4	69
41	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.	0.7	69
42	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.	1.1	66
43	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.	2.6	66
44	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.	1.8	65
45	A simulation study investigating power estimates in phenome-wide association studies. BMC Bioinformatics, 2018, 19, 120.	1.2	65
46	Pharmacogenomics Clinical Annotation Tool (Pharm<scp>CAT</scp>). Clinical Pharmacology and Therapeutics, 2020, 107, 203-210.	2.3	65
47	ATHENA: Identifying interactions between different levels of genomic data associated with cancer clinical outcomes using grammatical evolution neural network. BioData Mining, 2013, 6, 23.	2.2	64
48	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.	1.5	64
49	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
50	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.	0.6	63
51	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
52	Analysis pipeline for the epistasis search Ã¢â‚¬â€œ statistical versus biological filtering. Frontiers in Genetics, 2014, 5, 106.	1.1	57
53	Global increases in both common and rare copy number load associated with autism. Human Molecular Genetics, 2013, 22, 2870-2880.	1.4	56
54	From GWAS to Gene: Transcriptome-Wide Association Studies and Other Methods to Functionally Understand GWAS Discoveries. Frontiers in Genetics, 2021, 12, 713230.	1.1	55

#	Article	IF	Citations
55	Human-Disease Phenotype Map Derived from PheWAS across 38,682 Individuals. American Journal of Human Genetics, 2019, 104, 55-64.	2.6	54
56	Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature Genetics, 2022, 54, 1103-1116.	9.4	54
57	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003288.	3.9	51
58	Targeting the coronavirus nucleocapsid protein through GSK-3 inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	51
59	Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. BioData Mining, 2013, 6, 25.	2.2	50
60	COVID-19 outcomes and the human genome. Genetics in Medicine, 2020, 22, 1175-1177.	1.1	49
61	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.	2.6	47
62	Characterizing Heterogeneity in Neuroimaging, Cognition, Clinical Symptoms, and Genetics Among Patients With Late-Life Depression. JAMA Psychiatry, 2022, 79, 464.	6.0	47
63	ATHENA: the analysis tool for heritable and environmental network associations. Bioinformatics, 2014, 30, 698-705.	1.8	45
64	Exome-wide evaluation of rare coding variants using electronic health records identifies new geneâ€“phenotype associations. Nature Medicine, 2021, 27, 66-72.	15.2	44
65	ATHENA: A knowledge-based hybrid backpropagation-grammatical evolution neural network algorithm for discovering epistasis among quantitative trait Loci. BioData Mining, 2010, 3, 5.	2.2	43
66	Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. BioData Mining, 2010, 3, 10.	2.2	42
67	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
68	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.	1.1	42
69	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.	2.2	41
70	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	5.8	40
71	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.	1.8	40
72	Phenome-Wide Association Studies: Leveraging Comprehensive Phenotypic and Genotypic Data for Discovery. Current Genetic Medicine Reports, 2015, 3, 92-100.	1.9	39

