

Genetic effects on gene expression across human tissue

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Cracking the regulatory code. Nature, 2017, 550, 190-191.	27.8	18
2	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
3	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
4	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics, 2017, 49, 1664-1670.	21.4	179
5	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
6	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
7	Quantifying the regulatory effect size of <i>cis</i> -acting genetic variation using allelic fold change. Genome Research, 2017, 27, 1872-1884.	5.5	114
8	Estimating the causal tissues for complex traits and diseases. Nature Genetics, 2017, 49, 1676-1683.	21.4	166
10	Principles of gene regulation across tissues. Nature Reviews Genetics, 2017, 18, 701-701.	16.3	7
11	Molecular Epidemiology of Heart Failure. JACC Basic To Translational Science, 2017, 2, 757-769.	4.1	25
12	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	46.4	263
13	The importance of cohort studies in the post-GWAS era. Nature Genetics, 2018, 50, 322-328.	21.4	60
14	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. Nature Communications, 2018, 9, 804.	12.8	66
15	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. Nature Communications, 2018, 9, 859.	12.8	126
16	From gene networks to drugs: systems pharmacology approaches for AUD. Psychopharmacology, 2018, 235, 1635-1662.	3.1	15
17	2017 Presidential Address: Checking, Balancing, and Celebrating Diversity: Celebrating Some of the Women Who Paved the Way. American Journal of Human Genetics, 2018, 102, 342-349.	6.2	1
18	Advancing translational research and precision medicine with targeted proteomics. Journal of Proteomics, 2018, 189, 1-10.	2.4	72
19	Rare variants in axonogenesis genes connect three families with soundâ€‘color synesthesia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3168-3173.	7.1	34

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20	Cardiomyocytes have mosaic patterns of protein expression. <i>Cardiovascular Pathology</i> , 2018, 34, 50-57.	1.6	18
21	Single nucleotide variant counts computed from RNA sequencing and cellular traffic into human kidney allografts. <i>American Journal of Transplantation</i> , 2018, 18, 2429-2442.	4.7	11
22	Functional Assays to Screen and Dissect Genomic Hits. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002178.	3.6	18
23	Dissecting the sources of gene expression variation in a pan-cancer analysis identifies novel regulatory mutations. <i>Nucleic Acids Research</i> , 2018, 46, 4370-4381.	14.5	40
24	Widespread Enhancer Activity from Core Promoters. <i>Trends in Biochemical Sciences</i> , 2018, 43, 452-468.	7.5	54
25	Genetic variants in mRNA untranslated regions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1474.	6.4	118
26	High-throughput mouse phenomics for characterizing mammalian gene function. <i>Nature Reviews Genetics</i> , 2018, 19, 357-370.	16.3	78
27	Latexin and hematopoiesis. <i>Current Opinion in Hematology</i> , 2018, 25, 266-272.	2.5	4
28	Selection in the Introgressed Regions of the Chimpanzee Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 1132-1138.	2.5	13
29	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	21.4	143
30	Environmental microbiology: Too much food for thought? “An argument for reductionism. <i>Environmental Microbiology</i> , 2018, 20, 1929-1935.	3.8	2
31	The Extending Spectrum of NPC1-Related Human Disorders: From Niemann-Pick C1 Disease to Obesity. <i>Endocrine Reviews</i> , 2018, 39, 192-220.	20.1	32
32	Patterns of shared signatures of recent positive selection across human populations. <i>Nature Ecology and Evolution</i> , 2018, 2, 713-720.	7.8	63
33	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490.	12.8	198
34	Genetics of endometriosis: State of the art on genetic risk factors for endometriosis. <i>Best Practice and Research in Clinical Obstetrics and Gynaecology</i> , 2018, 50, 61-71.	2.8	30
35	Cloud computing for genomic data analysis and collaboration. <i>Nature Reviews Genetics</i> , 2018, 19, 208-219.	16.3	205
36	Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. <i>Nature Genetics</i> , 2018, 50, 424-431.	21.4	253
37	Reanalysis of clinical whole-exome sequence data yields multiple new diagnoses. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 264-265.	1.2	3

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38	The next generation of melanocyte data: Genetic, epigenetic, and transcriptional resource datasets and analysis tools. <i>Pigment Cell and Melanoma Research</i> , 2018, 31, 442-447.	3.3	3
39	The chromatin basis of neurodevelopmental disorders: Rethinking dysfunction along the molecular and temporal axes. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 84, 306-327.	4.8	73
40	Gene and MicroRNA Perturbations of Cellular Response to Pemetrexed Implicate Biological Networks and Enable Imputation of Response in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2018, 8, 733.	3.3	12
41	Asparagine bioavailability governs metastasis in a model of breast cancer. <i>Nature</i> , 2018, 554, 378-381.	27.8	362
42	The complex genetics of human insulin-like growth factor 2 are not reflected in public databases. <i>Journal of Biological Chemistry</i> , 2018, 293, 4324-4333.	3.4	21
43	Brain Transcriptome Databases: A User's Guide. <i>Journal of Neuroscience</i> , 2018, 38, 2399-2412.	3.6	68
44	GTEx project maps wide range of normal human genetic variation. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 263-264.	1.2	6
46	Bacterial genomics of plant adaptation. <i>Nature Genetics</i> , 2018, 50, 2-4.	21.4	1
47	Mapping regulatory variants in hiPSC models. <i>Nature Genetics</i> , 2018, 50, 1-2.	21.4	33
48	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, 1700148.	2.5	71
49	Genome-wide Analysis of Transcriptional Variability in a Large Maize-Teosinte Population. <i>Molecular Plant</i> , 2018, 11, 443-459.	8.3	87
51	Voltage-gated sodium channels: (Na ^V)igating the field to determine their contribution to visceral nociception. <i>Journal of Physiology</i> , 2018, 596, 785-807.	2.9	36
52	An APOE -independent cis -eSNP on chromosome 19q13.32 influences tau levels and late-onset Alzheimer's disease risk. <i>Neurobiology of Aging</i> , 2018, 66, 178.e1-178.e8.	3.1	12
53	Genetic variants influencing phenotypic variance heterogeneity. <i>Human Molecular Genetics</i> , 2018, 27, 799-810.	2.9	30
54	How to Consider Rare Genetic Variants in Personalized Drug Therapy. <i>Clinical Pharmacology and Therapeutics</i> , 2018, 103, 745-748.	4.7	36
55	FUN-LDA: A Latent Dirichlet Allocation Model for Predicting Tissue-Specific Functional Effects of Noncoding Variation: Methods and Applications. <i>American Journal of Human Genetics</i> , 2018, 102, 920-942.	6.2	75
56	RNAseq analysis of bronchial epithelial cells to identify COPD-associated genes and SNPs. <i>BMC Pulmonary Medicine</i> , 2018, 18, 42.	2.0	20
57	Effects on gene expression and behavior of untagged short tandem repeats: the case of arginine vasopressin receptor 1a (AVPR1a) and externalizing behaviors. <i>Translational Psychiatry</i> , 2018, 8, 72.	4.8	11

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58	Bayesian nonparametric discovery of isoforms and individual specific quantification. Nature Communications, 2018, 9, 1681.	12.8	8
59	Genetics in multiple sclerosis: Updates in the era of big data. Clinical and Experimental Neuroimmunology, 2018, 9, 19-24.	1.0	3
60	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. Genome Research, 2018, 28, 739-750.	5.5	324
61	Effect of hydrochlorothiazide on serum uric acid concentration: a genome-wide association study. Pharmacogenomics, 2018, 19, 517-527.	1.3	0
62	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
63	A genome-wide association study on photic sneeze syndrome in a Japanese population. Journal of Human Genetics, 2018, 63, 765-768.	2.3	3
64	Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family. EBioMedicine, 2018, 28, 168-179.	6.1	12
66	Lysosomal acid lipase and lipid metabolism: new mechanisms, new questions, and new therapies. Current Opinion in Lipidology, 2018, 29, 218-223.	2.7	57
67	Genetic regulation of <i>IL1RL1</i> methylation and IL1RL1-a protein levels in asthma. European Respiratory Journal, 2018, 51, 1701377.	6.7	24
68	A screen for deeply conserved non-coding GWAS SNPs uncovers a <i>MIR-9-2</i> functional mutation associated to retinal vasculature defects in human. Nucleic Acids Research, 2018, 46, 3517-3531.	14.5	33
69	Clinical and biological significance of a <i>rs73AA</i> variation in the CDH1 promoter of patients with sporadic gastric carcinoma. Gastric Cancer, 2018, 21, 606-616.	5.3	4
70	Genetic architecture: the shape of the genetic contribution to human traits and disease. Nature Reviews Genetics, 2018, 19, 110-124.	16.3	335
71	Neurodegeneration: the first mechanistic therapy and other progress in 2017. Lancet Neurology, The, 2018, 17, 3-5.	10.2	7
72	Copy number variation arising from gene conversion on the human Y chromosome. Human Genetics, 2018, 137, 73-83.	3.8	9
73	SNP association study in PMS2-associated Lynch syndrome. Familial Cancer, 2018, 17, 507-515.	1.9	7
74	InDePTH: detection of hub genes for developing gene expression networks under anticancer drug treatment. Oncotarget, 2018, 9, 29097-29111.	1.8	8
75	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. BMC Medical Genomics, 2018, 11, 112.	1.5	8
76	Complementing preclinical safety assessments through genomic analyses. Current Opinion in Toxicology, 2018, 11-12, 59-66.	5.0	0

