Integration of summary data from GWAS and eQTL stu targets

Nature Genetics

48, 481-487

DOI: 10.1038/ng.3538

Citation Report

#	Article	IF	Citations
2	Challenges and novel approaches for investigating molecular mediation. Human Molecular Genetics, 2016, 25, R149-R156.	1.4	104
3	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	1.5	143
4	Personalized medicine in rheumatology. Reumatologia, 2016, 54, 177-186.	0.5	14
5	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.	3.6	91
6	Expanding the Immunology Toolbox: Embracing Public-Data Reuse and Crowdsourcing. Immunity, 2016, 45, 1191-1204.	6.6	19
7	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
8	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome Medicine, 2016, 8, 78.	3.6	135
9	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
10	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
11	GLITTER: a web-based application for gene link inspection through tissue-specific coexpression. Scientific Reports, 2016, 6, 33460.	1.6	3
12	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	3.6	137
13	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	9.4	134
14	Sparse Simultaneous Signal Detection for Identifying Genetically Controlled Disease Genes. Journal of the American Statistical Association, 2017, 112, 1032-1046.	1.8	9
15	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	2.6	248
16	A functional SNP associated with atopic dermatitis controls cell type-specific methylation of the VSTM1 gene locus. Genome Medicine, 2017, 9, 18.	3.6	30
17	Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. Nature Genetics, 2017, 49, 600-605.	9.4	205
18	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 2017, 66, 1713-1722.	0.3	32
19	Genome-wide association study identifies four novel loci associated with Alzheimerâ€™s endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	3.9	199

#	Article	IF	Citations
20	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
21	TMEM175 deficiency impairs lysosomal and mitochondrial function and increases Î±-synuclein aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2389-2394.	3.3	164
22	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
23	Genetic regulation of gene expression in the epileptic human hippocampus. Human Molecular Genetics, 2017, 26, 1759-1769.	1.4	20
24	Multi-omics approaches to disease. Genome Biology, 2017, 18, 83.	3.8	1,439
25	Systems biology in the central nervous system: A brief perspective on essential recent advancements. Current Opinion in Systems Biology, 2017, 3, 67-76.	1.3	8
26	Exploring a causal role of DNA methylation in the relationship between maternal vitamin B12 during pregnancy and childâ€™s IQ at age 8, cognitive performance and educational attainment: a two-step Mendelian randomization study. Human Molecular Genetics, 2017, 26, 3001-3013.	1.4	50
27	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330
28	Pleiotropic Effects of Trait-Associated Genetic Variation on DNA Methylation: Utility for Refining GWAS Loci. American Journal of Human Genetics, 2017, 100, 954-959.	2.6	77
29	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. Nature Communications, 2017, 8, 15353.	5.8	92
30	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
31	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
32	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	9.4	130
33	Integrating genome-wide association study and expression quantitative trait loci data identifies multiple genes and gene set associated with neuroticism. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 78, 149-152.	2.5	12
34	Genetics of rheumatoid arthritis susceptibility, severity, and treatment response. Seminars in Immunopathology, 2017, 39, 395-408.	2.8	73
35	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	9.4	117
36	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	9.4	259
37	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951.	1.4	69

#	Article	IF	Citations
38	Integrative analysis of GWAS, eQTLs and meQTLs data suggests that multiple gene sets are associated with bone mineral density. Bone and Joint Research, 2017, 6, 572-576.	1.3	6
39	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. Nature Genetics, 2017, 49, 1576-1583.	9.4	395
40	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. American Journal of Human Genetics, 2017, 101, 590-602.	2.6	65
41	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
42	Mendelian randomization with fineâ€mapped genetic data: Choosing from large numbers of correlated instrumental variables. Genetic Epidemiology, 2017, 41, 714-725.	0.6	122
43	Genome-wide association studies of cancer: current insights and future perspectives. Nature Reviews Cancer, 2017, 17, 692-704.	12.8	285
44	A Dementia-Associated Risk Variant near TMEM106B Alters Chromatin Architecture and Gene Expression. American Journal of Human Genetics, 2017, 101, 643-663.	2.6	87
45	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. Carcinogenesis, 2017, 38, 1147-1154.	1.3	21
46	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	2.9	17
47	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	1.2	72
48	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93
49	A comparison of methods for inferring causal relationships between genotype and phenotype using additional biological measurements. Genetic Epidemiology, 2017, 41, 577-586.	0.6	20
50	Integrative Approaches to Understanding the Pathogenic Role of Genetic Variation in Rheumatic Diseases. Rheumatic Disease Clinics of North America, 2017, 43, 449-466.	0.8	9
51	Epigenetic research in multiple sclerosis: progress, challenges, and opportunities. Physiological Genomics, 2017, 49, 447-461.	1.0	30
52	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. Nature Communications, 2017, 8, 121.	5.8	82
53	Prioritising Causal Genes at Type 2 Diabetes Risk Loci. Current Diabetes Reports, 2017, 17, 76.	1.7	25
54	Transcriptional risk scores link GWAS to eQTLs and predict complications in Crohn's disease. Nature Genetics, 2017, 49, 1517-1521.	9.4	146
55	Recent Developments in Mendelian Randomization Studies. Current Epidemiology Reports, 2017, 4, 330-345.	1.1	553

#	Article	IF	Citations
56	High expression of interleukine-1 receptor antagonist in rheumatoid arthritis: Association with IL1RN*2/2 genotype. Autoimmunity, 2017, 50, 468-475.	1.2	11
57	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	40
58	High-resolution mapping of cis -regulatory variation in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10736-E10744.	3.3	50
59	The role of blood-based biomarkers in advancing personalized therapy of schizophrenia. Expert Review of Precision Medicine and Drug Development, 2017, 2, 363-370.	0.4	0
60	A cis-eQTL genetic variant of the cancerâ€“testis gene CCDC116 is associated with risk of multiple cancers. Human Genetics, 2017, 136, 987-997.	1.8	7
61	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
62	Context-specific effects of genetic variants associated with autoimmune disease. Human Molecular Genetics, 2017, 26, R185-R192.	1.4	38
63	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	2.6	2,793
64	Dissecting the genetics of complex traits using summary association statistics. Nature Reviews Genetics, 2017, 18, 117-127.	7.7	379
65	Statistical methods to detect pleiotropy in human complex traits. Open Biology, 2017, 7, 170125.	1.5	113
66	Prevalent function of genome loci associated with development of multiple sclerosis as revealed by GWAS and eQTL analysis. Russian Journal of Genetics, 2017, 53, 982-987.	0.2	0
67	Enhancing the Promise of Drug Repositioning through Genetics. Frontiers in Pharmacology, 2017, 8, 896.	1.6	59
68	Multidimensional Integrative Genomics Approaches to Dissecting Cardiovascular Disease. Frontiers in Cardiovascular Medicine, 2017, 4, 8.	1.1	25
69	Integrating Genome-Wide Association and eQTLs Studies Identifies the Genes and Gene Sets Associated with Diabetes. BioMed Research International, 2017, 2017, 1-4.	0.9	3
70	Parkinson's disease-associated genetic variation is linked to quantitative expression of inflammatory genes. PLoS ONE, 2017, 12, e0175882.	1.1	45
71	Genetic Risk Factors for Endometriosis. Journal of Endometriosis and Pelvic Pain Disorders, 2017, 9, 69-76.	0.3	3
72	Big knowledge from big data in functional genomics. Emerging Topics in Life Sciences, 2017, 1, 245-248.	1.1	4
73	Effects of Type 1 Diabetes Risk Alleles on Immune Cell Gene Expression. Genes, 2017, 8, 167.	1.0	17

#	Article	IF	Citations
74	Inferring causal relationships between phenotypes using summary statistics from genome-wide association studies. Human Genetics, 2018, 137, 247-255.	1.8	8
75	A novel variant associated with HDL-C levels by modifying DAGLB expression levels: An annotation-based genome-wide association study. European Journal of Human Genetics, 2018, 26, 838-847.	1.4	7
76	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
77	The human noncoding genome defined by genetic diversity. Nature Genetics, 2018, 50, 333-337.	9.4	137
78	Comprehensive integrative analyses identify GLT8D1 and CSNK2B as schizophrenia risk genes. Nature Communications, 2018, 9, 838.	5.8	80
79	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	1.4	7
80	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
81	Genetic Variation at Chromosome 2q13 and Its Potential Influence on Endometriosis Susceptibility Through Effects on the IL-1 Family. Reproductive Sciences, 2018, 25, 1307-1317.	1.1	22
82	The Evolution of Gene Expression in cis and trans. Trends in Genetics, 2018, 34, 532-544.	2.9	212
83	Recent Genetics and Epigenetics Approaches to PTSD. Current Psychiatry Reports, 2018, 20, 30.	2.1	89
84	From genome-wide association studies to Mendelian randomization: novel opportunities for understanding cardiovascular disease causality, pathogenesis, prevention, and treatment. Cardiovascular Research, 2018, 114, 1192-1208.	1.8	64
85	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	5.8	58
86	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	9.4	406
87	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	9.4	286
88	Identification of genetic risk factors in the Chinese population implicates a role of immune system in Alzheimerâ€™s disease pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1697-1706.	3.3	71
89	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. Annals of the Rheumatic Diseases, 2018, 77, 1039-1047.	0.5	57
90	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
91	Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. Nature Genetics, 2018, 50, 424-431.	9.4	253

#	Article	IF	Citations
92	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	5.8	629
93	Integrative expression quantitative trait locusâ€"based analysis of colorectal cancer identified a functional polymorphism regulating SLC22A5 expression. European Journal of Cancer, 2018, 93, 1-9.	1.3	47
94	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
95	An Osteoporosis Risk SNP at 1p36.12 Acts as an Allele-Specific Enhancer to Modulate LINC00339 Expression via Long-Range Loop Formation. American Journal of Human Genetics, 2018, 102, 776-793.	2.6	78
96	Polygenic Risk Scores in Clinical Psychology: Bridging Genomic Risk to Individual Differences. Annual Review of Clinical Psychology, 2018, 14, 119-157.	6.3	110
97	Genome-wide association study in ethnic Russians suggests an association of the MHC class III genomic region with the risk of primary varicose veins. Gene, 2018, 659, 93-99.	1.0	17
98	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	1.8	203
99	The integrated landscape of causal genes and pathways in schizophrenia. Translational Psychiatry, 2018, 8, 67.	2.4	75
100	Leveraging lung tissue transcriptome to uncover candidate causal genes in COPD genetic associations. Human Molecular Genetics, 2018, 27, 1819-1829.	1.4	37
101	Multiple Functional Variants at 13q14 Risk Locus for Osteoporosis Regulate RANKL Expression Through Long-Range Super-Enhancer. Journal of Bone and Mineral Research, 2018, 33, 1335-1346.	3.1	38
102	Genetic predictors of antipsychotic response to lurasidone identified in a genome wide association study and by schizophrenia risk genes. Schizophrenia Research, 2018, 192, 194-204.	1.1	64
103	A Decade of GWAS Results in Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 363-379.	1.1	162
104	A Genome-wide Expression Association Analysis Identifies Genes and Pathways Associated with Amyotrophic Lateral Sclerosis. Cellular and Molecular Neurobiology, 2018, 38, 635-639.	1.7	30
105	PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. Nucleic Acids Research, 2018, 46, D971-D976.	6.5	191
106	Estimation of cis-eQTL Effect Sizes Using a Log of Linear Model. Biometrics, 2018, 74, 616-625.	0.8	10
107	Integrating genome-wide association study and expression quantitative trait locus study identifies multiple genes and gene sets associated with schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 81, 50-54.	2.5	24
108	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. Psychological Medicine, 2018, 48, 1055-1067.	2.7	66
109	How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?. , 2018, , .		20

#	Article	IF	Citations
110	Statistical and integrative system-level analysis of DNA methylation data. Nature Reviews Genetics, 2018, 19, 129-147.	7.7	228
111	Genetic association of molecular traits: A help to identify causative variants in complex diseases. Clinical Genetics, 2018, 93, 520-532.	1.0	45
112	Sorting nexin 3 mutation impairs development and neuronal function in Caenorhabditis elegans. Cellular and Molecular Life Sciences, 2018, 75, 2027-2044.	2.4	12
113	Discovery of genetic risk factors for disease. Journal of the Royal Society of New Zealand, 2018, 48, 191-202.	1.0	0
114	Genetic Mapping of Head Size Related Traits in Common Carp (Cyprinus carpio). Frontiers in Genetics, 2018, 9, 448.	1.1	27
115	Integration of genetics and miRNAâ€“target gene network identified disease biology implicated in tissue specificity. Nucleic Acids Research, 2018, 46, 11898-11909.	6.5	39
116	Molecular insights into genome-wide association studies of chronic kidney disease-defining traits. Nature Communications, 2018, 9, 4800.	5.8	52
117	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. Genome Biology, 2018, 19, 194.	3.8	126
118	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. PLoS Genetics, 2018, 14, e1007799.	1.5	38
119	Leveraging Multilayered â€œOmicsâ€•Data for Atopic Dermatitis: A Road Map to Precision Medicine. Frontiers in Immunology, 2018, 9, 2727.	2.2	93
120	An integrative approach for building personalized gene regulatory networks for precision medicine. Genome Medicine, 2018, 10, 96.	3.6	49
121	regQTLs: Single nucleotide polymorphisms that modulate microRNA regulation of gene expression in tumors. PLoS Genetics, 2018, 14, e1007837.	1.5	24
122	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	1.5	30
123	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
124	Genomeâ€Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in Highâ€Quality Rice. Plant Genome, 2018, 11, 170076.	1.6	26
125	A network-based conditional genetic association analysis of the human metabolome. GigaScience, 2018, 7, .	3.3	13
126	Exploring the Genetic Correlation Between Growth and Immunity Based on Summary Statistics of Genome-Wide Association Studies. Frontiers in Genetics, 2018, 9, 393.	1.1	11
127	Prioritizing candidate genes post-GWAS using multiple sources of data for mastitis resistance in dairy cattle. BMC Genomics, 2018, 19, 656.	1.2	69

#	Article	IF	Citations
128	Renal compartmentâ€“specific genetic variation analyses identify new pathways in chronic kidney disease. Nature Medicine, 2018, 24, 1721-1731.	15.2	170
129	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	5.8	121
130	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
131	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. American Journal of Human Genetics, 2018, 103, 654-665.	2.6	126
132	eQTL discovery and their association with severe equine asthma in European Warmblood horses. BMC Genomics, 2018, 19, 581.	1.2	13
133	Coronary artery disease genes SMAD3 and TCF21 promote opposing interactive genetic programs that regulate smooth muscle cell differentiation and disease risk. PLoS Genetics, 2018, 14, e1007681.	1.5	41
134	Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	2.4	67
135	Distinguishing genetic correlation from causation across 52 diseases and complex traits. Nature Genetics, 2018, 50, 1728-1734.	9.4	262
136	Deciphering the Emerging Complexities of Molecular Mechanisms at GWAS Loci. American Journal of Human Genetics, 2018, 103, 637-653.	2.6	93
137	Integrative analysis identified mediation effects of lncRNAs on the correlations between methylation and mRNA. International Journal of Biochemistry and Cell Biology, 2018, 104, 66-72.	1.2	0
138	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
139	Another Round of â€œClueâ€•to Uncover the Mystery of Complex Traits. Genes, 2018, 9, 61.	1.0	7
140	OBSOLETE: Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , .		1
141	Additional common variants associated with type 2 diabetes and coronary artery disease detected using a pleiotropic cFDR method. Journal of Diabetes and Its Complications, 2018, 32, 1105-1112.	1.2	5
142	Forensic DNA Technological Advancements as an Emerging Perspective on Medico-Legal Autopsy: A Mini Review. , 2018, , .		0
143	A robust method to estimate regional polygenic correlation under misspecified linkage disequilibrium structure. Genetic Epidemiology, 2018, 42, 636-647.	0.6	3
144	Stratification of candidate genes for Parkinsonâ€™s disease using weighted protein-protein interaction network analysis. BMC Genomics, 2018, 19, 452.	1.2	35
145	Convergence of placenta biology and genetic risk for schizophrenia. Nature Medicine, 2018, 24, 792-801.	15.2	214

#	Article	IF	Citations
146	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
147	From genome-wide associations to candidate causal variants by statistical fine-mapping. Nature Reviews Genetics, 2018, 19, 491-504.	7.7	611
148	Elucidating the genetic architecture of reproductive ageing in the Japanese population. Nature Communications, 2018, 9, 1977.	5.8	44
149	Mendelian Randomization Studies of Cancer Risk: a Literature Review. Current Epidemiology Reports, 2018, 5, 184-196.	1.1	37
150	Evaluating the potential role of pleiotropy in Mendelian randomization studies. Human Molecular Genetics, 2018, 27, R195-R208.	1.4	804
151	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
152	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	0.6	59
153	Using Genomic Data to Find Disease-Modifying Loci in Huntingtonâ€™s Disease (HD). Methods in Molecular Biology, 2018, 1780, 443-461.	0.4	2
154	Japanese GWAS identifies variants for bust-size, dysmenorrhea, and menstrual fever that are eQTLs for relevant protein-coding or long non-coding RNAs. Scientific Reports, 2018, 8, 8502.	1.6	11
155	Constructing a Quantitative Fusion Layer over the Semantic Level for Scalable Inference. Lecture Notes in Computer Science, 2018, , 41-53.	1.0	0
156	Integration of summary data from GWAS and eQTL studies identified novel causal BMD genes with functional predictions. Bone, 2018, 113, 41-48.	1.4	29
157	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493.	0.6	23
158	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
159	A Genomewide Integrative Analysis of GWAS and eQTLs Data Identifies Multiple Genes and Gene Sets Associated with Obesity. BioMed Research International, 2018, 2018, 1-5.	0.9	27
160	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	2.8	3,639
161	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389
162	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. European Journal of Human Genetics, 2018, 26, 1361-1368.	1.4	3
163	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893