#	Article	IF	Citations
73	Discovery of gene-gene interactions across multiple independent data sets of late onset Alzheimer disease from the Alzheimer Disease Genetics Consortium. Neurobiology of Aging, 2016, 38, 141-150.	1.5	39
74	Medical records-based chronic kidney disease phenotype for clinical care and â€œbig dataâ€•observational and genetic studies. Npj Digital Medicine, 2021, 4, 70.	5.7	39
75	The joint effect of air pollution exposure and copy number variation on risk for autism. Autism Research, 2017, 10, 1470-1480.	2.1	38
76	Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. PLoS Genetics, 2016, 12, e1006186.	1.5	38
77	Disrupting upstream translation in mRNAs is associated with human disease. Nature Communications, 2021, 12, 1515.	5.8	37
78	Low Frequency Variants, Collapsed Based on Biological Knowledge, Uncover Complexity of Population Stratification in 1000 Genomes Project Data. PLoS Genetics, 2013, 9, e1003959.	1.5	35
79	Informatics and machine learning to define the phenotype. Expert Review of Molecular Diagnostics, 2018, 18, 219-226.	1.5	35
80	Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. Journal of Biomedical Informatics, 2015, 56, 220-228.	2.5	32
81	Efavirenz Pharmacogenetics and Weight Gain Following Switch to Integrase Inhibitorâ€“Containing Regimens. Clinical Infectious Diseases, 2021, 73, e2153-e2163.	2.9	32
82	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.	2.3	32
83	Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. Trends in Genetics, 2016, 32, 470-484.	2.9	31
84	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.	1.8	31
85	Incorporating inter-relationships between different levels of genomic data into cancer clinical outcome prediction. Methods, 2014, 67, 344-353.	1.9	30
86	Kidney disease genetic risk variants alter lysosomal beta-mannosidase (MANBA) expression and disease severity. Science Translational Medicine, 2021, 13, .	5.8	30
87	Real-world integration of genomic data into the electronic health record: the PennChart Genomics Initiative. Genetics in Medicine, 2021, 23, 603-605.	1.1	29
88	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. Nature Genetics, 2022, 54, 772-782.	9.4	29
89	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.	2.2	28
90	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. Personalized Medicine, 2019, 16, 247-257.	0.8	28

#	Article	IF	Citations
91	Genetically Downregulated Interleukin-6 Signaling Is Associated With a Favorable Cardiometabolic Profile. Circulation, 2021, 143, 1177-1180.	1.6	27
92	Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. Molecular Vision, 2014, 20, 1281-95.	1.1	27
93	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. BMC Medical Genomics, 2016, 9, 32.	0.7	26
94	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	1.7	26
95	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. Biological Psychiatry, 2021, 89, 236-245.	0.7	26
96	Rates of COVID-19â€“Related Outcomes in Cancer Compared With Noncancer Patients. JNCI Cancer Spectrum, 2021, 5, pkaa120.	1.4	26
97	ENVIRONMENT-WIDE ASSOCIATION STUDY (EWAS) FOR TYPE 2 DIABETES IN THE MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT BIOBANK. , 2013, , .		25
98	Celebrating parasites. Nature Genetics, 2017, 49, 483-484.	9.4	25
99	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
100	BINNING SOMATIC MUTATIONS BASED ON BIOLOGICAL KNOWLEDGE FOR PREDICTING SURVIVAL: AN APPLICATION IN RENAL CELL CARCINOMA. , 2014, , .		24
101	Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. Genome Medicine, 2015, 7, 67.	3.6	23
102	Phenome-Wide Association Study to Explore Relationships between Immune System Related Genetic Loci and Complex Traits and Diseases. PLoS ONE, 2016, 11, e0160573.	1.1	23
103	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	0.6	22
104	Collective feature selection to identify crucial epistatic variants. BioData Mining, 2018, 11, 5.	2.2	22
105	Knowledge-driven genomic interactions: an application in ovarian cancer. BioData Mining, 2014, 7, 20.	2.2	21
106	Regulatory Polymorphisms in Human DBH Affect Peripheral Gene Expression and Sympathetic Activity. Circulation Research, 2014, 115, 1017-1025.	2.0	21
107	The foundation of precision medicine: integration of electronic health records with genomics through basic, clinical, and translational research. Frontiers in Genetics, 2015, 6, 104.	1.1	21
108	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	1.6	21