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77	Expanded Insights Into Mechanisms of Gene Expression and Disease Related Disruptions. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 101.	3.5	13
78	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	1.6	16
79	Shared genetic risk contributes to type 1 and type 2 diabetes etiology. <i>Human Molecular Genetics</i> , 2018, , .	2.9	45
80	Integration of genetics and miRNAâ€target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018, 46, 11898-11909.	14.5	39
81	Polo-Like Kinase 4 (PLK4) Is Overexpressed in Central Nervous System Neuroblastoma (CNS-NB). <i>Bioengineering</i> , 2018, 5, 96.	3.5	20
82	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. <i>Nature Communications</i> , 2018, 9, 4774.	12.8	87
83	Large-scale associations between the leukocyte transcriptome and BOLD responses to speech differ in autism early language outcome subtypes. <i>Nature Neuroscience</i> , 2018, 21, 1680-1688.	14.8	69
84	Genetic variants influence on the placenta regulatory landscape. <i>PLoS Genetics</i> , 2018, 14, e1007785.	3.5	57
85	Germline genetic polymorphisms influence tumor gene expression and immune cell infiltration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11701-E11710.	7.1	108
86	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018, 19, 194.	8.8	126
87	Impact of Genetic Polymorphisms on Human Immune Cell Gene Expression. <i>Cell</i> , 2018, 175, 1701-1715.e16.	28.9	588
88	Systems Genetics Approaches in Rat Identify Novel Genes and Gene Networks Associated With Cardiac Conduction. <i>Journal of the American Heart Association</i> , 2018, 7, e009243.	3.7	18
89	A likelihood approach to testing hypotheses on the co-evolution of epigenome and genome. <i>PLoS Computational Biology</i> , 2018, 14, e1006673.	3.2	4
90	Into the Wild: GWAS Exploration of Non-coding RNAs. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 181.	2.4	94
91	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018, 10, 96.	8.2	49
92	Highâ€resolution mapping of cancer cell networks using coâ€functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	7.2	61
93	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755.	3.5	30
94	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	1.6	87

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95	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	12.6	805
96	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
97	Pathogenic copy number variants that affect gene expression contribute to genomic burden in cerebral palsy. <i>Npj Genomic Medicine</i> , 2018, 3, 33.	3.8	31
98	Bivariate Genome-Wide Association Scan Identifies 6 Novel Loci Associated With Lipid Levels and Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002239.	3.6	26
99	Tissue-Specific Down-Regulation of the Long Non-Coding RNAs PCAT18 and LINC01133 in Gastric Cancer Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3881.	4.1	37
100	Genome wide association analysis in a mouse advanced intercross line. <i>Nature Communications</i> , 2018, 9, 5162.	12.8	47
101	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. <i>Frontiers in Immunology</i> , 2018, 9, 2679.	4.8	4
103	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	12.8	75
104	Computational Methods for the Pharmacogenetic Interpretation of Next Generation Sequencing Data. <i>Frontiers in Pharmacology</i> , 2018, 9, 1437.	3.5	62
105	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	12.8	331
106	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. <i>Brain</i> , 2018, 141, 2895-2907.	7.6	39
107	High-throughput characterization of genetic effects on DNA-protein binding and gene transcription. <i>Genome Research</i> , 2018, 28, 1701-1708.	5.5	34
108	Transcription-driven genome organization: a model for chromosome structure and the regulation of gene expression tested through simulations. <i>Nucleic Acids Research</i> , 2018, 46, 9895-9906.	14.5	92
109	Vimentin Diversity in Health and Disease. <i>Cells</i> , 2018, 7, 147.	4.1	192
110	Evolutionary Divergence of Brain-specific Precursor miRNAs Drives Efficient Processing and Production of Mature miRNAs in Human. <i>Neuroscience</i> , 2018, 392, 141-159.	2.3	4
111	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , 2018, 50, 1514-1523.	21.4	497
112	Renal compartment-specific genetic variation analyses identify new pathways in chronic kidney disease. <i>Nature Medicine</i> , 2018, 24, 1721-1731.	30.7	170
113	A synthesis approach of mouse studies to identify genes and proteins in arterial thrombosis and bleeding. <i>Blood</i> , 2018, 132, e35-e46.	1.4	29

#	ARTICLE	IF	CITATIONS
114	Role of the SLC26A9 Chloride Channel as Disease Modifier and Potential Therapeutic Target in Cystic Fibrosis. <i>Frontiers in Pharmacology</i> , 2018, 9, 1112.	3.5	32
115	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	21.4	97
116	The Molecular and Neuropathological Consequences of Genetic Risk for Alzheimer's Dementia. <i>Frontiers in Neuroscience</i> , 2018, 12, 699.	2.8	47
117	Deconstructing and targeting the genomic architecture of human neurodegeneration. <i>Nature Neuroscience</i> , 2018, 21, 1310-1317.	14.8	42
118	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	3.7	15
119	Genome-wide association studies of brain imaging phenotypes in UK Biobank. <i>Nature</i> , 2018, 562, 210-216.	27.8	551
120	Defining the molecular signatures of Achilles tendinopathy and anterior cruciate ligament ruptures: A whole-exome sequencing approach. <i>PLoS ONE</i> , 2018, 13, e0205860.	2.5	16
121	Identification of a two-SNP PLA2R1 Haplotype and HLA-DRB1 Alleles as Primary Risk Associations in Idiopathic Membranous Nephropathy. <i>Scientific Reports</i> , 2018, 8, 15576.	3.3	8
122	Multiple genotype-phenotype association study reveals intronic variant pair on SIRT2 associated with metabolic syndrome in a Korean population. <i>Human Genomics</i> , 2018, 12, 48.	2.9	14
123	A reference haplotype panel for genome-wide imputation of short tandem repeats. <i>Nature Communications</i> , 2018, 9, 4397.	12.8	57
124	Multiplexed Targeted Resequencing Identifies Coding and Regulatory Variation Underlying Phenotypic Extremes of High-Density Lipoprotein Cholesterol in Humans. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002070.	3.6	5
125	Taking genomics research to the next level: The Genotype-Tissue expression project. <i>Movement Disorders</i> , 2018, 33, 1097-1097.	3.9	2
126	A comparative study of endoderm differentiation in humans and chimpanzees. <i>Genome Biology</i> , 2018, 19, 162.	8.8	32
127	Genetic determinants of childhood and adult height associated with osteosarcoma risk. <i>Cancer</i> , 2018, 124, 3742-3752.	4.1	20
128	Cell-type-specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. <i>Genome Research</i> , 2018, 28, 1621-1635.	5.5	67
129	Distinguishing genetic correlation from causation across 52 diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1728-1734.	21.4	262
130	The genetics of neuropsychiatric disorders. <i>Brain and Neuroscience Advances</i> , 2018, 2, 239821281879927.	3.4	53
131	Deciphering the Emerging Complexities of Molecular Mechanisms at GWAS Loci. <i>American Journal of Human Genetics</i> , 2018, 103, 637-653.	6.2	93