#	Article	IF	Citations
164	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	1.6	49
166	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	5.8	570
167	Integrating genome-wide association study, chromosomal enhancer maps and element-gene interaction networks detected brain regions related associations between elements and ADHD/IQ. Behavioural Brain Research, 2018, 353, 137-142.	1.2	3
168	A genome-wide pathway enrichment analysis identifies brain region related biological pathways associated with intelligence. Psychiatry Research, 2018, 268, 238-242.	1.7	4
169	Role of the Complement System in Chronic Central Serous Chorioretinopathy. JAMA Ophthalmology, 2018, 136, 1128.	1.4	49
170	Integrative Bioinformatics Approaches for Identification of Drug Targets in Hypertension. Frontiers in Cardiovascular Medicine, 2018, 5, 25.	1.1	3
171	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. Frontiers in Cardiovascular Medicine, 2018, 5, 56.	1.1	21
172	Using Gene Expression to Annotate Cardiovascular GWAS Loci. Frontiers in Cardiovascular Medicine, 2018, 5, 59.	1.1	13
173	Empirical Bayes Estimation of Semi-parametric Hierarchical Mixture Models for Unbiased Characterization of Polygenic Disease Architectures. Frontiers in Genetics, 2018, 9, 115.	1.1	10
174	Comparison of methods for transcriptome imputation through application to two common complex diseases. European Journal of Human Genetics, 2018, 26, 1658-1667.	1.4	22
175	A coding and non-coding transcriptomic perspective on the genomics of human metabolic disease. Nucleic Acids Research, 2018, 46, 7772-7792.	6.5	41
176	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
177	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	1.5	117
178	Genetic Regulatory Mechanisms of Smooth Muscle Cells Map to Coronary Artery Disease Risk Loci. American Journal of Human Genetics, 2018, 103, 377-388.	2.6	76
179	Identification of expression quantitative trait loci associated with schizophrenia and affective disorders in normal brain tissue. PLoS Genetics, 2018, 14, e1007607.	1.5	34
180	Meta-analysis of genome-wide association studies for height and body mass index in â^¼700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	1.4	1,541
181	Applicability of Precision Medicine Approaches to Managing Hypertension in Rural Populations. Journal of Personalized Medicine, 2018, 8, 16.	1.1	5
182	Genome-wide identification of directed gene networks using large-scale population genomics data. Nature Communications, 2018, 9, 3097.	5.8	18

#	Article	IF	Citations
183	Using genetic data to strengthen causal inference in observational research. Nature Reviews Genetics, 2018, 19, 566-580.	7.7	298
184	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. Human Molecular Genetics, 2018, 27, 3293-3304.	1.4	57
185	Genomic insights into the causes of type 2 diabetes. Lancet, The, 2018, 391, 2463-2474.	6.3	110
186	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
187	Integrative analysis of genome-wide association study and brain region related enhancer maps identifies biological pathways for insomnia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 86, 180-185.	2.5	14
188	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. Molecular Psychiatry, 2018, 23, 2254-2265.	4.1	19
189	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
190	Genome-wide association study in Japanese females identifies fifteen novel skin-related trait associations. Scientific Reports, 2018, 8, 8974.	1.6	59
191	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. Nature Communications, 2018, 9, 2427.	5.8	159
192	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
193	Immune-related genetic enrichment in frontotemporal dementia: An analysis of genome-wide association studies. PLoS Medicine, 2018, 15, e1002487.	3.9	111
194	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
195	eQTLs Weighted Genetic Correlation Analysis Detected Brain Region Differences in Genetic Correlations for Complex Psychiatric Disorders. Schizophrenia Bulletin, 2019, 45, 709-715.	2.3	6
196	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. Reproductive Sciences, 2019, 26, 496-502.	1.1	13
197	Computational Pipelines and Workflows in Bioinformatics. , 2019, , 113-134.		0
198	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	4.1	40
199	Comprehensive Analysis of Alzheimerâ€™s Disease Biologically Candidate Causal Genes Revealed by Function Association Study With GWAS. IEEE Access, 2019, 7, 114236-114245.	2.6	2
200	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	9.4	774

#	Article	IF	Citations
201	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	4.7	123
203	Integrative analysis revealed potential causal genetic and epigenetic factors for multiple sclerosis. Journal of Neurology, 2019, 266, 2699-2709.	1.8	34
204	Generalized meta-analysis for multiple regression models across studies with disparate covariate information. Biometrika, 2019, 106, 567-585.	1.3	35
205	The effect of X-linked dosage compensation on complex trait variation. Nature Communications, 2019, 10, 3009.	5.8	44
206	How humans can contribute to Mendelian randomization analyses. International Journal of Epidemiology, 2019, 48, 661-664.	0.9	23
207	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. Nature Communications, 2019, 10, 3300.	5.8	193
208	Ancestry-specific polygenic scores and SNP heritability of 25(OH)D in African- and European-ancestry populations. Human Genetics, 2019, 138, 1155-1169.	1.8	6
209	iFunMed: Integrative functional mediation analysis of GWAS and eQTL studies. Genetic Epidemiology, 2019, 43, 742-760.	0.6	1
210	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. Nature Genetics, 2019, 51, 1252-1262.	9.4	139
211	Mechanistic interpretation of non-coding variants for discovering transcriptional regulators of drug response. BMC Biology, 2019, 17, 62.	1.7	14
212	Dynamic genetic regulation of gene expression during cellular differentiation. Science, 2019, 364, 1287-1290.	6.0	142
213	A genetics-led approach defines the drug target landscape of 30 immune-related traits. Nature Genetics, 2019, 51, 1082-1091.	9.4	157
214	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. JAMA Psychiatry, 2019, 76, 1026.	6.0	51
215	TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. American Journal of Human Genetics, 2019, 105, 258-266.	2.6	84
216	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	13.5	174
217	Interactome of the Autoimmune Risk Protein ANKRD55. Frontiers in Immunology, 2019, 10, 2067.	2.2	13
218	Informing disease modelling with brain-relevant functional genomic annotations. Brain, 2019, 142, 3694-3712.	3.7	8
219	Mendelian randomization indicates that TNF is not causally associated with Alzheimer's disease. Neurobiology of Aging, 2019, 84, 241.e1-241.e3.	1.5	2

#	Article	IF	Citations
220	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. PLoS Genetics, 2019, 15, e1008431.	1.5	14
221	The genetic underpinnings of obesity. Current Opinion in Physiology, 2019, 12, 57-64.	0.9	0
222	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	4.9	1,414
223	Multi-breed genome-wide association studies across countries for electronically recorded behavior traits in local dual-purpose cows. PLoS ONE, 2019, 14, e0221973.	1.1	6
224	Use of Mendelian Randomization to Examine Causal Inference in Osteoporosis. Frontiers in Endocrinology, 2019, 10, 807.	1.5	23
225	Three Novel Loci for Infant Head Circumference Identified by a Joint Association Analysis. Frontiers in Genetics, 2019, 10, 947.	1.1	13
226	SNP eQTL status and eQTL density in the adjacent region of the SNP are associated with its statistical significance in GWA studies. BMC Genetics, 2019, 20, 85.	2.7	5
227	Systems genetics applications in metabolism research. Nature Metabolism, 2019, 1, 1038-1050.	5.1	35
228	The Genetic Architecture of Parkinson Disease in Spain: Characterizing Populationâ€Specific Risk, Differential Haplotype Structures, and Providing Etiologic Insight. Movement Disorders, 2019, 34, 1851-1863.	2.2	47
229	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	5.8	90
230	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	5.8	68
231	Genome-wide association analysis of 95â€‰549 individuals identifies novel loci and genes influencing optic disc morphology. Human Molecular Genetics, 2019, 28, 3680-3690.	1.4	19
232	â€œOmicsâ€•and â€œepi-omicsâ€•underlying the Î²-cell adaptation to insulin resistance. Molecular Metabolism, 2019, 27, S42-S48.	3.0	19
233	Integrating transcriptomic network reconstruction and eQTL analyses reveals mechanistic connections between genomic architecture and Brassica rapa development. PLoS Genetics, 2019, 15, e1008367.	1.5	15
234	Current achievements and future prospects in the genetic breeding of chrysanthemum: a review. Horticulture Research, 2019, 6, 109.	2.9	114
235	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
236	Joint Association Analysis Identified 18 New Loci for Bone Mineral Density. Journal of Bone and Mineral Research, 2019, 34, 1086-1094.	3.1	27
237	Association mapping in plants in the post-GWAS genomics era. Advances in Genetics, 2019, 104, 75-154.	0.8	100

#	Article	IF	Citations
238	The endocytic membrane trafficking pathway plays a major role in the risk of Parkinson's disease. Movement Disorders, 2019, 34, 460-468.	2.2	66
239	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. Molecular Plant, 2019, 12, 410-425.	3.9	69
240	Comprehensive functional annotation of susceptibility SNPs prioritized 10 genes for schizophrenia. Translational Psychiatry, 2019, 9, 56.	2.4	20
241	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 935-942.	1.1	21
242	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. Genome Medicine, 2019, 11, 6.	3.6	30
243	Genome-wide identification of circulating-miRNA expression quantitative trait loci reveals the role of several miRNAs in the regulation of cardiometabolic phenotypes. Cardiovascular Research, 2019, 115, 1629-1645.	1.8	55
244	Clinical and Genetic Aspects of BehÃ§et's Disease in Japan. Internal Medicine, 2019, 58, 1199-1207.	0.3	27
245	Innovative strategies for annotating the â€œrelationSNPâ€•between variants and molecular phenotypes. BioData Mining, 2019, 12, 10.	2.2	6
246	Mendelian randomization analysis of celiac GWAS reveals a blood expression signature with diagnostic potential in absence of gluten consumption. Human Molecular Genetics, 2019, 28, 3037-3042.	1.4	7
247	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
248	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. Human Molecular Genetics, 2019, 28, 3498-3513.	1.4	65
249	Integrating genome-wide association and eQTLs studies identifies the genes associated with age at menarche and age at natural menopause. PLoS ONE, 2019, 14, e0213953.	1.1	5
250	Comparison of quantitative trait loci methods: Total expression and allelic imbalance method in brain RNA-seq. PLoS ONE, 2019, 14, e0217765.	1.1	0
251	An evaluation of noncoding genome annotation tools through enrichment analysis of 15 genome-wide association studies. Briefings in Bioinformatics, 2019, 20, 995-1003.	3.2	3
252	The bidirectional causal relationships of insomnia with five major psychiatric disorders: A Mendelian randomization study. European Psychiatry, 2019, 60, 79-85.	0.1	45
253	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	5.8	183
254	Genetic correlations of polygenic disease traits: from theory to practice. Nature Reviews Genetics, 2019, 20, 567-581.	7.7	236
255	Identification of the primate-specific gene BTN3A2 as an additional schizophrenia risk gene in the MHC loci. EBioMedicine, 2019, 44, 530-541.	2.7	24

#	Article	IF	Citations
256	Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. Genetics, 2019, 212, 919-929.	1.2	12
257	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	3.8	105
258	Genomic Imprinting As a Window into Human Language Evolution. BioEssays, 2019, 41, 1800212.	1.2	5
259	Systems Chemical Genetics-Based Drug Discovery: Prioritizing Agents Targeting Multiple/Reliable Disease-Associated Genes as Drug Candidates. Frontiers in Genetics, 2019, 10, 474.	1.1	13
260	Integrative Analysis Identified IRF6 and NDST1 as Potential Causal Genes for Ischemic Stroke. Frontiers in Neurology, 2019, 10, 517.	1.1	13
261	Benefits and limitations of genome-wide association studies. Nature Reviews Genetics, 2019, 20, 467-484.	7.7	1,226
262	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. Cancer Research, 2019, 79, 3192-3204.	0.4	43
263	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	1.1	32
264	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
265	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10883-10888.	3.3	114
266	Novel Insight Into the Etiology of Autism Spectrum Disorder Gained by Integrating Expression Data With Genome-wide Association Statistics. Biological Psychiatry, 2019, 86, 265-273.	0.7	65
267	Weighting sequence variants based on their annotation increases the power of genome-wide association studies in dairy cattle. Genetics Selection Evolution, 2019, 51, 20.	1.2	15
268	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. Nature Genetics, 2019, 51, 933-940.	9.4	77
269	A genome-wide association study identifies susceptibility loci for primary central nervous system lymphoma at 6p25.3 and 3p22.1: a LOC Network study. Neuro-Oncology, 2019, 21, 1039-1048.	0.6	13
270	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	5.8	140
271	Varicose veins of lower extremities: Insights from the first large-scale genetic study. PLoS Genetics, 2019, 15, e1008110.	1.5	48
272	Genetic heterogeneity of Alzheimerâ€™s disease in subjects with and without hypertension. GeroScience, 2019, 41, 137-154.	2.1	23
273	Genome-Wide Association Studies of Endometrial Cancer: Latest Developments and Future Directions. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1095-1102.	1.1	32

#	Article	IF	Citations
274	Implementing MRâ€PRESSO and GCTAâ€GSMR for pleiotropy assessment in Mendelian randomization studies from a practitioner's perspective. Genetic Epidemiology, 2019, 43, 609-616.	0.6	126
275	Multi-SNP mediation intersection-union test. Bioinformatics, 2019, 35, 4724-4729.	1.8	23
276	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	9.4	89
277	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
278	Abundant associations with gene expression complicate GWAS follow-up. Nature Genetics, 2019, 51, 768-769.	9.4	210
279	Overlap between eQTL and QTL associated with production traits and fertility in dairy cattle. BMC Genomics, 2019, 20, 291.	1.2	25
280	Postmortem brain tissue as an underutilized resource to study the molecular pathology of neuropsychiatric disorders across different ethnic populations. Neuroscience and Biobehavioral Reviews, 2019, 102, 195-207.	2.9	9
281	The genetics of depression: successful genome-wide association studies introduce new challenges. Translational Psychiatry, 2019, 9, 114.	2.4	75
282	A genome-wide association analysis identifies 16 novel susceptibility loci for carpal tunnel syndrome. Nature Communications, 2019, 10, 1030.	5.8	57
283	Making Sense of the Epigenome Using Data Integration Approaches. Frontiers in Pharmacology, 2019, 10, 126.	1.6	58
284	Leveraging brain cortex-derived molecular data to elucidate epigenetic and transcriptomic drivers of complex traits and disease. Translational Psychiatry, 2019, 9, 105.	2.4	15
285	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
286	Regulation of MFGE8 by the intergenic coronary artery disease locus on 15q26.1. Atherosclerosis, 2019, 284, 11-17.	0.4	26
287	Identification of 22 novel loci associated withÂurinary biomarkers of albumin, sodium, andÂpotassium excretion. Kidney International, 2019, 95, 1197-1208.	2.6	33
288	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	2.0	14
289	An association analysis to identify genetic variants linked to asthma and rhino-conjunctivitis in a cohort of Sicilian children. Italian Journal of Pediatrics, 2019, 45, 16.	1.0	5
290	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. Human Molecular Genetics, 2019, 28, 2062-2077.	1.4	40
291	Mapping causal pathways from genetics to neuropsychiatric disorders using genomeâ€wide imaging genetics: Current status and future directions. Psychiatry and Clinical Neurosciences, 2019, 73, 357-369.	1.0	22

#	Article	IF	Citations
292	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	1.8	26
293	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	9.4	275
294	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
295	High-Resolution Regulatory Maps Connect Vascular Risk Variants to Disease-Related Pathways. Circulation Genomic and Precision Medicine, 2019, 12, e002353.	1.6	13
296	Integration of methylation QTL and enhancerâ€“target gene maps with schizophrenia GWAS summary results identifies novel genes. Bioinformatics, 2019, 35, 3576-3583.	1.8	19
297	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	9.4	262
298	Mendelian randomisation and the goal of inferring causation from observational studies in the vision sciences. Ophthalmic and Physiological Optics, 2019, 39, 11-25.	1.0	16
299	Dissecting closely linked association signals in combination with the mammalian phenotype database can identify candidate genes in dairy cattle. BMC Genetics, 2019, 20, 15.	2.7	20
300	Identification of Alzheimer's Disease-Related Genes Based on Data Integration Method. Frontiers in Genetics, 2018, 9, 703.	1.1	42
301	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. Current Genetic Medicine Reports, 2019, 7, 30-40.	1.9	4
302	Prediction of causal genes and gene expression analysis of attention-deficit hyperactivity disorder in the different brain region, a comprehensive integrative analysis of ADHD. Behavioural Brain Research, 2019, 364, 183-192.	1.2	18
303	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
304	Genome-wide analysis of genetic predisposition to Alzheimerâ€™s disease and related sex disparities. Alzheimer's Research and Therapy, 2019, 11, 5.	3.0	61
305	Adjusting for Principal Components of Molecular Phenotypes Induces Replicating False Positives. Genetics, 2019, 211, 1179-1189.	1.2	17
306	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. Journal of the American Society of Nephrology: JASN, 2019, 30, 421-441.	3.0	27
307	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
308	A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104.	1.5	83
309	Identification of loci of functional relevance to Barrettâ€™s esophagus and esophageal adenocarcinoma: Cross-referencing of expression quantitative trait loci data from disease-relevant tissues with genetic association data. PLoS ONE, 2019, 14, e0227072.	1.1	5