#	Article	IF	Citations
109	Biologyâ€Driven Geneâ€Gene Interaction Analysis of Ageâ€Related Cataract in the eMERGE Network. Genetic Epidemiology, 2015, 39, 376-384.	0.6	20
110	Current Scope and Challenges in Phenome-Wide Association Studies. Current Epidemiology Reports, 2017, 4, 321-329.	1.1	20
111	How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?. , 2018, , .		20
112	Real world scenarios in rare variant association analysis: the impact of imbalance and sample size on the power in silico. BMC Bioinformatics, 2019, 20, 46.	1.2	20
113	Ideas for how informaticians can get involved with COVID-19 research. BioData Mining, 2020, 13, 3.	2.2	20
114	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Mining, 2015, 8, 41.	2.2	17
115	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	9.4	17
116	A biologically informed method for detecting rare variant associations. BioData Mining, 2016, 9, 27.	2.2	16
117	Evaluation of PrediXcan for prioritizing GWAS associations and predicting gene expression. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 448-459.	0.7	16
118	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010113.	1.5	16
119	Admixture Mapping and Subsequent Fine-Mapping Suggests a Biologically Relevant and Novel Association on Chromosome 11 for Type 2 Diabetes in African Americans. PLoS ONE, 2014, 9, e86931.	1.1	15
120	Validation of PhenX measures in the personalized medicine research project for use in gene/environment studies. BMC Medical Genomics, 2014, 7, 3.	0.7	15
121	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. PLoS ONE, 2019, 14, e0226771.	1.1	15
122	Multi-trait association studies discover pleiotropic loci between Alzheimerâ€™s disease and cardiometabolic traits. Alzheimer's Research and Therapy, 2021, 13, 34.	3.0	15
123	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using GWAS Data. PLoS ONE, 2013, 8, e81503.	1.1	15
124	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.	1.1	14
125	eQTpLot: a user-friendly R package for the visualization of colocalization between eQTL and GWAS signals. BioData Mining, 2021, 14, 32.	2.2	14
126	How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 228-239.	0.7	14

#	Article	IF	Citations
127	Rare variants in drug target genes contributing to complex diseases, phenome-wide. Scientific Reports, 2018, 8, 4624.	1.6	13
128	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	5.8	13
129	Large-Scale Analysis of Genetic and Clinical Patient Data. Annual Review of Biomedical Data Science, 2018, 1, 263-274.	2.8	13
130	Why Is the Electronic Health Record So Challenging for Research and Clinical Care?. Methods of Information in Medicine, 2021, 60, 032-048.	0.7	13
131	Performance of polygenic risk scores for cancer prediction in a racially diverse academic biobank. Genetics in Medicine, 2022, 24, 601-609.	1.1	13
132	Interdisciplinary training to build an informatics workforce for precision medicine. Applied & Translational Genomics, 2015, 6, 28-30.	2.1	12
133	CLARITE Facilitates the Quality Control and Analysis Process for EWAS of Metabolic-Related Traits. Frontiers in Genetics, 2019, 10, 1240.	1.1	12
134	INTEGRATING CLINICAL LABORATORY MEASURES AND ICD-9 CODE DIAGNOSES IN PHENOME-WIDE ASSOCIATION STUDIES. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 168-79.	0.7	12
135	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	1.8	11
136	Novel features and enhancements in BioBin, a tool for the biologically inspired binning and association analysis of rare variants. Bioinformatics, 2018, 34, 527-529.	1.8	11
137	Tissue specificity-aware TWAS (TSA-TWAS) framework identifies novel associations with metabolic, immunologic, and virologic traits in HIV-positive adults. PLoS Genetics, 2021, 17, e1009464.	1.5	11
138	Evidence for extensive pleiotropy among pharmacogenes. Pharmacogenomics, 2016, 17, 853-866.	0.6	10
139	Genetic liability for substance use associated with medical comorbidities in electronic health records of Africanâ€•and Europeanâ€•ancestry individuals. Addiction Biology, 2022, 27, e13099.	1.4	9
140	KNOWLEDGE DRIVEN BINNING AND PHEWAS ANALYSIS IN MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT USING BIOBIN. , 2016, , .		9
141	Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. BioData Mining, 2016, 9, 18.	2.2	8
142	Pharmacogenetics of Between-Individual Variability in Plasma Clearance of Bedaquiline and Clofazimine in South Africa. Journal of Infectious Diseases, 2022, 226, 147-156.	1.9	8
143	Another Round of â€œClueâ€•to Uncover the Mystery of Complex Traits. Genes, 2018, 9, 61.	1.0	7
144	CNV Association of Diverse Clinical Phenotypes from eMERGE reveals novel disease biology underlying cardiovascular disease. International Journal of Cardiology, 2020, 298, 107-113.	0.8	7