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132	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2018, 9, 4264.	12.8	21
133	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. <i>Blood</i> , 2018, 132, 2040-2052.	1.4	17
134	Exome sequencing study in patients with multiple sclerosis reveals variants associated with disease course. <i>Journal of Neuroinflammation</i> , 2018, 15, 265.	7.2	25
135	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. <i>Nature Neuroscience</i> , 2018, 21, 1482-1492.	14.8	79
136	Epigenome-Wide Analyses Identify Two Novel Associations With Recurrent Stroke in the Vitamin Intervention for Stroke Prevention Clinical Trial. <i>Frontiers in Genetics</i> , 2018, 9, 358.	2.3	12
137	Power, false discovery rate and Winner's Curse in eQTL studies. <i>Nucleic Acids Research</i> , 2018, 46, e133-e133.	14.5	92
138	L1 retrotransposition in the soma: a field jumping ahead. <i>Mobile DNA</i> , 2018, 9, 22.	3.6	63
139	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, 280.	2.3	11
140	Evolutionary and Medical Consequences of Archaic Introgression into Modern Human Genomes. <i>Genes</i> , 2018, 9, 358.	2.4	28
141	Functionally distinct ERAP1 and ERAP2 are a hallmark of HLA-A29-(Birdshot) Uveitis. <i>Human Molecular Genetics</i> , 2018, 27, 4333-4343.	2.9	42
142	Transethnic and race-stratified genome-wide association study of fibroid characteristics in African American and European American women. <i>Fertility and Sterility</i> , 2018, 110, 737-745.e34.	1.0	12
143	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. <i>PLoS Genetics</i> , 2018, 14, e1007650.	3.5	43
144	Reduced monocyte and macrophage TNFSF15/TL1A expression is associated with susceptibility to inflammatory bowel disease. <i>PLoS Genetics</i> , 2018, 14, e1007458.	3.5	30
145	Decoding the non-coding genome: Opportunities and challenges of genomic and epigenomic consortium data. <i>Current Opinion in Systems Biology</i> , 2018, 11, 82-90.	2.6	4
146	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	21.4	55
147	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. <i>Nature Genetics</i> , 2018, 50, 1359-1365.	21.4	93
148	Variable Clinical Manifestations of Xia-Gibbs syndrome: Findings of Consecutively Identified Cases at a Single Children's Hospital. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1890-1896.	1.2	20
149	GWAS with Heterogeneous Data: Estimating the Fraction of Phenotypic Variation Mediated by Gene Expression Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3059-3068.	1.8	28

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150	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	21.4	482
151	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128
152	From genome-wide associations to candidate causal variants by statistical fine-mapping. <i>Nature Reviews Genetics</i> , 2018, 19, 491-504.	16.3	611
153	Rare-Variant Studies to Complement Genome-Wide Association Studies. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 97-112.	6.2	34
154	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> , 2018, 173, 1796-1809.e17.	28.9	165
155	Genetic-Driven Druggable Target Identification and Validation. <i>Trends in Genetics</i> , 2018, 34, 558-570.	6.7	44
156	A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018, 9, 1946.	12.8	33
157	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. <i>Nucleic Acids Research</i> , 2018, 46, W114-W120.	14.5	69
158	Genetics of Resistant Hypertension: the Missing Heritability and Opportunities. <i>Current Hypertension Reports</i> , 2018, 20, 48.	3.5	9
159	Large-Scale Analysis of Genetic and Clinical Patient Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 263-274.	6.5	13
160	Genomic approaches for the elucidation of genes and gene networks underlying cardiovascular traits. <i>Biophysical Reviews</i> , 2018, 10, 1053-1060.	3.2	5
161	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	21.4	389
162	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1041-1047.	21.4	154
163	Immunome differences between porcine ileal and jejunal Peyer's patches revealed by global transcriptome sequencing of gut-associated lymphoid tissues. <i>Scientific Reports</i> , 2018, 8, 9077.	3.3	12
164	Sex-specific genetic predictors of Alzheimer's disease biomarkers. <i>Acta Neuropathologica</i> , 2018, 136, 857-872.	7.7	87
165	A non-coding CRHR2 SNP rs255105, a cis-eQTL for a downstream lincRNA AC005154.6, is associated with heroin addiction. <i>PLoS ONE</i> , 2018, 13, e0199951.	2.5	11
166	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. <i>American Journal of Human Genetics</i> , 2018, 103, 45-57.	6.2	30
167	Transposable elements generate regulatory novelty in a tissue-specific fashion. <i>BMC Genomics</i> , 2018, 19, 468.	2.8	86

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168	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	3.3	49
169	Casein kinase 1 α : biological mechanisms and theranostic potential. Cell Communication and Signaling, 2018, 16, 23.	6.5	78
170	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
171	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 2018, 361, 511-516.	12.6	56
172	Similarity and variation in the insulin-like growth factor 2 - H19 locus in primates. Physiological Genomics, 2018, 50, 425-439.	2.3	7
173	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
174	Genome-wide association study of nocturnal blood pressure dipping in hypertensive patients. BMC Medical Genetics, 2018, 19, 110.	2.1	7
175	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16
176	An eQTL Landscape of Kidney Tissue in Human Nephrotic Syndrome. American Journal of Human Genetics, 2018, 103, 232-244.	6.2	147
177	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. BMC Genomics, 2018, 19, 395.	2.8	42
178	Integrative Bioinformatics Approaches for Identification of Drug Targets in Hypertension. Frontiers in Cardiovascular Medicine, 2018, 5, 25.	2.4	3
179	Using Gene Expression to Annotate Cardiovascular GWAS Loci. Frontiers in Cardiovascular Medicine, 2018, 5, 59.	2.4	13
180	DNA Damage Inducible Transcript 4 Gene: The Switch of the Metabolism as Potential Target in Cancer. Frontiers in Oncology, 2018, 8, 106.	2.8	76
181	Evidence that UBASH3 is a causal gene for type 1 diabetes. European Journal of Human Genetics, 2018, 26, 925-927.	2.8	16
182	Single Nucleotide Polymorphisms (SNPs) Distant from Xenobiotic Response Elements Can Modulate Aryl Hydrocarbon Receptor Function: SNP-Dependent CYP1A1 Induction. Drug Metabolism and Disposition, 2018, 46, 1372-1381.	3.3	11
183	Organic cation transporter 1 (OCT1) modulates multiple cardiometabolic traits through effects on hepatic thiamine content. PLoS Biology, 2018, 16, e2002907.	5.6	45
184	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid- β accumulation in Alzheimer's disease. Human Genetics, 2018, 137, 521-533.	3.8	22
185	Human urine-derived renal epithelial cells provide insights into kidney-specific alternate splicing variants. European Journal of Human Genetics, 2018, 26, 1791-1796.	2.8	22

#	ARTICLE	IF	CITATIONS
186	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , 2018, 50, 1171-1179.	21.4	375
187	Integrated genetic and epigenetic analysis of myxofibrosarcoma. <i>Nature Communications</i> , 2018, 9, 2765.	12.8	54
188	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	2.8	34
189	Normal Breast-Derived Epithelial Cells with Luminal and Intrinsic Subtype-Enriched Gene Expression Document Interindividual Differences in Their Differentiation Cascade. <i>Cancer Research</i> , 2018, 78, 5107-5123.	0.9	42
190	Long-range genomic regulators of <i>THBS1</i> and <i>LTBP4</i> modify disease severity in duchenne muscular dystrophy. <i>Annals of Neurology</i> , 2018, 84, 234-245.	5.3	53
191	Addendum: A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018, 9, 2861.	12.8	16
192	Chromatin 3D “ will it make understanding of cancer transformation finally possible?. <i>Bio-Algorithms and Med-Systems</i> , 2018, 14, .	2.4	0
193	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <i>Human Genomics</i> , 2018, 12, 1.	2.9	35
194	Analysis of circulating angiopoietin-like protein 3 and genetic variants in lipid metabolism and liver health: the DiOGenes study. <i>Genes and Nutrition</i> , 2018, 13, 7.	2.5	15
195	Disruption of a GATA1-binding motif upstream of XG/PBDX abolishes Xga expression and resolves the Xg blood group system. <i>Blood</i> , 2018, 132, 334-338.	1.4	26
196	Nitrite-dependent nitric oxide synthesis by molybdenum enzymes. <i>FEBS Letters</i> , 2018, 592, 2126-2139.	2.8	49
197	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. <i>Nature Genetics</i> , 2018, 50, 1327-1334.	21.4	167
198	Global genetic diversity of human apolipoproteins and effects on cardiovascular disease risk. <i>Journal of Lipid Research</i> , 2018, 59, 1987-2000.	4.2	19
199	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.	3.5	117
200	Genetic Regulatory Mechanisms of Smooth Muscle Cells Map to Coronary Artery Disease Risk Loci. <i>American Journal of Human Genetics</i> , 2018, 103, 377-388.	6.2	76
201	A compendium of conserved cleavage and polyadenylation events in mammalian genes. <i>Genome Research</i> , 2018, 28, 1427-1441.	5.5	81
202	Identification of expression quantitative trait loci associated with schizophrenia and affective disorders in normal brain tissue. <i>PLoS Genetics</i> , 2018, 14, e1007607.	3.5	34
203	Across-Experiment Transcriptomics of Sheep Rumen Identifies Expression of Lipid/Oxo-Acid Metabolism and Muscle Cell Junction Genes Associated With Variation in Methane-Related Phenotypes. <i>Frontiers in Genetics</i> , 2018, 9, 330.	2.3	13