#	Article	IF	Citations
310	Genetic correlations of psychiatric traits with body composition and glycemic traits are sex- and age-dependent. Nature Communications, 2019, 10, 5765.	5.8	59
311	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	5.8	58
312	Identification of genetic overlap and novel risk loci for attention-deficit/hyperactivity disorder and bipolar disorder. Molecular Psychiatry, 2021, 26, 4055-4065.	4.1	31
313	Genomics of human aggression. Psychiatric Genetics, 2019, 29, 170-190.	0.6	39
314	Associations between potentially functional CORIN SNPs and serum corin levels in the Chinese Han population. BMC Genetics, 2019, 20, 99.	2.7	6
315	Brain Banks Spur New Frontiers in Neuropsychiatric Research and Strategies for Analysis and Validation. Genomics, Proteomics and Bioinformatics, 2019, 17, 402-414.	3.0	12
316	Analysis of the Progeny of Sibling Matings Reveals Regulatory Variation Impacting the Transcriptome of Immune Cells in Commercial Chickens. Frontiers in Genetics, 2019, 10, 1032.	1.1	18
317	Insight into the genetic architecture of back pain and its risk factors from a study of 509,000 individuals. Pain, 2019, 160, 1361-1373.	2.0	74
318	Genomeâ€wide association study and identification of chromosomal enhancer maps in multiple brain regions related to autism spectrum disorder. Autism Research, 2019, 12, 26-32.	2.1	15
319	Integrating a genomeâ€wide association study with a largeâ€scale transcriptome analysis to predict genetic regions influencing the glycaemic index and texture in rice. Plant Biotechnology Journal, 2019, 17, 1261-1275.	4.1	56
320	Current perspectives in assessing humoral immunity after measles vaccination. Expert Review of Vaccines, 2019, 18, 75-87.	2.0	39
321	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
322	Widespread cis-regulation of RNA editing in a large mammal. Rna, 2019, 25, 319-335.	1.6	5
323	GDF11 antagonizes TNFâ€Î±â€induced inflammation and protects against the development of inflammatory arthritis in mice. FASEB Journal, 2019, 33, 3317-3329.	0.2	26
324	Bridging the Gap between Connectome and Transcriptome. Trends in Cognitive Sciences, 2019, 23, 34-50.	4.0	245
325	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	2.8	40
326	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
327	Multivariate genome-wide analyses of the well-being spectrum. Nature Genetics, 2019, 51, 445-451.	9.4	228

#	Article	IF	Citations
328	Association of a Schizophrenia-Risk Nonsynonymous Variant With Putamen Volume in Adolescents. JAMA Psychiatry, 2019, 76, 435.	6.0	51
329	Crosstalk of Genetic Variants, Allele-Specific DNA Methylation, and Environmental Factors for Complex Disease Risk. Frontiers in Genetics, 2018, 9, 695.	1.1	63
330	Established and emerging strategies to crack the genetic code of obesity. Obesity Reviews, 2019, 20, 212-240.	3.1	21
331	Crop genomeâ€wide association study: a harvest of biological relevance. Plant Journal, 2019, 97, 8-18.	2.8	151
332	eQTL analysis from co-localization of 2739 GWAS loci detects associated genes across 14 human cancers. Journal of Theoretical Biology, 2019, 462, 240-246.	0.8	1
333	simGWAS: a fast method for simulation of large scale caseâ€“control GWAS summary statistics. Bioinformatics, 2019, 35, 1901-1906.	1.8	23
334	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. Journal of Bone and Mineral Research, 2019, 34, 241-251.	3.1	47
335	Post-GWAS in prostate cancer: from genetic association to biological contribution. Nature Reviews Cancer, 2019, 19, 46-59.	12.8	73
336	1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes. Annual Review of Animal Biosciences, 2019, 7, 89-102.	3.6	241
337	A likelihoodâ€based approach to transcriptome association analysis. Statistics in Medicine, 2019, 38, 1357-1373.	0.8	7
338	Identification and characterization of <scp>GLDC</scp> as host susceptibility gene to severe influenza. EMBO Molecular Medicine, 2019, 11, .	3.3	20
339	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. Molecular Psychiatry, 2019, 24, 182-197.	4.1	47
340	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856.	3.2	16
341	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence. Molecular Psychiatry, 2019, 24, 169-181.	4.1	238
342	Beyond genomeâ€wide significance: integrative approaches to the interpretation and extension of GWAS findings for alcohol use disorder. Addiction Biology, 2019, 24, 275-289.	1.4	15
343	Genome-wide analysis reveals extensive genetic overlap between schizophrenia, bipolar disorder, and intelligence. Molecular Psychiatry, 2020, 25, 844-853.	4.1	156
344	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). Molecular Psychiatry, 2020, 25, 831-843.	4.1	36
345	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life. Molecular Psychiatry, 2020, 25, 3034-3052.	4.1	60

#	Article	IF	Citations
346	The three-dimensional landscape of the genome in human brain tissue unveils regulatory mechanisms leading to schizophrenia risk. Schizophrenia Research, 2020, 217, 17-25.	1.1	31
347	Clinical implications of recent advances in primary open-angle glaucoma genetics. Eye, 2020, 34, 29-39.	1.1	48
348	Three functional variants were identified to affect RPS24 expression and significantly associated with risk of colorectal cancer. Archives of Toxicology, 2020, 94, 295-303.	1.9	10
349	Mendelian Randomizationâ€"A Journey From Obscurity to Center Stage With a Few Potholes Along the Way. JAMA Neurology, 2020, 77, 7.	4.5	21
350	ncRNA-eQTL: a database to systematically evaluate the effects of SNPs on non-coding RNA expression across cancer types. Nucleic Acids Research, 2020, 48, D956-D963.	6.5	56
351	Integrating genome-wide association study and methylation functional annotation data identified candidate genes and pathways for schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2020, 96, 109736.	2.5	7
352	Identifying causal variants and genes using functional genomics in specialized cell types and contexts. Human Genetics, 2020, 139, 95-102.	1.8	16
353	BAGSE: a Bayesian hierarchical model approach for gene set enrichment analysis. Bioinformatics, 2020, 36, 1689-1695.	1.8	7
354	Integrative analysis of genomeâ€wide association study and expression quantitative trait loci datasets identified various immune cellâ€related pathways for rheumatoid arthritis. Annals of Human Genetics, 2020, 84, 72-79.	0.3	8
355	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
356	Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. Trends in Molecular Medicine, 2020, 26, 232-241.	3.5	31
357	The genetics of human ageing. Nature Reviews Genetics, 2020, 21, 88-101.	7.7	203
358	Mendelian randomization analysis revealed potential causal factors for systemic lupus erythematosus. Immunology, 2020, 159, 279-288.	2.0	18
359	A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. Human Molecular Genetics, 2020, 29, 159-167.	1.4	54
360	The genome-wide risk alleles for psychiatric disorders at 3p21.1 show convergent effects on mRNA expression, cognitive function, and mushroom dendritic spine. Molecular Psychiatry, 2020, 25, 48-66.	4.1	59
361	On Mendelian randomization analysis of caseâ€control study. Biometrics, 2020, 76, 380-391.	0.8	7
362	Linkageâ€linkage disequilibrium dissection of the epigenetic quantitative trait loci (epiQTLs) underlying growth and wood properties in Populus. New Phytologist, 2020, 225, 1218-1233.	3.5	25
363	Approximation of bias and meanâ€squared error in twoâ€sample Mendelian randomization analyses. Biometrics, 2020, 76, 369-379.	0.8	7

#	Article	IF	Citations
364	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature Communications, 2020, 11, 185.	5.8	45
365	Shared Genetic Loci Between Body Mass Index and Major Psychiatric Disorders. JAMA Psychiatry, 2020, 77, 503.	6.0	82
366	Integration analysis of methylation quantitative trait loci and GWAS identify three schizophrenia risk variants. Neuropsychopharmacology, 2020, 45, 1179-1187.	2.8	13
367	A Robust Method Uncovers Significant Context-Specific Heritability in Diverse Complex Traits. American Journal of Human Genetics, 2020, 106, 71-91.	2.6	54
368	Evaluating the Correlations Between Osteoporosis and Lifestyle-Related Factors Using Transcriptome-Wide Association Study. Calcified Tissue International, 2020, 106, 256-263.	1.5	10
369	Evaluation of muscarinic acetylcholine receptor typeÂ3 gene polymorphisms in patients with primary biliary cholangitis and primary sclerosing cholangitis. Hepatology Research, 2020, 50, 321-329.	1.8	4
370	Integrating genome-wide association study and expression quantitative trait loci data identifies NEGR1 as a causal risk gene of major depression disorder. Journal of Affective Disorders, 2020, 265, 679-686.	2.0	27
371	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. Nature Communications, 2020, 11, 45.	5.8	69
372	Multiomics Screening Identifies Molecular Biomarkers Causally Associated With the Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002876.	1.6	9
373	Association of blood-based transcriptional risk scores with biomarkers for Alzheimer disease. Neurology: Genetics, 2020, 6, e517.	0.9	13
374	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	2.4	40
375	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
376	Genome-wide identification of m6A-associated single-nucleotide polymorphisms in Parkinsonâ€™s disease. Neuroscience Letters, 2020, 737, 135315.	1.0	25
377	Genome-wide analysis of expression QTL (eQTL) and allele-specific expression (ASE) in pig muscle identifies candidate genes for meat quality traits. Genetics Selection Evolution, 2020, 52, 59.	1.2	22
378	Volumetric GWAS of medial temporal lobe structures identifies an ERC1 locus using ADNI high-resolution T2-weighted MRI data. Neurobiology of Aging, 2020, 95, 81-93.	1.5	7
379	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
380	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. Nature Communications, 2020, 11, 4930.	5.8	20
381	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. Nature Genetics, 2020, 52, 1239-1246.	9.4	134

#	Article	IF	Citations
382	Considerations for integrative multiâ€omic approaches to explore Alzheimer's disease mechanisms. Brain Pathology, 2020, 30, 984-991.	2.1	11
383	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. New Phytologist, 2020, 226, 1738-1752.	3.5	74
384	Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. Nature Communications, 2020, 11, 3570.	5.8	84
385	PWAS: proteome-wide association studyâ€"linking genes and phenotypes by functional variation in proteins. Genome Biology, 2020, 21, 173.	3.8	52
386	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. Nature Genetics, 2020, 52, 1303-1313.	9.4	163
387	Combining artificial intelligence: deep learning with Hi-C data to predict the functional effects of non-coding variants. Bioinformatics, 2021, 37, 1339-1344.	1.8	8
388	Massively parallel techniques for cataloguing the regulome of the human brain. Nature Neuroscience, 2020, 23, 1509-1521.	7.1	39
389	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	28
390	Genetics and major depressive disorder: clinical implications for disease risk, prognosis and treatment. International Clinical Psychopharmacology, 2020, 35, 233-242.	0.9	22
391	Gene mapping and functional annotation of GWAS of oral ulcers using FUMA software. Scientific Reports, 2020, 10, 12205.	1.6	6
392	Testing and controlling for horizontal pleiotropy with probabilistic Mendelian randomization in transcriptome-wide association studies. Nature Communications, 2020, 11, 3861.	5.8	79
393	Identification of susceptibility variants to benign childhood epilepsy with centro-temporal spikes (BECTS) in Chinese Han population. EBioMedicine, 2020, 57, 102840.	2.7	8
394	Genetic Fine Mapping and Genomic Annotation Defines Causal Mechanisms at A Novel Colorectal Cancer Susceptibility Locus in Han Chinese. Journal of Cancer, 2020, 11, 6841-6849.	1.2	2
395	Cyclic and multilevel causation in evolutionary processes. Biology and Philosophy, 2020, 35, 1.	0.7	1
396	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study. Communications Biology, 2020, 3, 608.	2.0	83
397	The Parkinson's Disease <scp>Genomeâ€Wide</scp> Association Study Locus Browser. Movement Disorders, 2020, 35, 2056-2067.	2.2	68
398	Integrative genomics analysis of various omics data and networks identify risk genes and variants vulnerable to childhood-onset asthma. BMC Medical Genomics, 2020, 13, 123.	0.7	15
399	Using Mendelian randomization to understand and develop treatments for neurodegenerative disease. Brain Communications, 2020, 2, fcaa031.	1.5	12

#	Article	IF	Citations
400	Identifying Risk Genes and Interpreting Pathogenesis for Parkinsonâ€™s Disease by a Multiomics Analysis. Genes, 2020, 11, 1100.	1.0	13
401	Epigenetic fine-mapping: identification of causal mechanisms for autoimmunity. Current Opinion in Immunology, 2020, 67, 50-56.	2.4	1
402	Integrative analysis identifies the association between CASZ1 methylation and ischemic stroke. Neurology: Genetics, 2020, 6, e509.	0.9	11
403	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. PLoS Genetics, 2020, 16, e1008947.	1.5	6
404	Genetic Architecture Modulates Diet-Induced Hepatic mRNA and miRNA Expression Profiles in Diversity Outbred Mice. Genetics, 2020, 216, 241-259.	1.2	6
405	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. Communications Biology, 2020, 3, 502.	2.0	36
406	Gene expression profiles complement the analysis of genomic modifiers of the clinical onset of Huntington disease. Human Molecular Genetics, 2020, 29, 2788-2802.	1.4	17
407	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. PLoS Genetics, 2020, 16, e1008780.	1.5	10
408	Summary-data-based Mendelian randomization prioritizes potential druggable targets for multiple sclerosis. Brain Communications, 2020, 2, fcaa119.	1.5	16
409	Genetic Pleiotropy of Bone-Related Phenotypes: Insights from Osteoporosis. Current Osteoporosis Reports, 2020, 18, 606-619.	1.5	2
410	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131.	9.4	298
411	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. Genome Biology, 2020, 21, 232.	3.8	46
412	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. Science Advances, 2020, 6, .	4.7	83
413	Convergent lines of evidence support NOTCH4 as a schizophrenia risk gene. Journal of Medical Genetics, 2021, 58, 666-678.	1.5	9
414	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. Genome Biology, 2020, 21, 235.	3.8	18
415	Gene Expression and RNA Splicing Imputation Identifies Novel Candidate Genes Associated with Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e4742-e4757.	1.8	12
416	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	1.5	41
417	Investigating DNA methylation as a potential mediator between pigmentation genes, pigmentary traits and skin cancer. Pigment Cell and Melanoma Research, 2021, 34, 892-904.	1.5	9

#	Article	IF	Citations
418	Functional annotation of genetic associations by transcriptome-wide association analysis provides insights into neutrophil development regulation. Communications Biology, 2020, 3, 790.	2.0	1
419	Genetic Risk Profiling in Parkinsonâ€™s Disease and Utilizing Genetics to Gain Insight into Disease-Related Biological Pathways. International Journal of Molecular Sciences, 2020, 21, 7332.	1.8	16
420	Single-cell expression and Mendelian randomization analyses identify blood genes associated with lifespan and chronic diseases. Communications Biology, 2020, 3, 206.	2.0	7
421	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	0.7	14
422	Quantifying genetic effects on disease mediated by assayed gene expression levels. Nature Genetics, 2020, 52, 626-633.	9.4	191
423	Summary-Based Methylome-Wide Association Analyses Suggest Potential Genetically Driven Epigenetic Heterogeneity of Alzheimerâ€™s Disease. Journal of Clinical Medicine, 2020, 9, 1489.	1.0	10
424	SZDB2.0: an updated comprehensive resource for schizophrenia research. Human Genetics, 2020, 139, 1285-1297.	1.8	35
425	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254.	5.8	140
426	The Integrated Landscape of Biological Candidate Causal Genes in Coronary Artery Disease. Frontiers in Genetics, 2020, 11, 320.	1.1	12
427	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. Frontiers in Genetics, 2020, 11, 424.	1.1	335
428	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohnâ€™s Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. Frontiers in Genetics, 2020, 11, 486.	1.1	15
429	Principles and approaches of association mapping in plant breeding. Tropical Plant Biology, 2020, 13, 212-224.	1.0	37
430	A practical view of fine-mapping and gene prioritization in the post-genome-wide association era. Open Biology, 2020, 10, 190221.	1.5	88
431	Association of TIM-1 (T-Cell Immunoglobulin and Mucin Domain 1) With Incidence of Stroke. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 1777-1786.	1.1	5
432	Transcriptomeâ€wide association studies: a view from Mendelian randomization. Quantitative Biology, 2021, 9, 107-121.	0.3	22
433	What do we know about the variability in survival of patients with amyotrophic lateral sclerosis?. Expert Review of Neurotherapeutics, 2020, 20, 921-941.	1.4	10
434	Identification of therapeutic targets from genetic association studies using hierarchical component analysis. BioData Mining, 2020, 13, 6.	2.2	3
435	Genomewide Association Study of Acute Anterior Uveitis Identifies New Susceptibility Loci. , 2020, 61, 3.		43