#	Article	IF	Citations
145	Mendelian pathway analysis of laboratory traits reveals distinct roles for ciliary subcompartments in common disease pathogenesis. American Journal of Human Genetics, 2021, 108, 482-501.	2.6	7
146	Genome-first approach to rare EYA4 variants and cardio-auditory phenotypes in adults. Human Genetics, 2021, 140, 957-967.	1.8	7
147	Impact of natural selection on global patterns of genetic variation and association with clinical phenotypes at genes involved in SARS-CoV-2 infection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123000119.	3.3	7
148	Innovative strategies for annotating the â€œrelationSNPâ€•between variants and molecular phenotypes. BioData Mining, 2019, 12, 10.	2.2	6
149	Mitochondrial DNA Haplogroups and Frailty in Adults Living with HIV. AIDS Research and Human Retroviruses, 2020, 36, 214-219.	0.5	6
150	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
151	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 272-283.	0.7	6
152	Large-scale genomic analyses reveal insights into pleiotropy across circulatory system diseases and nervous system disorders. Nature Communications, 2022, 13, .	5.8	6
153	Novel EDGE encoding method enhances ability to identify genetic interactions. PLoS Genetics, 2021, 17, e1009534.	1.5	5
154	CHARACTERIZATION OF THE METABOCHIP IN DIVERSE POPULATIONS FROM THE INTERNATIONAL HAPMAP PROJECT IN THE EPIDEMIOLOGIC ARCHITECTURE FOR GENES LINKED TO ENVIRONMENT (EAGLE) PROJECT. , 2012, , .		5
155	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	0.7	4
156	A genome-first approach to rare variants in hypertrophic cardiomyopathy genes MYBPC3 and MYH7 in a medical biobank. Human Molecular Genetics, 2022, 31, 827-837.	1.4	4
157	Translational Bioinformatics: Biobanks in the Precision Medicine Era. , 2019, , .		4
158	A research agenda to support the development and implementation of genomics-based clinical informatics tools and resources. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1342-1349.	2.2	4
159	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
160	Exploration of a diversity of computational and statistical measures of association for genome-wide genetic studies. BioData Mining, 2019, 12, 14.	2.2	3
161	A Genomeâ€First Approach to Rare Variants in Dominant Postlingual Hearing Loss Genes in a Large Adult Population. Otolaryngology - Head and Neck Surgery, 2022, 166, 746-752.	1.1	3
162	Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 296-307.	0.7	3

#	Article	IF	Citations
163	Multi-Trait Genome-Wide Association Study of Atherosclerosis Detects Novel Pleiotropic Loci. Frontiers in Genetics, 2021, 12, 787545.	1.1	3
164	Pharmacogenetics of Dolutegravir Plasma Exposure Among Southern Africans With Human Immunodeficiency Virus. Journal of Infectious Diseases, 2022, 226, 1616-1625.	1.9	3
165	Systematic characterization of germline variants from the DiscovEHR study endometrial carcinoma population. BMC Medical Genomics, 2019, 12, 59.	0.7	2
166	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. Nature Communications, 2021, 12, 168.	5.8	2
167	Genomic medicine implementation protocols in the PhenX Toolkit: tools for standardized data collection. Genetics in Medicine, 2021, 23, 1783-1788.	1.1	2
168	SARS-CoV-2 Seropositivity and Seroconversion in Patients Undergoing Active Cancer-Directed Therapy. JCO Oncology Practice, 2021, 17, e1879-e1886.	1.4	2
169	A Multi-Marker Test for Analyzing Paired Genetic Data in Transplantation. Frontiers in Genetics, 2021, 12, 745773.	1.1	2
170	BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR COMMON AND RARE COPY NUMBER BURDEN. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 357-68.	0.7	2
171	Translational Bioinformatics: Biobanks in the Precision Medicine Era. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 743-747.	0.7	2
172	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. Pharmacogenomics Journal, 2019, 19, 178-190.	0.9	0
173	Statistical Impact of Sample Size and Imbalance on Multivariate Analysis and A Case Study in the UK Biobank. AMIA ... Annual Symposium proceedings, 2020, 2020, 1383-1391.	0.2	0
174	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
175	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
176	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
177	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
178	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0