#	ARTICLE	IF	CITATIONS
204	A comprehensive analysis of <i>SNCA</i> -related genetic risk in sporadic parkinson disease. <i>Annals of Neurology</i> , 2018, 84, 117-129.	5.3	50
205	Meta-analysis of genome-wide association studies for height and body mass index in ~ 4700000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	2.9	1,541
206	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018, 5, 80-89.	4.1	19
207	Patterns and mechanisms of structural variations in human cancer. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-11.	7.7	73
208	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018, 9, 3097.	12.8	18
209	Variants at the APOE/C1/C2/C4 Locus Modulate Cholesterol Efflux Capacity Independently of High-Density Lipoprotein Cholesterol. <i>Journal of the American Heart Association</i> , 2018, 7, e009545.	3.7	25
210	Insights Into de novo Mutation Variation in Lithuanian Exome. <i>Frontiers in Genetics</i> , 2018, 9, 315.	2.3	9
211	Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. <i>Behavior Genetics</i> , 2018, 48, 374-385.	2.1	12
212	Prevalence Estimates of Polycystic Kidney and Liver Disease by Population Sequencing. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2593-2600.	6.1	173
213	Genome-wide association studies of multiple sclerosis. <i>Clinical and Translational Immunology</i> , 2018, 7, e1018.	3.8	58
214	Patient Similarity Networks for Precision Medicine. <i>Journal of Molecular Biology</i> , 2018, 430, 2924-2938.	4.2	93
215	Genetic study of multimodal imaging Alzheimer's disease progression score implicates novel loci. <i>Brain</i> , 2018, 141, 2167-2180.	7.6	56
216	Genomic atlas of the human plasma proteome. <i>Nature</i> , 2018, 558, 73-79.	27.8	1,180
217	First Giant Steps Toward a Cell Atlas of Atherosclerosis. <i>Circulation Research</i> , 2018, 122, 1632-1634.	4.5	6
218	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294
219	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	21.4	552
220	Genome-wide association study in Japanese females identifies fifteen novel skin-related trait associations. <i>Scientific Reports</i> , 2018, 8, 8974.	3.3	59
221	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. <i>Nature Communications</i> , 2018, 9, 2427.	12.8	159

#	ARTICLE	IF	CITATIONS
222	Common β -globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	3.5	45
223	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100
224	A Proteomic Variant Approach (ProVarA) for Personalized Medicine of Inherited and Somatic Disease. Journal of Molecular Biology, 2018, 430, 2951-2973.	4.2	32
225	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		0
226	Regulatory variants: from detection to predicting impact. Briefings in Bioinformatics, 2019, 20, 1639-1654.	6.5	82
227	Transcriptomic Databases. , 2019, , 341-351.		1
228	Differential Expression From Microarray and RNA-seq Experiments. , 2019, , 372-387.		0
229	Deciphering the Genetics of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 4-5.	5.6	5
230	Bioinformatic and biological avenues for understanding alcohol use disorder. Alcohol, 2019, 74, 65-71.	1.7	3
231	Statistical tests for detecting variance effects in quantitative trait studies. Bioinformatics, 2019, 35, 200-210.	4.1	28
232	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	21.4	774
233	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	6.2	175
234	Inherited and De Novo Genetic Risk for Autism Impacts Shared Networks. Cell, 2019, 178, 850-866.e26.	28.9	326
235	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. Science, 2019, 365, 786-793.	12.6	155
236	Family-Based Quantitative Trait Meta-Analysis Implicates Rare Noncoding Variants in DENND1A in Polycystic Ovary Syndrome. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 3835-3850.	3.6	51
237	A computational approach to identify blood cell-expressed Parkinson's disease biomarkers that are coordinately expressed in brain tissue. Computers in Biology and Medicine, 2019, 113, 103385.	7.0	23
238	Fast and covariate-adaptive method amplifies detection power in large-scale multiple hypothesis testing. Nature Communications, 2019, 10, 3433.	12.8	18
239	cindr, the Drosophila Homolog of the CD2AP Alzheimer's Disease Risk Gene, Is Required for Synaptic Transmission and Proteostasis. Cell Reports, 2019, 28, 1799-1813.e5.	6.4	27

#	ARTICLE	IF	CITATIONS
241	Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers. <i>American Journal of Human Genetics</i> , 2019, 105, 477-492.	6.2	27
242	Ligand-Free Estrogen Receptor α (ESR1) as Master Regulator for the Expression of CYP3A4 and Other Cytochrome P450 Enzymes in the Human Liver. <i>Molecular Pharmacology</i> , 2019, 96, 430-440.	2.3	26
243	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. <i>Nature Communications</i> , 2019, 10, 3472.	12.8	39
244	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. <i>Nature Biotechnology</i> , 2019, 37, 925-936.	17.5	622
245	Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. <i>Npj Genomic Medicine</i> , 2019, 4, 19.	3.8	163
246	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. <i>Science</i> , 2019, 365, .	12.6	152
247	The genetics of human hematopoiesis and its disruption in disease. <i>EMBO Molecular Medicine</i> , 2019, 11, e10316.	6.9	32
248	Integrative analysis revealed potential causal genetic and epigenetic factors for multiple sclerosis. <i>Journal of Neurology</i> , 2019, 266, 2699-2709.	3.6	34
249	Genetic Association Study of Eight Steroid Hormones and Implications for Sexual Dimorphism of Coronary Artery Disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 5008-5023.	3.6	37
250	Biological characterization of expression quantitative trait loci (eQTLs) showing tissue-specific opposite directional effects. <i>European Journal of Human Genetics</i> , 2019, 27, 1745-1756.	2.8	32
251	Future directions for high-throughput splicing assays in precision medicine. <i>Human Mutation</i> , 2019, 40, 1225-1234.	2.5	12
252	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
253	Using human urine-derived renal epithelial cells to model kidney disease in inherited ciliopathies. <i>Translational Science of Rare Diseases</i> , 2019, 4, 87-95.	1.5	1
254	Weighted elastic net for unsupervised domain adaptation with application to age prediction from DNA methylation data. <i>Bioinformatics</i> , 2019, 35, i154-i163.	4.1	11
255	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	30.7	177
256	Population Difference and Disease Status Affect the Association Between Genetic Variants and Gene Expression. <i>Gastroenterology</i> , 2019, 157, 894-896.	1.3	4
257	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	44
258	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. <i>Nature Communications</i> , 2019, 10, 3300.	12.8	193

#	ARTICLE	IF	CITATIONS
259	Eye in a Disk: eyeIntegratIon Human Pan-Eye and Body Transcriptome Database Version 1.0. , 2019, 60, 3236.		31
260	LOXL3 Function Beyond Amino Oxidase and Role in Pathologies, Including Cancer. International Journal of Molecular Sciences, 2019, 20, 3587.	4.1	20
261	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401.	14.8	145
262	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. Nature Genetics, 2019, 51, 1252-1262.	21.4	139
263	Dynamic genetic regulation of gene expression during cellular differentiation. Science, 2019, 364, 1287-1290.	12.6	142
264	The Effect of Genetic Variation on the Placental Transcriptome in Humans. Frontiers in Genetics, 2019, 10, 550.	2.3	15
265	High-throughput identification of human SNPs affecting regulatory element activity. Nature Genetics, 2019, 51, 1160-1169.	21.4	157
266	Interpreting and integrating big data in the life sciences. Emerging Topics in Life Sciences, 2019, 3, 335-341.	2.6	2
267	The insulin-like growth factor 2 gene in mammals: Organizational complexity within a conserved locus. PLoS ONE, 2019, 14, e0219155.	2.5	16
268	Three-way clustering of multi-tissue multi-individual gene expression data using semi-nonnegative tensor decomposition. Annals of Applied Statistics, 2019, 13, 1103-1127.	1.1	20
269	Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. Lancet Respiratory Medicine, the, 2019, 7, 509-522.	10.7	238
270	TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. American Journal of Human Genetics, 2019, 105, 258-266.	6.2	84
271	DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure. Clinical Epigenetics, 2019, 11, 142.	4.1	46
272	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	28.9	174
273	Genome-wide association study reveals dynamic role of genetic variation in infant and early childhood growth. Nature Communications, 2019, 10, 4448.	12.8	61
274	The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. Nature, 2019, 574, 187-192.	27.8	393
275	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	12.6	99
276	Mendelian randomization indicates that TNF is not causally associated with Alzheimer's disease. Neurobiology of Aging, 2019, 84, 241.e1-241.e3.	3.1	2