#	Article	IF	Citations
436	Integrative analysis of Mendelian randomization and Bayesian colocalization highlights four genes with putative BMI-mediated causal pathways to diabetes. Scientific Reports, 2020, 10, 7476.	1.6	7
437	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	9.4	304
438	Unravelling the complex genetics of common kidney diseases: from variants to mechanisms. Nature Reviews Nephrology, 2020, 16, 628-640.	4.1	33
439	Molecular mechanisms of coronary disease revealed using quantitative trait loci for TCF21 binding, chromatin accessibility, and chromosomal looping. Genome Biology, 2020, 21, 135.	3.8	16
440	Mendelian Randomization Identifies CpG Methylation Sites With Mediation Effects for Genetic Influences on BMD in Peripheral Blood Monocytes. Frontiers in Genetics, 2020, 11, 60.	1.1	9
441	Further confirmation of netrin 1 receptor (DCC) as a depression risk gene via integrations of multi-omics data. Translational Psychiatry, 2020, 10, 98.	2.4	26
442	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
443	Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia. Nature Genetics, 2020, 52, 401-407.	9.4	180
444	Large-scale pathway specific polygenic risk and transcriptomic community network analysis identifies novel functional pathways in Parkinson disease. Acta Neuropathologica, 2020, 140, 341-358.	3.9	68
445	Integrative analysis highlighted susceptibility genes for rheumatoid arthritis. International Immunopharmacology, 2020, 86, 106716.	1.7	8
446	Identifying Protein Biomarkers in Blood for Alzheimer's Disease. Frontiers in Cell and Developmental Biology, 2020, 8, 472.	1.8	7
447	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. Scientific Reports, 2020, 10, 10486.	1.6	22
448	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. Genome Biology, 2020, 21, 163.	3.8	76
449	The genetics of rheumatoid arthritis. Rheumatology, 2020, 59, 2661-2670.	0.9	80
450	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. Communications Biology, 2020, 3, 329.	2.0	42
451	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. PLoS Genetics, 2020, 16, e1008785.	1.5	29
452	Disentangling the genetics of sarcopenia: prioritization of NUDT3 and KLF5 as genes for lean mass & HLA-DQB1-AS1 for hand grip strength with the associated enhancing SNPs & a scoring system. BMC Medical Genetics, 2020, 21, 40.	2.1	18
453	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.4	43

#	Article	IF	Citations
454	IGREX for quantifying the impact of genetically regulated expression on phenotypes. NAR Genomics and Bioinformatics, 2020, 2, lqaa010.	1.5	15
455	A genome-wide multiphenotypic association analysis identified common candidate genes for subjective well-being, depressive symptoms and neuroticism. Journal of Psychiatric Research, 2020, 124, 22-28.	1.5	5
456	Large epigenome-wide association study of childhood ADHD identifies peripheral DNA methylation associated with disease and polygenic risk burden. Translational Psychiatry, 2020, 10, 8.	2.4	54
457	Expression quantitative trait loci-derived scores and white matter microstructure in UK Biobank: a novel approach to integrating genetics and neuroimaging. Translational Psychiatry, 2020, 10, 55.	2.4	8
458	Genome-wide association study of dietary intake in the UK biobank study and its associations with schizophrenia and other traits. Translational Psychiatry, 2020, 10, 51.	2.4	33
459	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
460	A Multi-Omics Perspective of Quantitative Trait Loci in Precision Medicine. Trends in Genetics, 2020, 36, 318-336.	2.9	41
461	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	15.2	384
462	Integrating Multi-Omics Data to Identify Novel Disease Genes and Single-Neucleotide Polymorphisms. Frontiers in Genetics, 2019, 10, 1336.	1.1	7
463	Variations and expression features of CYP2D6 contribute to schizophrenia risk. Molecular Psychiatry, 2021, 26, 2605-2615.	4.1	8
464	Power calculation for the general twoâ€sample Mendelian randomization analysis. Genetic Epidemiology, 2020, 44, 290-299.	0.6	25
465	A Multi-tissue Transcriptome Analysis of Human Metabolites Guides Interpretability of Associations Based on Multi-SNP Models for Gene Expression. American Journal of Human Genetics, 2020, 106, 188-201.	2.6	26
466	Integration of eQTL and a Single-Cell Atlas in the Human Eye Identifies Causal Genes for Age-Related Macular Degeneration. Cell Reports, 2020, 30, 1246-1259.e6.	2.9	151
467	Novel Approaches for Identifying the Molecular Background of Schizophrenia. Cells, 2020, 9, 246.	1.8	13
468	Allele-Specific QTL Fine Mapping with PLASMA. American Journal of Human Genetics, 2020, 106, 170-187.	2.6	14
469	Focus on Causality in ESC/iPSC-Based Modeling of Psychiatric Disorders. Cells, 2020, 9, 366.	1.8	12
470	Statistical Methods in Genome-Wide Association Studies. Annual Review of Biomedical Data Science, 2020, 3, 265-288.	2.8	6
471	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	5.8	8

#	Article	IF	Citations
472	Polygenic risk scores of several subtypes of epilepsies in a founder population. Neurology: Genetics, 2020, 6, e416.	0.9	17
473	A powerful and versatile colocalization test. PLoS Computational Biology, 2020, 16, e1007778.	1.5	10
474	Genome-wide meta-analysis identifies novel loci associated with age-related macular degeneration. Journal of Human Genetics, 2020, 65, 657-665.	1.1	59
475	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	5.8	211
476	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. Journal of Crohn's and Colitis, 2020, 14, 646-653.	0.6	5
477	Integrated Analysis of Summary Statistics to Identify Pleiotropic Genes and Pathways for the Comorbidity of Schizophrenia and Cardiometabolic Disease. Frontiers in Psychiatry, 2020, 11, 256.	1.3	24
478	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. PLoS Genetics, 2020, 16, e1008720.	1.5	180
479	An analysis of genetically regulated gene expression across multiple tissues implicates novel gene candidates in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2020, 12, 43.	3.0	20
480	Characterisation of genetic regulatory effects for osteoporosis risk variants in human osteoclasts. Genome Biology, 2020, 21, 80.	3.8	36
481	Comprehensive Analysis of the Genetic and Epigenetic Mechanisms of Osteoporosis and Bone Mineral Density. Frontiers in Cell and Developmental Biology, 2020, 8, 194.	1.8	10
482	A General Approach to Sensitivity Analysis for Mendelian Randomization. Statistics in Biosciences, 2021, 13, 34-55.	0.6	6
483	Emerging Methods and Resources for BiologicalÂInterrogation of Neuropsychiatric Polygenic Signal. Biological Psychiatry, 2021, 89, 41-53.	0.7	38
484	Genome-wide Association Analysis of Parkinsonâ€™s Disease and Schizophrenia Reveals Shared Genetic Architecture and Identifies Novel Risk Loci. Biological Psychiatry, 2021, 89, 227-235.	0.7	53
485	Genetic predictors of educational attainment and intelligence test performance predict voter turnout. Nature Human Behaviour, 2021, 5, 281-291.	6.2	15
486	Genetically determined intelligence and coronary artery disease risk. Clinical Research in Cardiology, 2021, 110, 211-219.	1.5	19
487	Transcriptomic Insight Into the Polygenic Mechanisms Underlying Psychiatric Disorders. Biological Psychiatry, 2021, 89, 54-64.	0.7	36
488	Where Are the Disease-Associated eQTLs?. Trends in Genetics, 2021, 37, 109-124.	2.9	163
489	Mendelian randomization integrating GWAS and mQTL data identified novel pleiotropic DNA methylation loci for neuropathology of Alzheimerâ€™s disease. Neurobiology of Aging, 2021, 97, 18-27.	1.5	14

#	Article	IF	Citations
490	CancerImmunityQTL: a database to systematically evaluate the impact of genetic variants on immune infiltration in human cancer. Nucleic Acids Research, 2021, 49, D1065-D1073.	6.5	22
491	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. Biological Psychiatry, 2021, 89, 246-255.	0.7	20
492	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	0.6	36
493	Prediction of Alzheimer's disease using multi-variants from a Chinese genome-wide association study. Brain, 2021, 144, 924-937.	3.7	30
494	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimerâ€™s Disease. Neuron, 2021, 109, 257-272.e14.	3.8	108
495	Mendelian randomization analysis identified genes pleiotropically associated with the risk and prognosis of COVID-19. Journal of Infection, 2021, 82, 126-132.	1.7	37
496	Computational Tools for Causal Inference in Genetics. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039248.	2.9	3
497	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome. Nature Human Behaviour, 2021, 5, 482-496.	6.2	30
498	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. Movement Disorders, 2021, 36, 449-459.	2.2	16
499	Independent replications and integrative analyses confirm TRANK1 as a susceptibility gene for bipolar disorder. Neuropsychopharmacology, 2021, 46, 1103-1112.	2.8	20
500	Causal Inference Methods to Integrate Omics and Complex Traits. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a040493.	2.9	9
501	A genome-wide association study of asthma hospitalizations in adults. Journal of Allergy and Clinical Immunology, 2021, 147, 933-940.	1.5	23
502	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224.	1.5	43
503	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
504	Novel directions in data pre-processing and genome-wide association study (GWAS) methodologies to overcome ongoing challenges. Informatics in Medicine Unlocked, 2021, 24, 100586.	1.9	2
505	Functional variants fineâ€mapping and gene function characterization provide insights into the role of ZNF323 in schizophrenia pathogenesis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 28-39.	1.1	8
506	Genetic analysis of amyotrophic lateral sclerosis identifies contributing pathways and cell types. Science Advances, 2021, 7, .	4.7	59
507	New Technologies to Study Functional Genomics of Age-Related Macular Degeneration. Frontiers in Cell and Developmental Biology, 2020, 8, 604220.	1.8	10

#	Article	IF	Citations
508	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	3.8	150
509	Convergent lines of evidence support BIN1 as a risk gene of Alzheimerâ€™s disease. Human Genomics, 2021, 15, 9.	1.4	8
510	Enhancer polymorphisms at the IKZF1 susceptibility locus for acute lymphoblastic leukemia impact B-cell proliferation and differentiation in both Down syndrome and non-Down syndrome genetic backgrounds. PLoS ONE, 2021, 16, e0244863.	1.1	3
512	Transcriptome wide association studies: general framework and methods. Quantitative Biology, 2021, 9, 141-150.	0.3	2
513	Mendelian randomization for studying the effects of perturbing drug targets. Wellcome Open Research, 2021, 6, 16.	0.9	90
514	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. Journal of Clinical Investigation, 2021, 131, .	3.9	23
515	Genetic risk factors for endometriosis near estrogen receptor 1 and coexpression of genes in this region in endometrium. Molecular Human Reproduction, 2021, 27, .	1.3	12
516	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
517	Revisiting the genome-wide significance threshold for common variant GWAS. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	59
518	Genetic loci shared between major depression and intelligence with mixed directions of effect. Nature Human Behaviour, 2021, 5, 795-801.	6.2	23
519	Multi-omics analysis to identify susceptibility genes for colorectal cancer. Human Molecular Genetics, 2021, 30, 321-330.	1.4	13
523	Genetic dissection of maize drought tolerance for trait improvement. Molecular Breeding, 2021, 41, 1.	1.0	49
524	The variant call format provides efficient and robust storage of GWAS summary statistics. Genome Biology, 2021, 22, 32.	3.8	82
525	GWAS of peptic ulcer disease implicates Helicobacter pylori infection, other gastrointestinal disorders and depression. Nature Communications, 2021, 12, 1146.	5.8	93
526	Identifying Thyroid Carcinoma-Related Genes by Integrating GWAS and eQTL Data. Frontiers in Cell and Developmental Biology, 2021, 9, 645275.	1.8	3
527	Genetic and functional interaction network analysis reveals global enrichment of regulatory T cell genes influencing basal cell carcinoma susceptibility. Genome Medicine, 2021, 13, 19.	3.6	20
528	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
529	Convergence of biomarkers and risk factor trait loci of coronary artery disease at 3p21.31 and HLA region. Npj Genomic Medicine, 2021, 6, 12.	1.7	6

#	Article	IF	Citations
533	E-MAGMA: an eQTL-informed method to identify risk genes using genome-wide association study summary statistics. Bioinformatics, 2021, 37, 2245-2249.	1.8	34
534	Genetic Architecture Underlying the Metabolites of Chlorogenic Acid Biosynthesis in Populus tomentosa. International Journal of Molecular Sciences, 2021, 22, 2386.	1.8	7
535	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. Human Molecular Genetics, 2021, 30, 603-618.	1.4	5
536	Aggregating multiple expression prediction models improves the power of transcriptome-wide association studies. Human Molecular Genetics, 2021, 30, 939-951.	1.4	24
537	Multi-omics highlights ABO plasma protein as a causal risk factor for COVID-19. Human Genetics, 2021, 140, 969-979.	1.8	36
538	Targeting Human lncRNAs for Treating Cardiometabolic Diseases. Cardiovascular Drugs and Therapy, 2021, 35, 655-662.	1.3	2
539	From the Genetics of Ankylosing Spondylitis to New Biology and Drug Target Discovery. Frontiers in Immunology, 2021, 12, 624632.	2.2	16
541	Multi-trait transcriptome-wide association studies with probabilistic Mendelian randomization. American Journal of Human Genetics, 2021, 108, 240-256.	2.6	35
542	Inference of phenotype-relevant transcriptional regulatory networks elucidates cancer type-specific regulatory mechanisms in a pan-cancer study. Npj Systems Biology and Applications, 2021, 7, 9.	1.4	5
543	Sex-Specific Associations of MIR137 Polymorphisms With Schizophrenia in a Han Chinese Cohort. Frontiers in Genetics, 2021, 12, 627874.	1.1	2
544	Deep transcriptome sequencing of subgenual anterior cingulate cortex reveals cross-diagnostic and diagnosis-specific RNA expression changes in major psychiatric disorders. Neuropsychopharmacology, 2021, 46, 1364-1372.	2.8	22
546	Power analysis of transcriptome-wide association study: Implications for practical protocol choice. PLoS Genetics, 2021, 17, e1009405.	1.5	50
547	Integrative Analysis of Omics Data Reveals Regulatory Network of CDK10 in Vitiligo Risk. Frontiers in Genetics, 2021, 12, 634553.	1.1	5
548	Mendelian randomization for studying the effects of perturbing drug targets. Wellcome Open Research, 2021, 6, 16.	0.9	48
549	Integrative analysis identifies potential causal methylation-mRNA regulation chains for rheumatoid arthritis. Molecular Immunology, 2021, 131, 89-96.	1.0	6
550	Integrating genomics with biomarkers and therapeutic targets to invigorate cardiovascular drug development. Nature Reviews Cardiology, 2021, 18, 435-453.	6.1	88
553	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. Nature Communications, 2021, 12, 1424.	5.8	23
555	A Bioinformatics Perspective on the Links Between Tetraspanin-Enriched Microdomains and Cardiovascular Pathophysiology. Frontiers in Cardiovascular Medicine, 2021, 8, 630471.	1.1	1

#	Article	IF	Citations
556	Single nucleotide variations in ZBTB46 are associated with post-thrombolytic parenchymal haematoma. Brain, 2021, 144, 2416-2426.	3.7	10
557	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
558	Integrative Analyses Followed by Functional Characterization Reveal TMEM180 as a Schizophrenia Risk Gene. Schizophrenia Bulletin, 2021, 47, 1364-1374.	2.3	7
559	An Integrative Transcriptome-Wide Analysis of Amyotrophic Lateral Sclerosis for the Identification of Potential Genetic Markers and Drug Candidates. International Journal of Molecular Sciences, 2021, 22, 3216.	1.8	12
560	Genetic control of the human brain proteome. American Journal of Human Genetics, 2021, 108, 400-410.	2.6	52
562	Phenome-wide investigation of the causal associations between childhood BMI and adult trait outcomes: a two-sample Mendelian randomization study. Genome Medicine, 2021, 13, 48.	3.6	23
563	A multi-ethnic genome-wide association study implicates collagen matrix integrity and cell differentiation pathways in keratoconus. Communications Biology, 2021, 4, 266.	2.0	36
564	Genetic Risk Stratification. JACC Basic To Translational Science, 2021, 6, 287-304.	1.9	19
565	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. Human Molecular Genetics, 2021, 30, 1259-1270.	1.4	8
566	Integration of summary data from GWAS and eQTL studies identified novel risk genes for coronary artery disease. Medicine (United States), 2021, 100, e24769.	0.4	9
567	DNA methylation and breast cancer-associated variants. Breast Cancer Research and Treatment, 2021, 188, 713-727.	1.1	7
568	Shared associations identify causal relationships between gene expression and immune cell phenotypes. Communications Biology, 2021, 4, 279.	2.0	3
569	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. Nature Genetics, 2021, 53, 445-454.	9.4	61
570	Editing GWAS: experimental approaches to dissect and exploit disease-associated genetic variation. Genome Medicine, 2021, 13, 41.	3.6	32
571	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	1.5	24
572	Utilising multi-large omics data to elucidate biological mechanisms within multiple sclerosis genetic susceptibility loci. Multiple Sclerosis Journal, 2021, 27, 2141-2149.	1.4	3
573	System Genetics Including Causal Inference Identify Immune Targets for Coronary Artery Disease and the Lifespan. Circulation Genomic and Precision Medicine, 2021, 14, e003196.	1.6	7
574	Multi-Omics Approaches to Define Calcific Aortic Valve Disease Pathogenesis. Circulation Research, 2021, 128, 1371-1397.	2.0	39