#	ARTICLE	IF	CITATIONS
277	Rare mutations in the complement regulatory gene CSMD1 are associated with male and female infertility. <i>Nature Communications</i> , 2019, 10, 4626.	12.8	24
278	Single-step access to a series of A β -conjugated oligomers with 3–10 nm chain lengths. <i>Polymer Chemistry</i> , 2019, 10, 325-330.	3.9	15
279	OncoBase: a platform for decoding regulatory somatic mutations in human cancers. <i>Nucleic Acids Research</i> , 2019, 47, D1044-D1055.	14.5	33
280	Intronic ATTC repeat expansions in STARD7 in familial adult myoclonic epilepsy linked to chromosome 2. <i>Nature Communications</i> , 2019, 10, 4920.	12.8	99
281	Causal Inference Engine: a platform for directional gene set enrichment analysis and inference of active transcriptional regulators. <i>Nucleic Acids Research</i> , 2019, 47, 11563-11573.	14.5	7
282	The Blessings of Multiple Causes. <i>Journal of the American Statistical Association</i> , 2019, 114, 1574-1596.	3.1	92
283	Association of Human iPSC Gene Signatures and X Chromosome Dosage with Two Distinct Cardiac Differentiation Trajectories. <i>Stem Cell Reports</i> , 2019, 13, 924-938.	4.8	44
284	The impact of short tandem repeat variation on gene expression. <i>Nature Genetics</i> , 2019, 51, 1652-1659.	21.4	164
285	TSEA-DB: a trait-tissue association map for human complex traits and diseases. <i>Nucleic Acids Research</i> , 2019, 48, D1022-D1030.	14.5	23
286	CoMM: A Collaborative Mixed Model That Integrates GWAS and eQTL Data Sets to Investigate the Genetic Architecture of Complex Traits. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221988143.	2.0	5
287	Copy number variation is highly correlated with differential gene expression: a pan-cancer study. <i>BMC Medical Genetics</i> , 2019, 20, 175.	2.1	174
288	Three Novel Loci for Infant Head Circumference Identified by a Joint Association Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 947.	2.3	13
289	Integrate GWAS, eQTL, and mQTL Data to Identify Alzheimer's Disease-Related Genes. <i>Frontiers in Genetics</i> , 2019, 10, 1021.	2.3	40
290	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. <i>Human Molecular Genetics</i> , 2019, 28, 4161-4172.	2.9	41
291	CAUSALdb: a database for disease/trait causal variants identified using summary statistics of genome-wide association studies. <i>Nucleic Acids Research</i> , 2019, 48, D807-D816.	14.5	34
292	DESE: estimating driver tissues by selective expression of genes associated with complex diseases or traits. <i>Genome Biology</i> , 2019, 20, 233.	8.8	15
293	Genetic regulation of gene expression and splicing during a 10-year period of human aging. <i>Genome Biology</i> , 2019, 20, 230.	8.8	57
294	Systems genetics applications in metabolism research. <i>Nature Metabolism</i> , 2019, 1, 1038-1050.	11.9	35

#	ARTICLE	IF	CITATIONS
295	Natural human genetic variation determines basal and inducible expression of <i>PM20D1</i> , an obesity-associated gene. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23232-23242.	7.1	35
296	Genetic Association Analyses Highlight <i>IL6</i> , <i>ALPL</i> , and <i>NAV1</i> As 3 New Susceptibility Genes Underlying Calcific Aortic Valve Stenosis. Circulation Genomic and Precision Medicine, 2019, 12, e002617.	3.6	45
297	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222.	8.8	47
298	Application of Computational Biology to Decode Brain Transcriptomes. Genomics, Proteomics and Bioinformatics, 2019, 17, 367-380.	6.9	7
299	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. EBioMedicine, 2019, 48, 203-211.	6.1	14
300	An expanded landscape of human long noncoding RNA. Nucleic Acids Research, 2019, 47, 7842-7856.	14.5	92
301	Die Rolle seltener Varianten bei häufigen Krankheiten. Medizinische Genetik, 2019, 31, 212-221.	0.2	1
302	Functional annotation of the cattle genome through systematic discovery and characterization of chromatin states and butyrate-induced variations. BMC Biology, 2019, 17, 68.	3.8	48
303	Characterization of disease-specific cellular abundance profiles of chronic inflammatory skin conditions from deconvolution of biopsy samples. BMC Medical Genomics, 2019, 12, 121.	1.5	19
304	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
305	Exercise and DNA methylation in skeletal muscle. , 2019, , 211-229.		10
306	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	28.9	144
307	The Length of the Expressed 3' UTR Is an Intermediate Molecular Phenotype Linking Genetic Variants to Complex Diseases. Frontiers in Genetics, 2019, 10, 714.	2.3	23
308	The RNA demethylase FTO is required for maintenance of bone mass and functions to protect osteoblasts from genotoxic damage. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17980-17989.	7.1	65
309	Ultrarare variants drive substantial cis heritability of human gene expression. Nature Genetics, 2019, 51, 1349-1355.	21.4	98
310	WNT5B governs the phenotype of basal-like breast cancer by activating WNT signaling. Cell Communication and Signaling, 2019, 17, 109.	6.5	45
311	Using Transcriptomic Hidden Variables to Infer Context-Specific Genotype Effects in the Brain. American Journal of Human Genetics, 2019, 105, 562-572.	6.2	7
312	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. Genomics, Proteomics and Bioinformatics, 2019, 17, 229-247.	6.9	42

#	ARTICLE	IF	CITATIONS
313	Evaluation of computational genotyping of structural variation for clinical diagnoses. GigaScience, 2019, 8, .	6.4	36
314	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
315	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19398-19408.	7.1	99
316	regBase: whole genome base-wise aggregation and functional prediction for human non-coding regulatory variants. Nucleic Acids Research, 2019, 47, e134-e134.	14.5	41
317	Enhancer variants associated with Alzheimer's disease affect gene expression via chromatin looping. BMC Medical Genomics, 2019, 12, 128.	1.5	51
318	NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis. Translational Psychiatry, 2019, 9, 230.	4.8	18
319	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
320	Evolutionary and functional impact of common polymorphic inversions in the human genome. Nature Communications, 2019, 10, 4222.	12.8	34
321	Hierarchical Classification of Cancers of Unknown Primary Using Multi-Omics Data. Cancer Informatics, 2019, 18, 117693511987216.	1.9	13
322	Mapping human cell phenotypes to genotypes with single-cell genomics. Science, 2019, 365, 1401-1405.	12.6	71
323	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. Current Biology, 2019, 29, 2926-2935.e4.	3.9	40
324	Transcriptome-wide association study of attention deficit hyperactivity disorder identifies associated genes and phenotypes. Nature Communications, 2019, 10, 4450.	12.8	56
325	Toward Robust Functional Neuroimaging Genetics of Cognition. Journal of Neuroscience, 2019, 39, 8778-8787.	3.6	16
326	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	6.2	45
327	Whole genome sequencing to identify predictive markers for the risk of drug-induced interstitial lung disease. PLoS ONE, 2019, 14, e0223371.	2.5	16
328	Genome-wide scan identified genetic variants associated with skin aging in a Chinese female population. Journal of Dermatological Science, 2019, 96, 42-49.	1.9	21
329	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. Nature Ecology and Evolution, 2019, 3, 1598-1606.	7.8	45
330	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	30.7	45

#	ARTICLE	IF	CITATIONS
331	High GILT Expression and an Active and Intact MHC Class II Antigen Presentation Pathway Are Associated with Improved Survival in Melanoma. <i>Journal of Immunology</i> , 2019, 203, 2577-2587.	0.8	21
332	Reply. <i>Gastroenterology</i> , 2019, 157, 896-897.	1.3	0
333	Synergistic effects of common schizophrenia risk variants. <i>Nature Genetics</i> , 2019, 51, 1475-1485.	21.4	184
334	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. <i>Nucleic Acids Research</i> , 2019, 47, 10597-10611.	14.5	39
335	Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects. <i>Nature Communications</i> , 2019, 10, 339.	12.8	163
336	Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. <i>Communications Biology</i> , 2019, 2, 28.	4.4	20
337	Functional SNPs in the Human Autoimmunity-Associated Locus 17q12-21. <i>Genes</i> , 2019, 10, 77.	2.4	11
338	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	16.3	932
339	hiPSCs in cardio-oncology: deciphering the genomics. <i>Cardiovascular Research</i> , 2019, 115, 935-948.	3.8	21
340	Tissue-Specific <i>Trans</i> Regulation of the Mouse Epigenome. <i>Genetics</i> , 2019, 211, 831-845.	2.9	15
341	Tissue-specific epigenetics of atherosclerosis-related <i>ANGPT</i> and <i>ANGPTL</i> genes. <i>Epigenomics</i> , 2019, 11, 169-186.	2.1	30
342	Lessons Learned From GWAS of Asthma. <i>Allergy, Asthma and Immunology Research</i> , 2019, 11, 170.	2.9	77
343	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
344	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019, 10, 409.	12.8	121
345	Integrative Functional Annotation of 52 Genetic Loci Influencing Myocardial Mass Identifies Candidate Regulatory Variants and Target Genes. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002328.	3.6	7
346	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. <i>Genome Medicine</i> , 2019, 11, 6.	8.2	30
347	Repeated Evolution of Asexuality Involves Convergent Gene Expression Changes. <i>Molecular Biology and Evolution</i> , 2019, 36, 350-364.	8.9	26
348	Large-scale analysis of human gene expression variability associates highly variable drug targets with lower drug effectiveness and safety. <i>Bioinformatics</i> , 2019, 35, 3028-3037.	4.1	24

#	ARTICLE	IF	CITATIONS
349	Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330.	12.8	44
350	Innovative strategies for annotating the “relationSNP” between variants and molecular phenotypes. <i>BioData Mining</i> , 2019, 12, 10.	4.0	6
351	A Genetic Locus on Chromosome 2q24 Predicting Peripheral Neuropathy Risk in Type 2 Diabetes: Results From the ACCORD and BARI 2D Studies. <i>Diabetes</i> , 2019, 68, 1649-1662.	0.6	22
352	Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. <i>Communications Biology</i> , 2019, 2, 186.	4.4	20
353	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. <i>Nucleic Acids Research</i> , 2019, 47, W242-W247.	14.5	11
354	Mendelian randomization analysis of celiac GWAS reveals a blood expression signature with diagnostic potential in absence of gluten consumption. <i>Human Molecular Genetics</i> , 2019, 28, 3037-3042.	2.9	7
355	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019, 51, 973-980.	21.4	216
356	Genetic and Epigenetic Fine Mapping of Complex Trait Associated Loci in the Human Liver. <i>American Journal of Human Genetics</i> , 2019, 105, 89-107.	6.2	35
357	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. <i>PLoS ONE</i> , 2019, 14, e0218073.	2.5	61
358	Role of MEIS1 in restless legs syndrome: From GWAS to functional studies in mice. <i>Advances in Pharmacology</i> , 2019, 84, 175-184.	2.0	21
359	Genetic Variation in Human Gene Regulatory Factors Uncovers Regulatory Roles in Local Adaptation and Disease. <i>Genome Biology and Evolution</i> , 2019, 11, 2178-2193.	2.5	17
360	Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. <i>Nature Communications</i> , 2019, 10, 2760.	12.8	22
361	Genomics of disease risk in globally diverse populations. <i>Nature Reviews Genetics</i> , 2019, 20, 520-535.	16.3	217
362	Inferring Interaction Networks From Multi-Omics Data. <i>Frontiers in Genetics</i> , 2019, 10, 535.	2.3	105
363	PhenoScanner V2: an expanded tool for searching human genotype “phenotype associations. <i>Bioinformatics</i> , 2019, 35, 4851-4853.	4.1	1,036
364	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S114-S125.	3.8	16
365	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	2.4	6
366	Comparative Analyses of Chromatin Landscape in White Adipose Tissue Suggest Humans May Have Less Beigeing Potential than Other Primates. <i>Genome Biology and Evolution</i> , 2019, 11, 1997-2008.	2.5	23

#	ARTICLE	IF	CITATIONS
367	Evidence that 6q25.1 variant rs6931104 confers susceptibility to chronic myeloid leukemia through RMND1 regulation. PLoS ONE, 2019, 14, e0218968.	2.5	1
368	Genome-wide association study identifies loci for arterial stiffness index in 127,121 UK Biobank participants. Scientific Reports, 2019, 9, 9143.	3.3	28
369	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. Journal of Bone and Mineral Research, 2019, 34, 1824-1836.	2.8	24
370	Combined genetic and transcriptome analysis of patients with SLE: distinct, targetable signatures for susceptibility and severity. Annals of the Rheumatic Diseases, 2019, 78, 1079-1089.	0.9	109
371	A massively parallel 3' UTR reporter assay reveals relationships between nucleotide content, sequence conservation, and mRNA destabilization. Genome Research, 2019, 29, 896-906.	5.5	34
372	The Translational Landscape of the Human Heart. Cell, 2019, 178, 242-260.e29.	28.9	407
373	Oligogenic inheritance of a human heart disease involving a genetic modifier. Science, 2019, 364, 865-870.	12.6	142
374	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	8.8	105
375	Association between MBL2 haplotypes and dengue severity in children from Rio de Janeiro, Brazil. Memorias Do Instituto Oswaldo Cruz, 2019, 114, e190004.	1.6	11
376	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
377	Mouse Models and Online Resources for Functional Analysis of Osteoporosis Genome-Wide Association Studies. Frontiers in Endocrinology, 2019, 10, 277.	3.5	16
378	A comparison of two workflows for regulome and transcriptome-based prioritization of genetic variants associated with myocardial mass. Genetic Epidemiology, 2019, 43, 717-726.	1.3	1
379	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. Neuron, 2019, 103, 217-234.e4.	8.1	518
380	Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919.	30.7	221
381	A genomic atlas of systemic interindividual epigenetic variation in humans. Genome Biology, 2019, 20, 105.	8.8	70
382	Integrative Analysis Identified IRF6 and NDST1 as Potential Causal Genes for Ischemic Stroke. Frontiers in Neurology, 2019, 10, 517.	2.4	13
383	Learning Causal Biological Networks With the Principle of Mendelian Randomization. Frontiers in Genetics, 2019, 10, 460.	2.3	36
384	BarkBase: Epigenomic Annotation of Canine Genomes. Genes, 2019, 10, 433.	2.4	25

#	ARTICLE	IF	CITATIONS
385	A Differential Host Response to Viral Infection Defines a Subset of Earlier-Onset Diverticulitis Patients. <i>Journal of Gastrointestinal and Liver Diseases</i> , 2019, 27, 249-255.	0.9	5
386	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	12.8	62
387	Risk of spontaneous preterm birth and fetal growth associates with fetal SLIT2. <i>PLoS Genetics</i> , 2019, 15, e1008107.	3.5	38
388	Genome-wide association study of multisite chronic pain in UK Biobank. <i>PLoS Genetics</i> , 2019, 15, e1008164.	3.5	144
389	Detection of circular RNA expression and related quantitative trait loci in the human dorsolateral prefrontal cortex. <i>Genome Biology</i> , 2019, 20, 99.	8.8	57
390	Characterising the genetic basis of immune response variation to identify causal mechanisms underlying disease susceptibility. <i>Hla</i> , 2019, 94, 275-284.	0.6	5
392	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	12.8	82
393	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	27.8	2,149
394	Identification of regulatory variants associated with genetic susceptibility to meningococcal disease. <i>Scientific Reports</i> , 2019, 9, 6966.	3.3	3
395	Genome-wide association study of white-coat effect in hypertensive patients. <i>Blood Pressure</i> , 2019, 28, 239-249.	1.5	6
396	Genetic Insights Into Smooth Muscle Cell Contributions to Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 1006-1017.	2.4	26
397	Progressive optic nerve changes in cavitory optic disc anomaly: integration of copy number alteration and cis-expression quantitative trait loci to assess disease etiology. <i>BMC Medical Genetics</i> , 2019, 20, 63.	2.1	1
398	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. <i>Cancer Research</i> , 2019, 79, 3192-3204.	0.9	43
399	Genome-wide association study identifies loci associated with liability to alcohol and drug dependence that is associated with variability in reward-related ventral striatum activity in African- and European-Americans. <i>Genes, Brain and Behavior</i> , 2019, 18, e12580.	2.2	15
400	epiTAD: a web application for visualizing chromosome conformation capture data in the context of genetic epidemiology. <i>Bioinformatics</i> , 2019, 35, 4462-4464.	4.1	2
401	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
402	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10883-10888.	7.1	114
403	Association of Economic Status and Educational Attainment With Posttraumatic Stress Disorder. <i>JAMA Network Open</i> , 2019, 2, e193447.	5.9	40