#	Article	IF	Citations
575	Evidence forGRNconnecting multiple neurodegenerative diseases. Brain Communications, 2021, 3, fcab095.	1.5	24
576	Educational attainment protects against epilepsy independent of cognitive function: A Mendelian randomization study. Epilepsia, 2021, 62, 1362-1368.	2.6	11
577	Genetic evidence suggests posttraumatic stress disorder as a subtype of major depressive disorder. Journal of Clinical Investigation, 2022, 132, .	3.9	68
578	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
579	Mendelian randomization integrating GWAS and eQTL data revealed genes pleiotropically associated with major depressive disorder. Translational Psychiatry, 2021, 11, 225.	2.4	19
580	Effect of selection bias on two sample summary data based Mendelian randomization. Scientific Reports, 2021, 11, 7585.	1.6	10
581	Gene Expression Imputation Across Multiple Tissue Types Provides Insight Into the Genetic Architecture of Frontotemporal Dementia and Its Clinical Subtypes. Biological Psychiatry, 2021, 89, 825-835.	0.7	10
582	Pleiotropic effects of telomere length loci with brain morphology and brain tissue expression. Human Molecular Genetics, 2021, 30, 1360-1370.	1.4	4
583	Beyond association: successes and challenges in linking non-coding genetic variation to functional consequences that modulate Alzheimerâ€™s disease risk. Molecular Neurodegeneration, 2021, 16, 27.	4.4	20
584	Defining functional variants associated with Alzheimerâ€™s disease in the induced immune response. Brain Communications, 2021, 3, fcab083.	1.5	14
585	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. Nature Neuroscience, 2021, 24, 810-817.	7.1	85
586	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
587	Transâ€Ethnic Fineâ€Mapping of the Major Histocompatibility Complex Region Linked to Parkinson's Disease. Movement Disorders, 2021, 36, 1805-1814.	2.2	14
588	Chromatin accessibility in neuropsychiatric disorders. Neurobiology of Learning and Memory, 2021, 181, 107438.	1.0	2
589	Sorting Out Sorting Nexins Functions in the Nervous System in Health and Disease. Molecular Neurobiology, 2021, 58, 4070-4106.	1.9	15
591	Downregulation by CNNM2 of ATP5MD expression in the 10q24.32 schizophrenia-associated locus involved in impaired ATP production and neurodevelopment. NPJ Schizophrenia, 2021, 7, 27.	2.0	3
592	Multi-tissue neocortical transcriptome-wide association study implicates 8 genes across 6 genomic loci in Alzheimerâ€™s disease. Genome Medicine, 2021, 13, 76.	3.6	19
594	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12

#	Article	IF	Citations
595	Identification of Gingivitis-Related Genes Across Human Tissues Based on the Summary Mendelian Randomization. Frontiers in Cell and Developmental Biology, 2020, 8, 624766.	1.8	4
597	Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis. Journal of Clinical Investigation, 2021, 131, .	3.9	49
598	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
599	Joint Genome-Wide Association Analyses Identified 49 Novel Loci For Age at Natural Menopause. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 2574-2591.	1.8	6
600	Brain gene co-expression networks link complement signaling with convergent synaptic pathology in schizophrenia. Nature Neuroscience, 2021, 24, 799-809.	7.1	44
601	Variance-component-based meta-analysis of geneâ€“environment interactions for rare variants. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
602	Interaction Between SNP Genotype and Efficacy of Anastrozole and Exemestane in Earlyâ€Stage Breast Cancer. Clinical Pharmacology and Therapeutics, 2021, 110, 1038-1049.	2.3	5
603	Association of Antihypertensive Drug Target Genes With Psychiatric Disorders. JAMA Psychiatry, 2021, 78, 623.	6.0	56
604	Shared genetic architecture between neuroticism, coronary artery disease and cardiovascular risk factors. Translational Psychiatry, 2021, 11, 368.	2.4	10
605	Multitrait transcriptomeâ€wide association study (TWAS) tests. Genetic Epidemiology, 2021, 45, 563-576.	0.6	9
606	Epigenome-Wide Study Identified Methylation Sites Associated with the Risk of Obesity. Nutrients, 2021, 13, 1984.	1.7	8
607	Shared genetic links between amyotrophic lateral sclerosis and obesity-related traits: a genome-wide association study. Neurobiology of Aging, 2021, 102, 211.e1-211.e9.	1.5	12
608	Evaluating marginal genetic correlation of associated loci for complex diseases and traits between European and East Asian populations. Human Genetics, 2021, 140, 1285-1297.	1.8	12
609	Regulatory SNPs: Altered Transcription Factor Binding Sites Implicated in Complex Traits and Diseases. International Journal of Molecular Sciences, 2021, 22, 6454.	1.8	29
611	Genetic mechanisms of COVID-19 and its association with smoking and alcohol consumption. Briefings in Bioinformatics, 2021, 22, .	3.2	31
612	eQTpLot: a user-friendly R package for the visualization of colocalization between eQTL and GWAS signals. BioData Mining, 2021, 14, 32.	2.2	14
613	GWAS-Top Polymorphisms Associated With Late-Onset Alzheimer Disease in Brazil: Pointing Out Possible New Culprits Among Non-Coding RNAs. Frontiers in Molecular Biosciences, 2021, 8, 632314.	1.6	3
614	Proteome-wide Association Study Provides Insights Into the Genetic Component of Protein Abundance in Psychiatric Disorders. Biological Psychiatry, 2021, 90, 781-789.	0.7	34

#	Article	IF	Citations
615	SNX19 restricts endolysosome motility through contacts with the endoplasmic reticulum. Nature Communications, 2021, 12, 4552.	5.8	33
616	Investigation of convergent and divergent genetic influences underlying schizophrenia and alcohol use disorder. Psychological Medicine, 2023, 53, 1196-1204.	2.7	7
617	Mendelian randomization analysis identified genes potentially pleiotropically associated with periodontitis. Saudi Journal of Biological Sciences, 2021, 28, 4089-4095.	1.8	4
620	rs12537 Is a Novel Susceptibility SNP Associated With Estrogen Receptor Positive Breast Cancer in Chinese Han Population. Frontiers in Medicine, 2021, 8, 708644.	1.2	4
621	Mendelian randomization analysis identified genes pleiotropically associated with central corneal thickness. BMC Genomics, 2021, 22, 517.	1.2	9
626	Identification of Parkinsonâ€™s Disease-Causing Genes via Omics Data. Frontiers in Genetics, 2021, 12, 712164.	1.1	7
628	Demystifying emerging bulk RNA-Seq applications: the application and utility of bioinformatic methodology. Briefings in Bioinformatics, 2021, 22, .	3.2	31
629	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
630	DeepGP: An Integrated Deep Learning Method for Endocrine Disease Gene Prediction Using Omics Data. Frontiers in Cell and Developmental Biology, 2021, 9, 700061.	1.8	1
632	Extensive bidirectional genetic overlap between bipolar disorder and cardiovascular disease phenotypes. Translational Psychiatry, 2021, 11, 407.	2.4	16
634	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. PLoS Genetics, 2021, 17, e1009331.	1.5	25
635	Automated AI labeling of optic nerve head enables insights into cross-ancestry glaucoma risk and genetic discovery in >280,000 images from UKB and CLSA. American Journal of Human Genetics, 2021, 108, 1204-1216.	2.6	39
637	Genetic architecture modulates diet-induced hepatic mRNA and miRNA expression profiles in Diversity Outbred mice. Genetics, 2021, 218, .	1.2	4
638	Integration of Multiple-Omics Data to Analyze the Population-Specific Differences for Coronary Artery Disease. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-11.	0.7	40
639	Genes with specificity for expression in the round cell layer of the growth plate are enriched in genomewide association study (GWAS) of human height. Journal of Bone and Mineral Research, 2020, 36, 2300-2308.	3.1	9
640	GIS-based ensemble computational models for flood susceptibility prediction in the Quang Binh Province, Vietnam. Journal of Hydrology, 2021, 599, 126500.	2.3	31
642	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome Biology, 2021, 22, 241.	3.8	3
644	Novel DNA methylation loci and genes showing pleiotropic association with Alzheimerâ€™s dementia: a network Mendelian randomization analysis. Epigenetics, 2022, 17, 746-758.	1.3	8

#	Article	IF	Citations
645	Identification of novel drug targets for Alzheimerâ€™s disease by integrating genetics and proteomes from brain and blood. Molecular Psychiatry, 2021, 26, 6065-6073.	4.1	38
647	Integrative Transcriptome-Wide Analyses Uncover Novel Risk-Associated MicroRNAs in Hormone-Dependent Cancers. Frontiers in Genetics, 2021, 12, 716236.	1.1	3
653	Model checking via testing for direct effects in Mendelian Randomization and transcriptome-wide association studies. PLoS Computational Biology, 2021, 17, e1009266.	1.5	4
654	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
657	Association of Variants Near the Bradykinin Receptor B2 Gene With Angioedema in Patients Taking ACEÂInhibitors. Journal of the American College of Cardiology, 2021, 78, 696-709.	1.2	10
658	Effect of Metabolite Levels on Type 2 Diabetes Mellitus and Glycemic Traits: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 3439-3447.	1.8	2
660	Chromatin Alterations in Neurological Disorders and Strategies of (Epi)Genome Rescue. Pharmaceuticals, 2021, 14, 765.	1.7	3
661	Unraveling Risk Genes of COVID-19 by Multi-Omics Integrative Analyses. Frontiers in Medicine, 2021, 8, 738687.	1.2	22
662	Relationship between genetically determined telomere length and glioma risk. Neuro-Oncology, 2022, 24, 171-181.	0.6	21
663	Identification of New Genes and Loci Associated With Bone Mineral Density Based on Mendelian Randomization. Frontiers in Genetics, 2021, 12, 728563.	1.1	4
664	Genetic variations of DNA bindings of FOXA1 and co-factors in breast cancer susceptibility. Nature Communications, 2021, 12, 5318.	5.8	14
665	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
666	Integrative Functional Genomics Implicated the Key T-/B-Cell Deficiency Regulator RAG1 in Transarterial Chemoembolization of Hepatocellular Carcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 720791.	1.8	2
667	Pleiotropy or linkage? Their relative contributions to the genetic correlation of quantitative traits and detection by multitrait GWA studies. Genetics, 2021, 219, .	1.2	24
668	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. Nature Communications, 2021, 12, 5251.	5.8	37
669	Mendelian randomization study reveals a population-specific putative causal effect of type 2 diabetes in risk of cataract. International Journal of Epidemiology, 2022, 50, 2024-2037.	0.9	11
670	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. Epigenetics and Chromatin, 2021, 14, 44.	1.8	3
671	Causal Associations Between Blood Lipids and COVID-19 Risk: A Two-Sample Mendelian Randomization Study. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2802-2810.	1.1	15

#	Article	IF	Citations
672	Genetic Association Between Schizophrenia and Cortical Brain Surface Area and Thickness. JAMA Psychiatry, 2021, 78, 1020.	6.0	43
673	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
675	Integration of functional genomics data to uncover cell type-specific pathways affected in Parkinson's disease. Biochemical Society Transactions, 2021, 49, 2091-2100.	1.6	1
676	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
678	Estimation of Simultaneous Signals Using Absolute Inner Product with Applications to Integrative Genomics. Statistica Sinica, 2022, , .	0.2	0
679	Gene-based association analysis identifies 190 genes affecting neuroticism. Scientific Reports, 2021, 11, 2484.	1.6	12
680	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimerâ€™s disease pathogenesis. Nature Genetics, 2021, 53, 143-146.	9.4	158
681	Multi-omics analyses of cognitive traits and psychiatric disorders highlight brain-dependent mechanisms. Human Molecular Genetics, 2023, 32, 885-896.	1.4	11
683	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. Cancer Research, 2021, 81, 1230-1239.	0.4	14
684	Polygenic overlap and shared genetic loci between loneliness, severe mental disorders, and cardiovascular disease risk factors suggest shared molecular mechanisms. Translational Psychiatry, 2021, 11, 3.	2.4	29
685	MungeSumstats: a Bioconductor package for the standardization and quality control of many GWAS summary statistics. Bioinformatics, 2021, 37, 4593-4596.	1.8	32
686	Multiâ€tissue transcriptomeâ€wide association studies. Genetic Epidemiology, 2021, 45, 324-337.	0.6	8
687	Genetic Risk Factors for Sporadic Frontotemporal Dementia. , 2018, , 147-186.		1
688	Genetic architecture of photosynthesis energy partitioning as revealed by a genome-wide association approach. Photosynthesis Research, 2021, 150, 97-115.	1.6	8
689	Artificial Intelligence in Drug Discovery: A Comprehensive Review of Data-driven and Machine Learning Approaches. Biotechnology and Bioprocess Engineering, 2020, 25, 895-930.	1.4	43
690	Effect of Human Genetic Variability on Gene Expression in Dorsal Root Ganglia and Association with Pain Phenotypes. Cell Reports, 2017, 19, 1940-1952.	2.9	83
691	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	9.4	391
692	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. Nature Neuroscience, 2017, 20, 1418-1426.	7.1	377

#	Article	IF	Citations
693	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	4.1	48
694	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
695	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. Nature Neuroscience, 2020, 23, 809-818.	7.1	242
696	Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29013-29024.	3.3	46
697	Intricacies of aetiology in intrafamilial degenerative disease. Brain Communications, 2020, 2, fcaa120.	1.5	4
698	PheLiGe: an interactive database of billions of human genotypeâ€“phenotype associations. Nucleic Acids Research, 2021, 49, D1347-D1350.	6.5	13
814	Using single-cell entropy to describe the dynamics of reprogramming and differentiation of induced pluripotent stem cells. International Journal of Modern Physics B, 2020, 34, 2050288.	1.0	8
815	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	2.3	15
816	Multiomics dissection of molecular regulatory mechanisms underlying autoimmune-associated noncoding SNPs. JCI Insight, 2020, 5, .	2.3	13
817	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. F1000Research, 2018, 7, 121.	0.8	4
818	Efficient and accurate causal inference with hidden confounders from genome-transcriptome variation data. PLoS Computational Biology, 2017, 13, e1005703.	1.5	36
819	C-reactive protein upregulates the whole blood expression of CD59 - an integrative analysis. PLoS Computational Biology, 2017, 13, e1005766.	1.5	44
820	LocusFocus: Web-based colocalization for the annotation and functional follow-up of GWAS. PLoS Computational Biology, 2020, 16, e1008336.	1.5	28
821	Integrating molecular QTL data into genome-wide genetic association analysis: Probabilistic assessment of enrichment and colocalization. PLoS Genetics, 2017, 13, e1006646.	1.5	205
822	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194
823	The relative contribution of DNA methylation and genetic variants on protein biomarkers for human diseases. PLoS Genetics, 2017, 13, e1007005.	1.5	54
824	Orienting the causal relationship between imprecisely measured traits using GWAS summary data. PLoS Genetics, 2017, 13, e1007081.	1.5	969
825	Inferring causal direction between two traits in the presence of horizontal pleiotropy with GWAS summary data. PLoS Genetics, 2020, 16, e1009105.	1.5	18

#	Article	IF	Citations
826	Epigenome-wide association study of leukocyte telomere length. Aging, 2019, 11, 5876-5894.	1.4	19
827	Identification of Genes Associated with Lung Adenocarcinoma Prognosis. Combinatorial Chemistry and High Throughput Screening, 2019, 22, 220-224.	0.6	2
828	Transcriptomic analyses of humans and mice provide insights into depression. Zoological Research, 2020, 41, 632-643.	0.9	9
829	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	2.8	170
830	A generally conserved response to hypoxia in iPSC-derived cardiomyocytes from humans and chimpanzees. ELife, 2019, 8, .	2.8	35
831	Causal associations of intelligence with schizophrenia and bipolar disorder: A Mendelian randomization analysis. European Psychiatry, 2021, 64, e61.	0.1	6
832	A Bioinformatic Pipeline to Integrate GWAS and eQTL Datasets to Identify Disease Relevant Human Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 93-110.	0.4	0
833	A comprehensive review of the analysis and integration of omics data for SARS-CoV-2 and COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	9
834	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. Nature Communications, 2021, 12, 5641.	5.8	46
835	Beyond GWAS: from simple associations to functional insights. Seminars in Immunopathology, 2022, 44, 3-14.	2.8	13
836	FOXA1 of regulatory variant associated with risk of breast cancer through allele-specific enhancer in the Chinese population. Breast Cancer, 2021, , 1.	1.3	0
837	SCFD1 expression quantitative trait loci in amyotrophic lateral sclerosis are differentially expressed. Brain Communications, 2021, 3, fcab236.	1.5	14
838	Joint-Tissue Integrative Analysis Identified Hundreds of Schizophrenia Risk Genes. Molecular Neurobiology, 2021, , 1.	1.9	4
839	White Matter Integrity and Nicotine Dependence: Evaluating Vertical and Horizontal Pleiotropy. Frontiers in Neuroscience, 2021, 15, 738037.	1.4	6
841	Mendelian Randomization Analysis Identified Potential Genes Pleiotropically Associated with Polycystic Ovary Syndrome. Reproductive Sciences, 2022, 29, 1028-1037.	1.1	6
842	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	2.0	11
863	Pan-Cancer Analysis of Heritable Genetic Variations Reveals Cancer-Specific Activation of Dormant Oncogenic Pathways. SSRN Electronic Journal, 0, , .	0.4	0
864	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. F1000Research, 2018, 7, 121.	0.8	3

#	Article	IF	Citations
915	Sequence variation at 8q24.21 and risk of back pain. F1000Research, 0, 9, 424.	0.8	1
927	High-Dimensional Mediation Analysis with Applications to Causal Gene Identification. Statistics in Biosciences, 2022, 14, 432-451.	0.6	8
928	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	9.4	208
929	Identification of soybean phosphorous efficiency QTLs and genes using chlorophyll fluorescence parameters through GWAS and RNA-seq. Planta, 2021, 254, 110.	1.6	8
931	Genetics and Pharmacogenetics of COPD. Respiratory Medicine, 2020, , 39-55.	0.1	0
936	The GWAS-MAP platform for aggregation of results of genome-wide association studies and the GWAS-MAP|homo database of 70 billion genetic associations of human traits. Vavilovskii Zhurnal Genetiki I Selektsii, 2020, 24, 876-884.	0.4	7
938	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. PLoS Genetics, 2020, 16, e1009060.	1.5	11
939	Genetic susceptibility to CRC. , 2022, , 513-518.		0
940	Genome-wide association study toward efficient selection breeding of resistance to Vibrio alginolyticus in Pacific oyster, Crassostrea gigas. Aquaculture, 2022, 548, 737592.	1.7	14
948	Functional Annotations of Single-Nucleotide Polymorphism (SNP)-Based and Gene-Based Genome-Wide Association Studies Show Genes Affecting Keratitis Susceptibility. Medical Science Monitor, 2020, 26, e922710.	0.5	3
949	Insight into the genetic architecture of back pain and its risk factors from a study of 509.000 individuals. BÃ³l, 2020, 20, 1-14.	0.1	0
953	Integrative genomics analysis of eQTL and GWAS summary data identifies PPP1CB as a novel bone mineral density risk genes. Bioscience Reports, 2020, 40, .	1.1	0
954	Systematic Exploration in Tissue-Pathway Associations of Complex Traits Using Comprehensive eQTLs Catalog. Frontiers in Big Data, 2021, 4, 719737.	1.8	1
955	Heritability Enrichment of Immunoglobulin G N-Glycosylation in Specific Tissues. Frontiers in Immunology, 2021, 12, 741705.	2.2	6
956	Genome-wide association studies identify the role of caspase-9 in kidney disease. Science Advances, 2021, 7, eabi8051.	4.7	14
958	Dysregulated expression levels of APH1B in peripheral blood are associated with brain atrophy and amyloid-Î² deposition in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2021, 13, 183.	3.0	13
965	Integrative genomics analysis identifies five promising genes implicated in insomnia risk based on multiple omics datasets. Bioscience Reports, 2020, 40, .	1.1	8
969	Could personalised risk prediction for type 2 diabetes using polygenic risk scores direct prevention, enhance diagnostics, or improve treatment?. Wellcome Open Research, 0, 5, 206.	0.9	4

#	Article	IF	Citations
973	kTWAS: integrating kernel machine with transcriptome-wide association studies improves statistical power and reveals novel genes. Briefings in Bioinformatics, 2021, 22, .	3.2	30
979	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. ELife, 2020, 9, .	2.8	18
981	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
982	Stress, Cortisol and NR3C1 in At-Risk Individuals for Psychosis: A Mendelian Randomization Study. Frontiers in Psychiatry, 2020, 11, 680.	1.3	3
983	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk based on multiple omics datasets. Aging, 2020, 12, 19173-19220.	1.4	2
984	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 172-183.	0.7	0
985	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. Frontiers in Genetics, 2021, 12, 609657.	1.1	1
986	Deep learning enables genetic analysis of the human thoracic aorta. Nature Genetics, 2022, 54, 40-51.	9.4	90
988	Strong and weak cross-inheritance of substance use disorders in a nationally representative sample. Molecular Psychiatry, 2022, 27, 1742-1753.	4.1	4
993	A Comprehensive Evaluation of Cross-Omics Blood-Based Biomarkers for Neuropsychiatric Disorders. Journal of Personalized Medicine, 2021, 11, 1247.	1.1	3
994	Integrative metabolomicsâ€genomics approach reveals key metabolic pathways and regulators of Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1260-1278.	0.4	57
995	Graph Embedding Based Novel Gene Discovery Associated With Diabetes Mellitus. Frontiers in Genetics, 2021, 12, 779186.	1.1	2
996	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300.	2.6	31
997	Genetic Association and Mendelian Randomization for Hypothyroidism Highlight Immune Molecular Mechanisms. SSRN Electronic Journal, 0, , .	0.4	0
998	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	3.7	6
999	Quantitative Genetics of Human Protein N-Glycosylation. Advances in Experimental Medicine and Biology, 2021, 1325, 151-171.	0.8	1
1000	Genetics of common cerebral small vessel disease. Nature Reviews Neurology, 2022, 18, 84-101.	4.9	30
1003	A CNN-Based Method for Counting Grains within a Panicle. Machines, 2022, 10, 30.	1.2	7

#	Article	IF	Citations
1004	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	9.4	60
1005	Genetic Regulation of Transcription in the Endometrium in Health and Disease. Frontiers in Reproductive Health, 2022, 3, .	0.6	8
1006	A novel cis-regulatory variant modulating TIE1 expression associated with attention deficit hyperactivity disorder in Han Chinese children. Journal of Affective Disorders, 2022, 300, 179-188.	2.0	4
1007	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk based on multiple omics datasets. Aging, 2020, 12, 19173-19220.	1.4	6
1009	Genome-Wide Analysis of Disordered Eating Behavior in the Mexican Population. Nutrients, 2022, 14, 394.	1.7	1
1010	A flexible summary statistics-based colocalization method with application to the mucin cystic fibrosis lung disease modifier locus. American Journal of Human Genetics, 2022, 109, 253-269.	2.6	5
1011	Mendelian randomization analyses for PCOS: evidence, opportunities, and challenges. Trends in Genetics, 2022, 38, 468-482.	2.9	21
1012	The use of machine learning to discover regulatory networks controlling biological systems. Molecular Cell, 2022, 82, 260-273.	4.5	11
1014	Promoter DNA Methylation in GWAS-Identified Genes as Potential Functional Elements for Blood Pressure: An Observational and Mendelian Randomization Study. Frontiers in Genetics, 2021, 12, 791146.	1.1	2
1015	Polycystic Ovary Syndrome: An Evolutionary Adaptation to Lifestyle and the Environment. International Journal of Environmental Research and Public Health, 2022, 19, 1336.	1.2	30
1017	Genome-wide analysis of genetic predisposition to common polygenic cancers. Journal of Applied Genetics, 2022, 63, 315.	1.0	2
1018	Genome-Wide Association Study Identifies Two Common Loci Associated with Pigment Dispersion Syndrome/Pigmentary Glaucoma and Implicates Myopia in its Development. Ophthalmology, 2022, 129, 626-636.	2.5	10
1019	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	1.8	5
1020	Genetic common variants associated with cerebellar volume and their overlap with mental disorders: a study on 33,265 individuals from the UK-Biobank. Molecular Psychiatry, 2022, 27, 2282-2290.	4.1	17
1021	Interpreting Functional Impact of Genetic Variations by Network QTL for Genotypeâ€“Phenotype Association Study. Frontiers in Cell and Developmental Biology, 2021, 9, 720321.	1.8	3
1022	MODAS: exploring maize germplasm with multi-omics data association studies. Science Bulletin, 2022, 67, 903-906.	4.3	6
1023	Whole exome sequence analysis in 51â€‰624 participants identifies novel genes and variants associated with refractive error and myopia. Human Molecular Genetics, 2022, , .	1.4	10
1024	Genetic approaches for increasing fitness in endangered species. Trends in Ecology and Evolution, 2022, 37, 332-345.	4.2	14

#	Article	IF	Citations
1025	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. Genome Medicine, 2022, 14, 7.	3.6	12
1026	Adaptive eQTLs reveal the evolutionary impacts of pleiotropy and tissue-specificity while contributing to health and disease. Human Genetics and Genomics Advances, 2022, 3, 100083.	1.0	9
1027	Functional variant rs2270363 on 16p13.3 confers schizophrenia risk by regulating NMRAL1. Brain, 2022, 145, 2569-2585.	3.7	4
1028	Harnessing tissue-specific genetic variation to dissect putative causal pathways between body mass index and cardiometabolic phenotypes. American Journal of Human Genetics, 2022, 109, 240-252.	2.6	15
1030	The association between the CASP5 rs7939842 polymorphism and the risk of rheumatoid arthritis in Chinese Han individuals. Arabian Journal of Chemistry, 2022, 15, 103667.	2.3	0
1031	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	3.2	3
1032	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	1.4	6
1035	Partitioning gene-mediated disease heritability without eQTLs. American Journal of Human Genetics, 2022, 109, 405-416.	2.6	8
1036	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. Nature Communications, 2022, 13, 826.	5.8	31
1037	Molecular mapping for fruit-related traits, and joint identification of candidate genes and selective sweeps for seed size in melon. Genomics, 2022, 114, 110306.	1.3	5
1038	A comprehensive gene-centric pleiotropic association analysis for 14 psychiatric disorders with GWAS summary statistics. BMC Medicine, 2021, 19, 314.	2.3	20
1039	Meta-Analysis of Transcriptome-Wide Association Studies across 13 Brain Tissues Identified Novel Clusters of Genes Associated with Nicotine Addiction. Genes, 2022, 13, 37.	1.0	1
1040	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	9.4	223
1042	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. Frontiers in Genetics, 2021, 12, 609657.	1.1	8
1043	Genetics of bipolar disorder. , 2022, , 43-61.		0
1044	Integration with systems biology approaches and -omics data to characterize risk variation. , 2022, , 289-315.		4
1045	Proxied Therapeutic Inhibition on Wnt Signaling Antagonists and Risk of Cardiovascular Diseases: Multi-Omics Analyses. SSRN Electronic Journal, 0, , .	0.4	0
1046	Multi-ancestry GWAS reveals excitotoxicity associated with outcome after ischaemic stroke. Brain, 2022, 145, 2394-2406.	3.7	15

#	Article	IF	Citations
1047	A genome-wide association study in a large community-based cohort identifies multiple loci associated with susceptibility to bacterial and viral infections. Scientific Reports, 2022, 12, 2582.	1.6	9
1048	An analysis of genetically regulated gene expression and the role of co-expression networks across 16 psychiatric and substance use phenotypes. European Journal of Human Genetics, 2022, 30, 560-566.	1.4	3
1049	Integrative analysis prioritizes the relevant genes and risk factors for chronic venous disease. Journal of Vascular Surgery: Venous and Lymphatic Disorders, 2022, 10, 738-748.e5.	0.9	3
1050	Predicting genotype-specific gene regulatory networks. Genome Research, 2022, 32, 524-533.	2.4	9
1051	Large-scale association study on daily weight gain in pigs reveals overlap of genetic factors for growth in humans. BMC Genomics, 2022, 23, 133.	1.2	8
1052	Effect of corporate environmental strategies on firmsâ€™ competitiveness, the mediating role of supply chain collaboration. Journal of Global Responsibility, 2022, ahead-of-print, .	1.1	3
1053	A genome-wide analysis of 340â€‰318 participants identifies four novel loci associated with the age of first spectacle wear. Human Molecular Genetics, 2022, , .	1.4	0
1054	PSRC1 May Affect Coronary Artery Disease Risk by Altering CELSR2, PSRC1, and SORT1 Gene Expression and Circulating Granulin and Apolipoprotein B Protein Levels. Frontiers in Cardiovascular Medicine, 2022, 9, 763015.	1.1	3
1055	Integrative Prioritization of Causal Genes for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003365.	1.6	11
1056	The molecular genetic basis of creativity: a mini review and perspectives. Psychological Research, 2023, 87, 1-16.	1.0	1
1058	Leveraging a Surrogate Outcome to Improve Inference on a Partially Missing Target Outcome. Biometrics, 2023, 79, 1472-1484.	0.8	1
1062	Likelihood-based Mendelian randomization analysis with automated instrument selection and horizontal pleiotropic modeling. Science Advances, 2022, 8, eabl5744.	4.7	13
1063	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. Frontiers in Psychiatry, 2022, 13, 797329.	1.3	9
1064	Genetic regulation of post-translational modification of two distinct proteins. Nature Communications, 2022, 13, 1586.	5.8	19
1065	Genetic and phenotypic links between obesity and extracellular vesicles. Human Molecular Genetics, 2022, 31, 3643-3651.	1.4	2
1066	ICA1L Is Associated with Small Vessel Disease: A Proteome-Wide Association Study in Small Vessel Stroke and Intracerebral Haemorrhage. International Journal of Molecular Sciences, 2022, 23, 3161.	1.8	11
1067	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	0.6	2
1068	Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes. Genome Medicine, 2022, 14, 31.	3.6	7

#	Article	IF	Citations
1070	Gene-based association tests using GWAS summary statistics and incorporating eQTL. Scientific Reports, 2022, 12, 3553.	1.6	1
1071	Association of Circulating Cathepsin B Levels With Blood Pressure and Aortic Dilation. Frontiers in Cardiovascular Medicine, 2022, 9, 762468.	1.1	7
1072	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	9.4	23
1073	Alcohol, Coffee, and Milk Intake in Relation to Epilepsy Risk. Nutrients, 2022, 14, 1153.	1.7	5
1074	The Potential of Current Polygenic Risk Scores to Predict High Myopia and Myopic Macular Degeneration in Multiethnic Singapore Adults. Ophthalmology, 2022, 129, 890-902.	2.5	5
1075	Identifying causal genes for depression via integration of the proteome and transcriptome from brain and blood. Molecular Psychiatry, 2022, 27, 2849-2857.	4.1	27
1076	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	3.3	26
1077	Single-cell eQTL mapping identifies cell typeâ€“specific genetic control of autoimmune disease. Science, 2022, 376, eabf3041.	6.0	171
1080	Genome-wide identification of the shared genetic basis of cannabis and cigarette smoking and schizophrenia implicates NCAM1 and neuronal abnormality. Psychiatry Research, 2022, 310, 114453.	1.7	7
1081	Investigating the transparency of reporting in two-sample summary data Mendelian randomization studies using the MR-Base platform. International Journal of Epidemiology, 2022, 51, 1943-1956.	0.9	17
1082	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
1083	Twenty-Five Novel Loci for Carotid Intima-Media Thickness: A Genome-Wide Association Study in >45â€‰000 Individuals and Meta-Analysis of >100â€‰000 Individuals. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 484-501.	1.1	17
1084	Identifying Genetic Biomarkers Predicting Response to Anti-Vascular Endothelial Growth Factor Injections in Diabetic Macular Edema. International Journal of Molecular Sciences, 2022, 23, 4042.	1.8	5
1086	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. Human Molecular Genetics, 2021, , .	1.4	2
1087	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	5.8	31
1088	Association of lipid-lowering drugs with COVID-19 outcomes from a Mendelian randomization study. ELife, 2021, 10, .	2.8	49
1089	Understanding the Function of a Locus Using the Knowledge Available at Single-Nucleotide Polymorphisms. Neurology International, 2021, 11, 255-262.	0.2	2
1091	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance. Alzheimer's and Dementia, 2022, 18, 1797-1811.	0.4	5

#	Article	IF	Citations
1092	Single cell sequencing analysis identifies genetics-modulated ORMDL3+ cholangiocytes having higher metabolic effects on primary biliary cholangitis. Journal of Nanobiotechnology, 2021, 19, 406.	4.2	16
1093	Neuropathologic Correlates of Human Cortical Proteins in Alzheimer Disease and Related Dementias. Neurology, 2022, 98, .	1.5	9
1094	Exploration of Lung Cancer-Related Genetic Factors via Mendelian Randomization Method Based on Genomic and Transcriptomic Summarized Data. Frontiers in Cell and Developmental Biology, 2021, 9, 800756.	1.8	1
1095	Advances in Multi-Omics Approaches for Molecular Breeding of Black Rot Resistance in Brassica oleracea L.. Frontiers in Plant Science, 2021, 12, 742553.	1.7	7
1096	Finding genetically-supported drug targets for Parkinsonâ€™s disease using Mendelian randomization of the druggable genome. Nature Communications, 2021, 12, 7342.	5.8	44
1097	Mendelian Randomization Integrating GWAS, eQTL, and mQTL Data Identified Genes Pleiotropically Associated With Atrial Fibrillation. Frontiers in Cardiovascular Medicine, 2021, 8, 745757.	1.1	2
1098	Stroke Genetics: Discovery, Insight Into Mechanisms, and Clinical Perspectives. Circulation Research, 2022, 130, 1095-1111.	2.0	18
1101	Integrating human brain proteomes with genome-wide association data implicates novel proteins in post-traumatic stress disorder. Molecular Psychiatry, 2022, 27, 3075-3084.	4.1	13
1102	Genome-Wide Association Study Identifies New Risk Loci for Progression of Schistosomiasis Among the Chinese Population. Frontiers in Cellular and Infection Microbiology, 2022, 12, 871545.	1.8	0
1103	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge. Molecular Psychiatry, 2022, 27, 3095-3106.	4.1	4
1171	Association between MAP3K4 gene polymorphisms and the risk of schizophrenia susceptibility in a Northeast Chinese Han population. Metabolic Brain Disease, 2022, 37, 1365.	1.4	1
1172	Combining evidence from Mendelian randomization and colocalization: Review and comparison of approaches. American Journal of Human Genetics, 2022, 109, 767-782.	2.6	101
1173	Powerful and robust inference of complex phenotypes' causal genes with dependent expression quantitative loci by a median-based Mendelian randomization. American Journal of Human Genetics, 2022, 109, 838-856.	2.6	8
1174	Comorbidities in osteoarthritis (ComOA): a combined cross-sectional, caseâ€“control and cohort study using large electronic health records in four European countries. BMJ Open, 2022, 12, e052816.	0.8	6
1175	Integrative analysis of eQTL and GWAS summary statistics reveals transcriptomic alteration in Alzheimer brains. BMC Medical Genomics, 2022, 15, 93.	0.7	2
1176	Stress, Cortisol and NR3C1 in At-Risk Individuals for Psychosis: A Mendelian Randomization Study. Frontiers in Psychiatry, 2020, 11, 680.	1.3	3
1177	DNA Methylation in Noncancerous Liver Tissues as Biomarker for Multicentric Occurrence of Hepatitis C Virusâ€“Related Hepatocellular Carcinoma. , 2022, 1, 555-562.		0
1178	Analytical Considerations of Large-Scale Aptamer-Based Datasets for Translational Applications. Cancers, 2022, 14, 2227.	1.7	3