#	ARTICLE	IF	CITATIONS
405	Molecular Origins of Complex Heritability in Natural Genotype-to-Phenotype Relationships. <i>Cell Systems</i> , 2019, 8, 363-379.e3.	6.2	26
406	Novel Insight Into the Etiology of Autism Spectrum Disorder Gained by Integrating Expression Data With Genome-wide Association Statistics. <i>Biological Psychiatry</i> , 2019, 86, 265-273.	1.3	65
407	Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. <i>Stem Cell Reports</i> , 2019, 12, 1342-1353.	4.8	32
408	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. <i>Nature Genetics</i> , 2019, 51, 933-940.	21.4	77
409	The Legacy of Sexual Ancestors in Phenotypic Variability, Gene Expression, and Homoeolog Regulation of Asexual Hybrids and Polyploids. <i>Molecular Biology and Evolution</i> , 2019, 36, 1902-1920.	8.9	21
410	UBR5 is a novel E3 ubiquitin ligase involved in skeletal muscle hypertrophy and recovery from atrophy. <i>Journal of Physiology</i> , 2019, 597, 3727-3749.	2.9	53
411	Joint analyses of multi-tissue Hi-C and eQTL data demonstrate close spatial proximity between eQTLs and their target genes. <i>BMC Genetics</i> , 2019, 20, 43.	2.7	20
412	On Using Local Ancestry to Characterize the Genetic Architecture of Human Traits: Genetic Regulation of Gene Expression in Multiethnic or Admixed Populations. <i>American Journal of Human Genetics</i> , 2019, 104, 1097-1115.	6.2	50
413	Correction of IVS I-110(G>A) β -thalassemia by CRISPR/Cas-and TALEN-mediated disruption of aberrant regulatory elements in human hematopoietic stem and progenitor cells. <i>Haematologica</i> , 2019, 104, e497-e501.	3.5	32
414	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. <i>Nature Communications</i> , 2019, 10, 1847.	12.8	55
415	TCF21 and AP-1 interact through epigenetic modifications to regulate coronary artery disease gene expression. <i>Genome Medicine</i> , 2019, 11, 23.	8.2	43
416	Expression estimation and eQTL mapping for HLA genes with a personalized pipeline. <i>PLoS Genetics</i> , 2019, 15, e1008091.	3.5	75
417	Selective vulnerability in α -synucleinopathies. <i>Acta Neuropathologica</i> , 2019, 138, 681-704.	7.7	58
418	Resequencing Study Confirms That Host Defense and Cell Senescence Gene Variants Contribute to the Risk of Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 199-208.	5.6	90
419	Chromatin three-dimensional interactions mediate genetic effects on gene expression. <i>Science</i> , 2019, 364, .	12.6	163
420	Differential methylation of enhancer at IGF2 is associated with abnormal dopamine synthesis in major psychosis. <i>Nature Communications</i> , 2019, 10, 2046.	12.8	55
421	Tissue-specific sex differences in human gene expression. <i>Human Molecular Genetics</i> , 2019, 28, 2976-2986.	2.9	41
422	Mouse genome-wide association and systems genetics identifies Lhfp as a regulator of bone mass. <i>PLoS Genetics</i> , 2019, 15, e1008123.	3.5	22

#	ARTICLE	IF	CITATIONS
423	Trouble With Tribbles-1. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 998-1005.	2.4	14
424	A Convergent Study of Genetic Variants Associated With Crohn's Disease: Evidence From GWAS, Gene Expression, Methylation, eQTL and TWAS. Frontiers in Genetics, 2019, 10, 318.	2.3	19
425	The Role of Tertiary Structure in MicroRNA Target Recognition. Methods in Molecular Biology, 2019, 1970, 43-64.	0.9	9
426	Hemostatic Genes Exhibit a High Degree of Allele-Specific Regulation in Liver. Thrombosis and Haemostasis, 2019, 119, 1072-1083.	3.4	2
427	FunSPU: A versatile and adaptive multiple functional annotation-based association test of whole-genome sequencing data. PLoS Genetics, 2019, 15, e1008081.	3.5	16
428	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.	21.4	89
429	Abundant associations with gene expression complicate GWAS follow-up. Nature Genetics, 2019, 51, 768-769.	21.4	210
430	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. Plant Journal, 2019, 99, 895-909.	5.7	19
431	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	6.2	46
432	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. Cell, 2019, 177, 1022-1034.e6.	28.9	385
433	Data showing atherosclerosis-associated differentially methylated regions are often at enhancers. Data in Brief, 2019, 23, 103812.	1.0	9
434	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
435	Genome-wide analysis revealed sex-specific gene expression in asthmatics. Human Molecular Genetics, 2019, 28, 2600-2614.	2.9	29
436	Transposable Elements Are Important Contributors to Standing Variation in Gene Expression in Capsella Grandiflora. Molecular Biology and Evolution, 2019, 36, 1734-1745.	8.9	34
437	Functional genomics of CDHR3 confirms its role in HRV-C infection and childhood asthma exacerbations. Journal of Allergy and Clinical Immunology, 2019, 144, 962-971.	2.9	63
438	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. Nature Communications, 2019, 10, 1338.	12.8	38
439	Using Whole Genome Sequencing in an African Subphenotype of Myasthenia Gravis to Generate a Pathogenetic Hypothesis. Frontiers in Genetics, 2019, 10, 136.	2.3	12
440	Gene expression variability: the other dimension in transcriptome analysis. Physiological Genomics, 2019, 51, 145-158.	2.3	61

#	ARTICLE	IF	CITATIONS
441	Genome-scale Capture C promoter interactions implicate effector genes at GWAS loci for bone mineral density. <i>Nature Communications</i> , 2019, 10, 1260.	12.8	101
442	An UNC5C Allele Predicts Cognitive Decline and Hippocampal Atrophy in Clinically Normal Older Adults. <i>Journal of Alzheimer's Disease</i> , 2019, 68, 1161-1170.	2.6	5
443	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. <i>Journal of Molecular Biology</i> , 2019, 431, 2477-2484.	4.2	32
444	A genome-wide association analysis identifies 16 novel susceptibility loci for carpal tunnel syndrome. <i>Nature Communications</i> , 2019, 10, 1030.	12.8	57
445	Amelioration of Autoimmune Arthritis in Mice Treated With the DNA Methyltransferase Inhibitor 5-azacytidine. <i>Arthritis and Rheumatology</i> , 2019, 71, 1265-1275.	5.6	22
446	Regulation of Intronic Polyadenylation by PCF11 Impacts mRNA Expression of Long Genes. <i>Cell Reports</i> , 2019, 26, 2766-2778.e6.	6.4	77
447	Maternity Log study: a longitudinal lifelog monitoring and multiomics analysis for the early prediction of complicated pregnancy. <i>BMJ Open</i> , 2019, 9, e025939.	1.9	10
448	Hidden Treasures in Contemporary RNA Sequencing. <i>SpringerBriefs in Computer Science</i> , 2019, , 1-93.	0.2	0
449	Shortage of Cellular ATP as a Cause of Diseases and Strategies to Enhance ATP. <i>Frontiers in Pharmacology</i> , 2019, 10, 98.	3.5	91
450	Interrogating the Genetic Determinants of Tourette's Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. <i>American Journal of Psychiatry</i> , 2019, 176, 217-227.	7.2	242
451	Hidden Treasures in Contemporary RNA Sequencing. <i>SpringerBriefs in Computer Science</i> , 2019, , .	0.2	0
452	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. <i>Cell</i> , 2019, 177, 162-183.	28.9	331
453	Genomic Analysis in the Age of Human Genome Sequencing. <i>Cell</i> , 2019, 177, 70-84.	28.9	205
454	Genome-wide association analysis reveals KCTD12 and miR-383-binding genes in the background of rumination. <i>Translational Psychiatry</i> , 2019, 9, 119.	4.8	18
455	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	12.8	37
456	The long noncoding <i>ROCK1</i> RNA regulates inflammatory gene expression. <i>EMBO Journal</i> , 2019, 38, .	7.8	76
457	Gene regulation and the architecture of complex human traits in the genomics era. <i>Current Opinion in Psychology</i> , 2019, 27, 93-97.	4.9	0
458	AMPK variant, a candidate of novel predictor for chemotherapy in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC and FIRE3. <i>International Journal of Cancer</i> , 2019, 145, 2082-2090.	5.1	4