#	Article	IF	Citations
1182	Comprehensive and integrative analyses identify TYW5 as a schizophrenia risk gene. BMC Medicine, 2022, 20, 169.	2.3	5
1183	GEMmaker: process massive RNA-seq datasets on heterogeneous computational infrastructure. BMC Bioinformatics, 2022, 23, 156.	1.2	2
1185	Analyzing and reconciling colocalization and transcriptome-wide association studies from the perspective of inferential reproducibility. American Journal of Human Genetics, 2022, 109, 825-837.	2.6	17
1186	Transcriptomeâ€wide association study identifies <scp> PSMB9 </scp> as a susceptibility gene for coal workers' pneumoconiosis. Environmental Toxicology, 2022, , .	2.1	1
1187	Shared genetic loci between depression and cardiometabolic traits. PLoS Genetics, 2022, 18, e1010161.	1.5	18
1188	A protocol for recruiting and analyzing the disease-oriented Russian disc degeneration study (RuDDS) biobank for functional omics studies of lumbar disc degeneration. PLoS ONE, 2022, 17, e0267384.	1.1	1
1189	Molecular Quantitative Trait Locus Mapping in Human Complex Diseases. Current Protocols, 2022, 2, e426.	1.3	3
1190	Genetic regulation and variation of expression of miRNA and mRNA transcripts in fetal muscle tissue in the context of sex, dam and variable fetal weight. Biology of Sex Differences, 2022, 13, 24.	1.8	5
1191	Genetic Variations of Vitamin A-Absorption and Storage-Related Genes, and Their Potential Contribution to Vitamin A Deficiency Risks Among Different Ethnic Groups. Frontiers in Nutrition, 2022, 9, 861619.	1.6	6
1192	Genome-Wide Mapping of Plasma IgG N-Glycan Quantitative Trait Loci Identifies a Potentially Causal Association between IgG N-Glycans and Rheumatoid Arthritis. Journal of Immunology, 2022, 208, 2508-2514.	0.4	7
1194	ezQTL: A Web Platform for Interactive Visualization and Colocalization of QTLs and GWAS Loci. Genomics, Proteomics and Bioinformatics, 2022, 20, 541-548.	3.0	17
1195	Novel Insight into the Etiology of Rheumatoid Arthritis Gained by a Cross-Tissue Transcriptome-Wide Association Study. SSRN Electronic Journal, 0, , .	0.4	0
1197	Exploring and mitigating potential bias when genetic instrumental variables are associated with multiple non-exposure traits in Mendelian randomization. European Journal of Epidemiology, 2022, 37, 683-700.	2.5	27
1199	Recent Advances for Drought Stress Tolerance in Maize (Zea mays L.): Present Status and Future Prospects. Frontiers in Plant Science, 2022, 13, .	1.7	24
1201	Integrative analysis of summary data from GWAS and eQTL studies implicates genes differentially expressed in Alzheimerâ€™s disease. BMC Genomics, 2022, 23, .	1.2	6
1202	Genome-wide association analysis and replication in 810,625 individuals with varicose veins. Nature Communications, 2022, 13, .	5.8	8
1205	Screening of Phytochemicals against Osteoporosis: Molecular Docking and Simulation-Based Computational Approaches. International Journal of Pharmaceutical Research and Allied Sciences, 2022, 11, 87-98.	0.1	1
1206	Two-sample Mendelian Randomization Study for Schizophrenia and Cancers. , 2022, , .		0

#	Article	IF	Citations
1208	Genome-wide association studies in non-anxiety individuals identified novel risk loci for depression. European Psychiatry, 2022, 65, .	0.1	1
1209	A Brief Atlas of Insulin. Current Diabetes Reviews, 2022, 19, .	0.6	2
1210	Distributed genetic architecture across the hippocampal formation implies common neuropathology across brain disorders. Nature Communications, 2022, 13, .	5.8	12
1213	Bioinformatic Prioritization and Functional Annotation of GWAS-Based Candidate Genes for Primary Open-Angle Glaucoma. Genes, 2022, 13, 1055.	1.0	12
1215	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nature Genetics, 2022, 54, 950-962.	9.4	71
1216	The HDAC9-associated risk locus promotes coronary artery disease by governing TWIST1. PLoS Genetics, 2022, 18, e1010261.	1.5	2
1217	Prioritizing Suggestive Candidate Genes in Migraine: An Opinion. Frontiers in Neurology, 0, 13, .	1.1	1
1218	Causal Inference of Genetic Variants and Genes in Amyotrophic Lateral Sclerosis. Frontiers in Genetics, 0, 13, .	1.1	4
1219	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .	1.1	1
1220	Pinpointing novel risk loci for Lewy body dementia and the shared genetic etiology with Alzheimerâ€™s disease and Parkinsonâ€™s disease: a large-scale multi-trait association analysis. BMC Medicine, 2022, 20, .	2.3	10
1221	Epigenomic analysis reveals a dynamic and context-specific macrophage enhancer landscape associated with innate immune activation and tolerance. Genome Biology, 2022, 23, .	3.8	9
1222	Non-Steroidal Anti-Inflammatory Drug Target Gene Associations with Major Depressive Disorders: A Mendelian Randomisation Study Integrating GWAS, eQTLand mQTL Data. SSRN Electronic Journal, 0, , .	0.4	0
1223	dbBIP: a comprehensive bipolar disorder database for genetic research. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	3
1224	Systemic inflammatory markers in relation to cognitive function and measures of brain atrophy: a Mendelian randomization study. GeroScience, 2022, 44, 2259-2270.	2.1	21
1225	Investigating the Effect of Estradiol Levels on the Risk of Breast, Endometrial, and Ovarian Cancer. Journal of the Endocrine Society, 2022, 6, .	0.1	10
1226	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots. Nature Communications, 2022, 13, .	5.8	43
1227	Genetic variant rs9848497 up-regulates MST1R expression, thereby influencing leadership phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
1228	Variance-quantitative trait loci enable systematic discovery of gene-environment interactions for cardiometabolic serum biomarkers. Nature Communications, 2022, 13, .	5.8	14

#	Article	IF	Citations
1229	Identification of Putative Causal Relationships Between Type 2 Diabetes and Blood-Based Biomarkers in East Asians by Mendelian Randomization. American Journal of Epidemiology, 2022, 191, 1867-1876.	1.6	5
1231	Large-Scale Multi-Omics Studies Provide New Insights into Blood Pressure Regulation. International Journal of Molecular Sciences, 2022, 23, 7557.	1.8	10
1233	Genome-wide analyses of 200,453 individuals yield new insights into the causes and consequences of clonal hematopoiesis. Nature Genetics, 2022, 54, 1155-1166.	9.4	109
1234	Genome-wide meta-analysis of insomnia prioritizes genes associated with metabolic and psychiatric pathways. Nature Genetics, 2022, 54, 1125-1132.	9.4	61
1235	Exploring Potential Causal Genes for Uterine Leiomyomas: A Summary Data-Based Mendelian Randomization and FUMA Analysis. Frontiers in Genetics, 0, 13, .	1.1	3
1236	Patterns of Convergence and Divergence Between Bipolar Disorder Type I and Type II: Evidence From Integrative Genomic Analyses. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	6
1237	Including diverse and admixed populations in genetic epidemiology research. Genetic Epidemiology, 2022, 46, 347-371.	0.6	11
1238	Genome-Wide Association and Transcriptome-Wide Association Studies Identify Novel Susceptibility Genes Contributing to Colorectal Cancer. Journal of Immunology Research, 2022, 2022, 1-14.	0.9	4
1239	Genetic Elements at the Alpha-Synuclein Locus. Frontiers in Neuroscience, 0, 16, .	1.4	1
1241	The Parkinsonâ€™s disease variant rs356182 regulates neuronal differentiation independently from alpha-synuclein. Human Molecular Genetics, 2023, 32, 1-14.	1.4	4
1242	Identification of RNA modification-associated single-nucleotide polymorphisms in genomic loci for low-density lipoprotein cholesterol concentrations. Pharmacogenomics, 2022, 23, 655-665.	0.6	0
1243	Fine-mapping from summary data with the â€œSum of Single Effectsâ€•model. PLoS Genetics, 2022, 18, e1010299.	1.5	84
1244	Shared mechanisms across the major psychiatric and neurodegenerative diseases. Nature Communications, 2022, 13, .	5.8	48
1246	RNA modification-related variants in genomic loci associated with body mass index. Human Genomics, 2022, 16, .	1.4	3
1247	GWAS meta-analysis of 16 790 patients with Barrettâ€™s oesophagus and oesophageal adenocarcinoma identifies 16 novel genetic risk loci and provides insights into disease aetiology beyond the single marker level. Gut, 2023, 72, 612-623.	6.1	6
1248	Fatty Acid Amide Hydrolase: An Integrative Clinical Perspective. Cannabis and Cannabinoid Research, 2023, 8, 56-76.	1.5	4
1249	High throughput CRISPRi and CRISPRa technologies in 3D genome regulation for neuropsychiatric diseases. Human Molecular Genetics, 0, , .	1.4	1
1250	Genetic identification of tissues and cell types underlying attention-deficit/hyperactivity disorder. Frontiers in Psychiatry, 0, 13, .	1.3	1

#	Article	IF	Citations
1251	Genetic association and Mendelian randomization for hypothyroidism highlight immune molecular mechanisms. IScience, 2022, 25, 104992.	1.9	7
1252	Clinical opportunity awaits at the intersection of genomics and brain imaging. Journal of Psychiatry and Neuroscience, 2022, 47, E293-E298.	1.4	1
1255	Multi-ancestry fine-mapping improves precision to identify causal genes in transcriptome-wide association studies. American Journal of Human Genetics, 2022, 109, 1388-1404.	2.6	18
1256	SUMMER: a Mendelian randomization interactive serverÂto systematically evaluate the causal effects of risk factors and circulating biomarkers on pan-cancer survival. Nucleic Acids Research, 2023, 51, D1160-D1167.	6.5	7
1257	Novel genes/loci validate the small effect size of ERBB2 in patients with myasthenia gravis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
1258	Human Genetic Variants Associated with COVID-19 Severity are Enriched in Immune and Epithelium Regulatory Networks. Phenomics, 2022, 2, 389-403.	0.9	5
1260	Novel functional genomics approaches bridging neuroscience and psychiatry. Biological Psychiatry Global Open Science, 2022, , .	1.0	1
1261	Limited evidence for blood eQTLs in human sexual dimorphism. Genome Medicine, 2022, 14, .	3.6	5
1263	Immunodeficiency, autoimmunity, and increased risk of B cell malignancy in humans with TRAF3 mutations. Science Immunology, 2022, 7, .	5.6	9
1264	Using expression quantitative trait loci data and graph-embedded neural networks to uncover genotypeâ€“phenotype interactions. Frontiers in Genetics, 0, 13, .	1.1	0
1266	Genetic control of RNA splicing and its distinct role in complex trait variation. Nature Genetics, 2022, 54, 1355-1363.	9.4	53
1268	Gene Set Enrichment Analysis Detected Immune Cell-Related Pathways Associated with Primary Sclerosing Cholangitis. BioMed Research International, 2022, 2022, 1-9.	0.9	0
1269	Integrating human brain proteomic data with genome-wide association study findings identifies novel brain proteins in substance use traits. Neuropsychopharmacology, 2022, 47, 2292-2299.	2.8	6
1270	Identification of novel proteins associated with movement-related adverse antipsychotic effects by integrating GWAS data and human brain proteomes. Psychiatry Research, 2022, 317, 114791.	1.7	3
1272	Multi-Omics Analyses Identify Pleiotropy and Causality Between Circulating Sclerostin and Atrial Fibrillation. SSRN Electronic Journal, 0, , .	0.4	0
1273	Genetic evidence for a causal relationship between type 2 diabetes and peripheral artery disease in both Europeans and East Asians. BMC Medicine, 2022, 20, .	2.3	6
1274	Effects of Coronary Artery Diseaseâ€“Associated Variants on Vascular Smooth Muscle Cells. Circulation, 2022, 146, 917-929.	1.6	11
1275	Huntingtonâ€™s disease age at motor onset is modified by the tandem hexamer repeat in TCERG1. Npj Genomic Medicine, 2022, 7, .	1.7	5

#	Article	IF	Citations
1276	Cross-ancestry meta-analysis of opioid use disorder uncovers novel loci with predominant effects in brain regions associated with addiction. Nature Neuroscience, 2022, 25, 1279-1287.	7.1	26
1277	From classical mendelian randomization to causal networks for systematic integration of multi-omics. Frontiers in Genetics, 0, 13, .	1.1	8
1278	Mediation analysis of multiple mediators with incomplete omics data. Genetic Epidemiology, 2023, 47, 61-77.	0.6	0
1279	Genetics and mechanisms of thoracic aortic disease. Nature Reviews Cardiology, 2023, 20, 168-180.	6.1	17
1280	Gene set enrichment analysis of pathophysiological pathways highlights oxidative stress in psychosis. Molecular Psychiatry, 2022, 27, 5135-5143.	4.1	5
1281	Genome-wide association analyses of physical activity and sedentary behavior provide insights into underlying mechanisms and roles in disease prevention. Nature Genetics, 2022, 54, 1332-1344.	9.4	64
1282	Integrating multi-omics summary data using a Mendelian randomization framework. Briefings in Bioinformatics, 0, , .	3.2	2
1285	Mendelian Randomization and GWAS Meta Analysis Revealed the Risk-Increasing Effect of Schizophrenia on Cancers. Biology, 2022, 11, 1345.	1.3	6
1286	Genome-wide Mendelian randomization identifies actionable novel drug targets for psychiatric disorders. Neuropsychopharmacology, 2023, 48, 270-280.	2.8	12
1288	Novel insight into the aetiology of rheumatoid arthritis gained by a cross-tissue transcriptome-wide association study. RMD Open, 2022, 8, e002529.	1.8	2
1289	3D chromatin maps of the human pancreas reveal lineage-specific regulatory architecture of T2D risk. Cell Metabolism, 2022, 34, 1394-1409.e4.	7.2	26
1290	Coronary artery disease risk factors affected by RNA modification-related genetic variants. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	5
1291	Gene mapping methodology powered by induced genome rearrangements. Scientific Reports, 2022, 12, .	1.6	1
1293	Integrating transcriptomics, metabolomics, and GWAS helps reveal molecular mechanisms for metabolite levels and disease risk. American Journal of Human Genetics, 2022, 109, 1727-1741.	2.6	16
1294	A causal association of ANKRD37 with human hippocampal volume. Molecular Psychiatry, 2022, 27, 4432-4445.	4.1	2
1295	Transcriptomeâ€wide summary dataâ€based Mendelian randomization analysis reveals 38 novel genes associated with severe COVIDâ€19. Journal of Medical Virology, 2023, 95, .	2.5	15
1296	Benchmarking post-GWAS analysis tools in major depression: Challenges and implications. Frontiers in Genetics, 0, 13, .	1.1	1
1297	Identify novel, shared and disorder-specific genetic architecture of major depressive disorder, insomnia and chronic pain. Journal of Psychiatric Research, 2022, 155, 511-517.	1.5	5

#	Article	IF	Citations
1299	A transcriptome-wide association study provides new insights into the etiology of osteoarthritis. Annals of Translational Medicine, 2022, 10, 1116-1116.	0.7	3
1302	TWAS Atlas: a curated knowledgebase of transcriptome-wide association studies. Nucleic Acids Research, 2023, 51, D1179-D1187.	6.5	13
1303	Genome-Wide Association Analysis of Over 170,000 Individuals from the UK Biobank Identifies Seven Loci Associated with Dietary Approaches to Stop Hypertension (DASH) Diet. Nutrients, 2022, 14, 4431.	1.7	3
1304	Stem Cell Models for Context-Specific Modeling in Psychiatric Disorders. Biological Psychiatry, 2023, 93, 642-650.	0.7	9
1305	The regulatory landscape of multiple brain regions in outbred heterogeneous stock rats. Nucleic Acids Research, 2022, 50, 10882-10895.	6.5	20
1306	A saturated map of common genetic variants associated with human height. Nature, 2022, 610, 704-712.	13.7	205
1308	Brain Catalog: a comprehensive resource for the genetic landscape of brain-related traits. Nucleic Acids Research, 2023, 51, D835-D844.	6.5	5
1309	Network regression analysis for binary and ordinal categorical phenotypes in transcriptome-wide association studies. Genetics, 0, , .	1.2	1
1310	Using human genetics to improve safety assessment of therapeutics. Nature Reviews Drug Discovery, 2023, 22, 145-162.	21.5	20
1311	Genetic determinants of polygenic prediction accuracy within a population. Genetics, 2022, 222, .	1.2	4
1312	SumStatsRehab: an efficient algorithm for GWAS summary statistics assessment and restoration. BMC Bioinformatics, 2022, 23, .	1.2	2
1313	Expression Quantitative Trait Locus Study of Non-Syndromic Cleft Lip with or without Cleft Palate GWAS Variants in Lip Tissues. Cells, 2022, 11, 3281.	1.8	0
1315	Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. Nature Neuroscience, 2022, 25, 1559-1568.	7.1	19
1316	Genetic regulation of serum IgA levels and susceptibility to common immune, infectious, kidney, and cardio-metabolic traits. Nature Communications, 2022, 13, .	5.8	19
1317	Collective genomic segments with differential pleiotropic patterns between cognitive dimensions and psychopathology. Nature Communications, 2022, 13, .	5.8	3
1319	Toward Best Practices for Imaging Transcriptomics of the Human Brain. Biological Psychiatry, 2023, 93, 391-404.	0.7	23
1320	Novel plasma and brain proteins that are implicated in multiple sclerosis. Brain, 2023, 146, 2464-2475.	3.7	2
1321	Multi-ancestry genome-wide association analyses identify novel genetic mechanisms in rheumatoid arthritis. Nature Genetics, 2022, 54, 1640-1651.	9.4	68

#	Article	IF	Citations
1323	Identification of potentially common loci between childhood obesity and coronary artery disease using pleiotropic approaches. Scientific Reports, 2022, 12, .	1.6	0
1324	Identification of novel <scp>meQTLs</scp> strongly associated with rheumatoid arthritis by largeâ€scale epigenomeâ€wide analysis. FEBS Open Bio, 2022, 12, 2227-2235.	1.0	1
1325	Comprehensive transcriptional variability analysis reveals gene networks regulating seed oil content of Brassica napus. Genome Biology, 2022, 23, .	3.8	6
1326	Integrating transcription factor occupancy with transcriptome-wide association analysis identifies susceptibility genes in human cancers. Nature Communications, 2022, 13, .	5.8	12
1327	Investigating genetic causal relationships between blood pressure and anxiety, depressive symptoms, neuroticism and subjective well-being. Annals of General Psychiatry, 2022, 35, e100877.	1.1	7
1331	Detection of potential functional variants based on systems-biology: the case of feed efficiency in beef cattle. BMC Genomics, 2022, 23, .	1.2	0
1332	Mendelian Randomization Study Using Dopaminergic Neuron-Specific eQTL Identifies Novel Risk Genes for Schizophrenia. Molecular Neurobiology, 2023, 60, 1537-1546.	1.9	2
1333	Pleiotropic architectures of porcine immune and growth trait pairs revealed by a selfâ€productâ€based transcriptome method. Animal Genetics, 0, , .	0.6	0
1334	NetMix2: A Principled Network Propagation Algorithm for Identifying Altered Subnetworks. Journal of Computational Biology, 2022, 29, 1305-1323.	0.8	0
1335	Bidirectional Causality Between Immunoglobulin G N-Glycosylation and Metabolic Traits: A Mendelian Randomization Study. Engineering, 2022, , .	3.2	0
1336	Association of genetically predicted lipid traits and lipid-modifying targets with heart failure. European Journal of Preventive Cardiology, 2023, 30, 358-366.	0.8	8
1337	Deciphering colorectal cancer genetics through multi-omic analysis of 100,204 cases and 154,587 controls of European and east Asian ancestries. Nature Genetics, 2023, 55, 89-99.	9.4	39
1338	Cis-eQTL Analysis and Functional Validation of Candidate Genes for Carcass Yield Traits in Beef Cattle. International Journal of Molecular Sciences, 2022, 23, 15055.	1.8	4
1339	Quantifying the role of transcript levels in mediating DNA methylation effects on complex traits and diseases. Nature Communications, 2022, 13, .	5.8	15
1340	Mendelian randomisation studies of Attention Deficit Hyperactivity Disorder. JCPP Advances, 2022, 2, .	1.4	2
1343	Probabilistic integration of transcriptome-wide association studies and colocalization analysis identifies key molecular pathways of complex traits. American Journal of Human Genetics, 2023, 110, 44-57.	2.6	5
1344	mBAT-combo: A more powerful test to detect gene-trait associations from GWAS data. American Journal of Human Genetics, 2023, 110, 30-43.	2.6	6
1345	Recent Advances in Genetic Epidemiology of Colorectal Cancer in Chinese Population. , 2022, , 187-214.		0

#	Article	IF	Citations
1347	Advances in sequencing technologies for amyotrophic lateral sclerosis research. Molecular Neurodegeneration, 2023, 18, .	4.4	4
1348	New â€œdrugs and targetsâ€•in the GWAS era of bipolar disorder. Bipolar Disorders, 2023, 25, 410-421.	1.1	2
1349	Genetic Regulation of SMC Gene Expression and Splicing Predict Causal CAD Genes. Circulation Research, 2023, 132, 323-338.	2.0	11
1351	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. ELife, 0, 12, .	2.8	2
1352	Support Interval for Two-Sample Summary Data-Based Mendelian Randomization. Genes, 2023, 14, 211.	1.0	1
1355	Mitochondrial related genome-wide Mendelian randomization identifies putatively causal genes for multiple cancer types. EBioMedicine, 2023, 88, 104432.	2.7	6
1357	Associations of Lipids and Lipid-Lowering Drugs with Risk of Vascular Dementia: A Mendelian Randomization Study. Nutrients, 2023, 15, 69.	1.7	4
1358	Shared genetic architecture of hernias: A genome-wide association study with multivariable meta-analysis of multiple hernia phenotypes. PLoS ONE, 2022, 17, e0272261.	1.1	4
1359	Genetic and phenotypic relationships between coronary atherosclerotic heart disease and electrocardiographic traits. , 2022, , .		0
1361	Investigating the potential impact of PCSK9-inhibitors on mood disorders using eQTL-based Mendelian randomization. PLoS ONE, 2022, 17, e0279381.	1.1	3
1362	Exploring genetic mechanisms underlying EEG endophenotypes via summary-data-based Mendelian randomization. , 2022, , .		0
1363	Genome- and Transcriptome-Wide Association Studies Identify Susceptibility Genes and Pathways for Periodontitis. Cells, 2023, 12, 70.	1.8	2
1364	Leveraging pleiotropy to discover and interpret GWAS results for sleep-associated traits. PLoS Genetics, 2022, 18, e1010557.	1.5	4
1365	Association between periodontitis and COVID-19 infection: a two-sample Mendelian randomization study. PeerJ, 0, 11, e14595.	0.9	4
1366	The relationship between caseâ€“control differential gene expression from brain tissue and genetic associations in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2023, 192, 85-92.	1.1	2
1367	Exploring genes for immunoglobulin A nephropathy: a summary data-based mendelian randomization and FUMA analysis. BMC Medical Genomics, 2023, 16, .	0.7	1
1369	A phenome-wide comparative analysis of genetic discordance between obesity and type 2 diabetes. Nature Metabolism, 2023, 5, 237-247.	5.1	18
1370	Estimation and implications of the genetic architecture of fasting and non-fasting blood glucose. Nature Communications, 2023, 14, .	5.8	1

#	Article	IF	Citations
1372	Large scale phenotype imputation and in vivo functional validation implicate ADAMTS14 as an adiposity gene. Nature Communications, 2023, 14, .	5.8	0
1373	Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. Nature Communications, 2023, 14, .	5.8	11
1374	Multi-omics data integration methods and their applications in psychiatric disorders. European Neuropsychopharmacology, 2023, 69, 26-46.	0.3	19
1375	Genetic and clinical analysis of TP73 gene in amyotrophic lateral sclerosis patients from Chinese mainland. Frontiers in Aging Neuroscience, 0, 15, .	1.7	1
1376	Evidence of a causal effect of genetic tendency to gain muscle mass on uterine leiomyomata. Nature Communications, 2023, 14, .	5.8	3
1377	Effect of tissue-grouped regulatory variants associated to type 2 diabetes in related secondary outcomes. Scientific Reports, 2023, 13, .	1.6	2
1379	Insight into the causality between basal metabolic rate and endometrial and ovarian cancers: Analysis utilizing systematic Mendelian randomization and genetic association data from over 331,000 UK biobank participants. European Journal of Clinical Investigation, 2023, 53, .	1.7	5
1380	Widespread allele-specific topological domains in the human genome are not confined to imprinted gene clusters. Genome Biology, 2023, 24, .	3.8	5
1381	Investigating the potential anti-depressive mechanisms of statins: a transcriptomic and Mendelian randomization analysis. Translational Psychiatry, 2023, 13, .	2.4	4
1382	Integration of Mendelian randomisation and systems biology models to identify novel blood-based biomarkers for stroke. Journal of Biomedical Informatics, 2023, 141, 104345.	2.5	3
1383	Loci for insulin processing and secretion provide insight into type 2 diabetes risk. American Journal of Human Genetics, 2023, 110, 284-299.	2.6	9
1384	Causal effects of maternal circulating amino acids on offspring birthweight: a Mendelian randomisation study. EBioMedicine, 2023, 88, 104441.	2.7	6
1385	The shared genetic landscape of blood cell traits and risk of neurological and psychiatric disorders. Cell Genomics, 2023, 3, 100249.	3.0	3
1387	Glucagon-like peptide-1 receptor agonists and diabetic retinopathy: nationwide cohort and Mendelian randomization studies. BMC Medicine, 2023, 21, .	2.3	8
1389	Identification of MKNK1 and TOP3A as ovarian endometriosis risk-associated genes using integrative genomic analyses and functional experiments. Computational and Structural Biotechnology Journal, 2023, 21, 1510-1522.	1.9	6
1390	Perturbed iron biology in the prefrontal cortex of people with schizophrenia. Molecular Psychiatry, 2023, 28, 2058-2070.	4.1	8
1391	Genomic regulatory sequences in the pathogenesis of bipolar disorder. Frontiers in Psychiatry, 0, 14, .	1.3	1
1393	GWAS on retinal vasculometry phenotypes. PLoS Genetics, 2023, 19, e1010583.	1.5	3

#	Article	IF	Citations
1394	Migraine genetics: Status and road forward. Cephalalgia, 2023, 43, 033310242211459.	1.8	8
1395	A cross-tissue transcriptome association study identifies key genes in essential hypertension. Frontiers in Genetics, 0, 14, .	1.1	1
1396	Associations of genetically determined lipid traits and lipid-modifying agents with the risk of diabetic retinopathy: A Mendelian randomization study. Atherosclerosis, 2023, 369, 9-16.	0.4	3
1397	The Joint Link of the rs1051730 and rs1902341 Polymorphisms and Cigarette Smoking to Peripheral Artery Disease and Atherosclerotic Lesions of Different Arterial Beds. Life, 2023, 13, 496.	1.1	0
1401	Exploiting the mediating role of the metabolome to unravel transcript-to-phenotype associations. ELife, 0, 12, .	2.8	10
1402	Rare genetic variants underlie outlying levels of DNA methylation and gene-expression. Human Molecular Genetics, 0, , .	1.4	0
1403	An integrated strategy to identify COVIDâ€19 causal genes and characteristics represented by LRRC37A2. Journal of Medical Virology, 2023, 95, .	2.5	2
1404	Candidate Genes and Gene Networks Change with Age in Japanese Black Cattle by Blood Transcriptome Analysis. Genes, 2023, 14, 504.	1.0	2
1405	Genome-wide genotype-serum proteome mapping provides insights into the cross-ancestry differences in cardiometabolic disease susceptibility. Nature Communications, 2023, 14, .	5.8	6
1406	Genetic Insights of Schizophrenia via Single Cell RNA-Sequencing Analyses. Schizophrenia Bulletin, 2023, 49, 914-922.	2.3	1
1407	Causal Inference in Transcriptome-Wide Association Studies with Invalid Instruments and GWAS Summary Data. Journal of the American Statistical Association, 2023, 118, 1525-1537.	1.8	6
1408	Brain expression quantitative trait locus and network analyses reveal downstream effects and putative drivers for brain-related diseases. Nature Genetics, 2023, 55, 377-388.	9.4	54
1409	Cross-trait analyses identify shared genetics between migraine, headache, and glycemic traits, and a causal relationship with fasting proinsulin. Human Genetics, 2023, 142, 1149-1172.	1.8	3
1410	Network expansion of genetic associations defines a pleiotropy map of human cell biology. Nature Genetics, 2023, 55, 389-398.	9.4	19
1411	Genetic overlap between cortical brain morphometry and frontotemporal dementia risk. Cerebral Cortex, 0, , .	1.6	0
1412	Therapeutic targets for inflammatory bowel disease: proteome-wide Mendelian randomization and colocalization analyses. EBioMedicine, 2023, 89, 104494.	2.7	27
1413	Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus. Nature Human Behaviour, 2023, 7, 790-801.	6.2	6
1414	Using QTL to Identify Genes and Pathways Underlying the Regulation and Production of Milk Components in Cattle. Animals, 2023, 13, 911.	1.0	1

#	Article	IF	Citations
1416	Genome-wide Survival Study Identifies PARL as a Novel Locus for Clinical Progression and Neurodegeneration in Alzheimerâ€™s Disease. Biological Psychiatry, 2023, 94, 732-742.	0.7	1
1417	De novo mutations disturb early brain development more frequently than common variants in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2023, 192, 62-70.	1.1	0
1418	A unifying statistical framework to discover disease genes from GWASs. Cell Genomics, 2023, 3, 100264.	3.0	1
1421	Larger cerebral cortex is genetically correlated with greater frontal area and dorsal thickness. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	0
1422	Genetically predicted levels of folate, vitamin B12, and risk of autoimmune diseases: A Mendelian randomization study. Frontiers in Immunology, 0, 14, .	2.2	3
1424	The genetic basis of endometriosis and comorbidity with other pain and inflammatory conditions. Nature Genetics, 2023, 55, 423-436.	9.4	50
1427	BnIR: A multi-omics database with various tools for Brassica napus research and breeding. Molecular Plant, 2023, 16, 775-789.	3.9	19
1432	Non-steroidal anti-inflammatory drug target gene associations with major depressive disorders: a Mendelian randomisation study integrating GWAS, eQTL and mQTL Data. Pharmacogenomics Journal, 2023, 23, 95-104.	0.9	1
1434	Genome-wide identification of RNA modification-related single nucleotide polymorphisms associated with rheumatoid arthritis. BMC Genomics, 2023, 24, .	1.2	7
1435	Multiâ€omics cannot replace sample size in genomeâ€wide association studies. Genes, Brain and Behavior, 2023, 22, .	1.1	0
1440	OTTERS: a powerful TWAS framework leveraging summary-level reference data. Nature Communications, 2023, 14, .	5.8	7
1441	FHL5 Controls Vascular Diseaseâ€“Associated Gene Programs in Smooth Muscle Cells. Circulation Research, 2023, 132, 1144-1161.	2.0	5
1442	Exploring the genetic and genomic connection underlying neurodegeneration with brain iron accumulation and the risk for Parkinsonâ€™s disease. Npj Parkinson's Disease, 2023, 9, .	2.5	2
1443	Shared genetic loci and causal relations between schizophrenia and obsessive-compulsive disorder. , 2023, 9, .		1
1444	Identification of Genetic Markers Linked to The Activity of Indoleamine 2,3-Dioxygenase and Kidney Function. Metabolites, 2023, 13, 541.	1.3	0
1445	Integrative Post-Genome-Wide Association Study Analyses Relevant to Psychiatric Disorders: Imputing Transcriptome and Proteome Signals. Complex Psychiatry, 2023, 9, 130-144.	1.3	0
1447	The effects of blood pressure and antihypertensive drugs on heart failure: A Mendelian randomization study. Nutrition, Metabolism and Cardiovascular Diseases, 2023, 33, 1420-1428.	1.1	1
1448	A systems biology approach uncovers novel disease mechanisms in age-related macular degeneration. Cell Genomics, 2023, 3, 100302.	3.0	6

#	Article	IF	Citations
1449	Interactions between the lipidome and genetic and environmental factors in autism. Nature Medicine, 2023, 29, 936-949.	15.2	5
1458	Artificial Intelligence and Machine Learning in Drug Discovery. , 2023, , 205-230.		0
1463	Genetic Enhancement of Nutraceuticals in Linseed: Breeding and Molecular Strategies. , 2023, , 1-25.		0
1513	AI in Genomics and Epigenomics. Healthy Ageing and Longevity, 2023, , 217-243.	0.2	0
1540	Transcriptome-wide association studies: recent advances in methods, applications and available databases. Communications Biology, 2023, 6, .	2.0	7
1553	Leveraging molecular quantitative trait loci to comprehend complex diseases/traits from the omics perspective. Human Genetics, 2023, 142, 1543-1560.	1.8	1
1564	Editorial: Statistical methods for genome-wide association studies (GWAS) and transcriptome-wide association studies (TWAS) and their applications. Frontiers in Genetics, 0, 14, .	1.1	0
1620	Transcriptomic analysis reveals associations of blood-based A-to-I editing with Parkinsonâ€™s disease. Journal of Neurology, 2024, 271, 976-985.	1.8	0
1660	Genetic Enhancement of Nutraceuticals in Linseed: Breeding and Molecular Strategies. , 2023, , 519-543.		0
1692	Identification of risk genes and biological pathways influencing myopia via transcriptome association study and biomedical ontology methods. , 2023, , .		0