#	ARTICLE	IF	CITATIONS
459	Regulation of MFGE8 by the intergenic coronary artery disease locus on 15q26.1. <i>Atherosclerosis</i> , 2019, 284, 11-17.	0.8	26
460	Alcohol-responsive genes identified in human iPSC-derived neural cultures. <i>Translational Psychiatry</i> , 2019, 9, 96.	4.8	14
461	GREP: genome for REPositioning drugs. <i>Bioinformatics</i> , 2019, 35, 3821-3823.	4.1	35
462	Discovering heritable modes of MEG spectral power. <i>Human Brain Mapping</i> , 2019, 40, 1391-1402.	3.6	17
463	Integrative Analysis Revealing Human Adipose-Specific Genes and Consolidating Obesity Loci. <i>Scientific Reports</i> , 2019, 9, 3087.	3.3	23
464	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019, 28, 2062-2077.	2.9	40
465	Mapping causal pathways from genetics to neuropsychiatric disorders using genome-wide imaging genetics: Current status and future directions. <i>Psychiatry and Clinical Neurosciences</i> , 2019, 73, 357-369.	1.8	22
466	The responses of lungs and adjacent lymph nodes in responding to <i>Yersinia pestis</i> infection: A transcriptomic study using a non-human primate model. <i>PLoS ONE</i> , 2019, 14, e0209592.	2.5	2
467	Variation in the repulsive guidance molecule family in human populations. <i>Physiological Reports</i> , 2019, 7, e13959.	1.7	3
468	Genetic variations in miR-125 family and the survival of non-small cell lung cancer in Chinese population. <i>Cancer Medicine</i> , 2019, 8, 2636-2645.	2.8	7
469	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. <i>Cell Systems</i> , 2019, 8, 122-135.e7.	6.2	45
470	A Role of Oxytocin Receptor Gene Brain Tissue Expression Quantitative Trait Locus rs237895 in the Intergenerational Transmission of the Effects of Maternal Childhood Maltreatment. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2019, 58, 1207-1216.	0.5	15
471	Genomic and epigenomic mapping of leptin-responsive neuronal populations involved in body weight regulation. <i>Nature Metabolism</i> , 2019, 1, 475-484.	11.9	17
472	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , 2019, 2, 115.	4.4	66
473	Genome-wide Association Study of Maximum Habitual Alcohol Intake in >140,000 U.S. European and African American Veterans Yields Novel Risk Loci. <i>Biological Psychiatry</i> , 2019, 86, 365-376.	1.3	82
474	Identification of trans-eQTLs using mediation analysis with multiple mediators. <i>BMC Bioinformatics</i> , 2019, 20, 126.	2.6	34
475	Gene Expression Networks Across Multiple Tissues Are Associated with Rates of Molecular Evolution in Wild House Mice. <i>Genes</i> , 2019, 10, 225.	2.4	12
476	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.	4.1	120

#	ARTICLE	IF	CITATIONS
477	Probabilistic fine-mapping of transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 675-682.	21.4	275
478	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
479	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. <i>Genome Medicine</i> , 2019, 11, 19.	8.2	33
480	Genetic overlap of chronic obstructive pulmonary disease and cardiovascular disease-related traits: a large-scale genome-wide cross-trait analysis. <i>Respiratory Research</i> , 2019, 20, 64.	3.6	73
481	Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. <i>PLoS Genetics</i> , 2019, 15, e1007973.	3.5	5
482	Imputed gene associations identify replicable <i>trans-acting</i> genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019, 43, 596-608.	1.3	19
483	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
484	A statistical framework for cross-tissue transcriptome-wide association analysis. <i>Nature Genetics</i> , 2019, 51, 568-576.	21.4	262
485	The genomics of major psychiatric disorders in a large pedigree from Northern Sweden. <i>Translational Psychiatry</i> , 2019, 9, 60.	4.8	15
486	Emerging links between pediatric lysosomal storage diseases and adult parkinsonism. <i>Movement Disorders</i> , 2019, 34, 614-624.	3.9	37
487	Pandemrix-induced narcolepsy is associated with genes related to immunity and neuronal survival. <i>EBioMedicine</i> , 2019, 40, 595-604.	6.1	39
488	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. <i>Current Genetic Medicine Reports</i> , 2019, 7, 30-40.	1.9	4
489	ALK rearrangements: Biology, detection and opportunities of therapy in non-small cell lung cancer. <i>Critical Reviews in Oncology/Hematology</i> , 2019, 136, 48-55.	4.4	33
490	Mucosal RNA and protein expression as the next frontier in IBS: abnormal function despite morphologically intact small intestinal mucosa. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, G701-G719.	3.4	7
491	Open Targets Platform: new developments and updates two years on. <i>Nucleic Acids Research</i> , 2019, 47, D1056-D1065.	14.5	364
492	Prediction of causal genes and gene expression analysis of attention-deficit hyperactivity disorder in the different brain region, a comprehensive integrative analysis of ADHD. <i>Behavioural Brain Research</i> , 2019, 364, 183-192.	2.2	18
493	Functional genomics reveal gene regulatory mechanisms underlying schizophrenia risk. <i>Nature Communications</i> , 2019, 10, 670.	12.8	94
494	Genetic Ancestry-dependent Differences in Breast Cancer-induced Field Defects in the Tumor-adjacent Normal Breast. <i>Clinical Cancer Research</i> , 2019, 25, 2848-2859.	7.0	23

#	ARTICLE	IF	CITATIONS
495	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	21.4	201
496	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	21.4	350
497	Shared genetic architecture between metabolic traits and Alzheimer's disease: a large-scale genome-wide cross-trait analysis. <i>Human Genetics</i> , 2019, 138, 271-285.	3.8	52
498	Allele specific chromatin signals, 3D interactions, and motif predictions for immune and B cell related diseases. <i>Scientific Reports</i> , 2019, 9, 2695.	3.3	24
499	Discovery and Functional Annotation of Quantitative Trait Loci Affecting Resistance to Sea Lice in Atlantic Salmon. <i>Frontiers in Genetics</i> , 2019, 10, 56.	2.3	59
500	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. <i>Human Genetics</i> , 2019, 138, 307-326.	3.8	44
501	Expanding the Boundaries of RNA Sequencing as a Diagnostic Tool for Rare Mendelian Disease. <i>American Journal of Human Genetics</i> , 2019, 104, 466-483.	6.2	176
502	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	28.9	345
503	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β , tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	21.4	1,962
504	Integration of GWAS and brain eQTL identifies FLOT1 as a risk gene for major depressive disorder. <i>Neuropsychopharmacology</i> , 2019, 44, 1542-1551.	5.4	37
505	Rejoinder: "Gene hunting with hidden Markov model knockoffs". <i>Biometrika</i> , 2019, 106, 35-45.	2.4	15
506	Genome-wide analysis of genetic predisposition to Alzheimer's disease and related sex disparities. <i>Alzheimer's Research and Therapy</i> , 2019, 11, 5.	6.2	61
507	Genomic annotation of disease-associated variants reveals shared functional contexts. <i>Diabetologia</i> , 2019, 62, 735-743.	6.3	5
508	Adjusting for Principal Components of Molecular Phenotypes Induces Replicating False Positives. <i>Genetics</i> , 2019, 211, 1179-1189.	2.9	17
509	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 421-441.	6.1	27
510	Discussion of "Gene hunting with hidden Markov model knockoffs". <i>Biometrika</i> , 2019, 106, 27-28.	2.4	5
511	Data Mining Approaches for Understanding of Regulation of Expression of the Urea Cycle Genes. , 2019, , .		0
512	Elimination of Reference Mapping Bias Reveals Robust Immune Related Allele-Specific Expression in Crossbred Sheep. <i>Frontiers in Genetics</i> , 2019, 10, 863.	2.3	38

#	ARTICLE	IF	CITATIONS
513	Genetic biomarkers in the VEGF pathway predicting response to anti-VEGF therapy in age-related macular degeneration. <i>BMJ Open Ophthalmology</i> , 2019, 4, e000273.	1.6	10
514	Foundations and new horizons for causal inference. <i>Oberwolfach Reports</i> , 2019, 16, 1499-1571.	0.0	2
515	Interpreting Coronary Artery Disease Risk Through Gene-Environment Interactions in Gene Regulation. <i>Genetics</i> , 2019, 213, 651-663.	2.9	20
516	High-Dimensional Bayesian Network Inference From Systems Genetics Data Using Genetic Node Ordering. <i>Frontiers in Genetics</i> , 2019, 10, 1196.	2.3	14
517	Impact of glycemic traits, type 2 diabetes and metformin use on breast and prostate cancer risk: a Mendelian randomization study. <i>BMJ Open Diabetes Research and Care</i> , 2019, 7, e000872.	2.8	34
519	DNA Sequence Variations Contribute to Variability in Fitness and Trainability. <i>Medicine and Science in Sports and Exercise</i> , 2019, 51, 1781-1785.	0.4	18
520	An automated quality control pipeline for eQTL analysis with RNA-seq data. , 2019, , .		8
521	Retrospective Association Analysis of Longitudinal Binary Traits Identifies Important Loci and Pathways in Cocaine Use. <i>Genetics</i> , 2019, 213, 1225-1236.	2.9	13
522	A network-based approach to identify deregulated pathways and drug effects in metabolic syndrome. <i>Nature Communications</i> , 2019, 10, 5215.	12.8	47
523	DNA Methylation-Governed Gene Expression in Autoimmune Arthritis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5646.	4.1	20
524	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	3.5	83
525	Ranking of non-coding pathogenic variants and putative essential regions of the human genome. <i>Nature Communications</i> , 2019, 10, 5241.	12.8	65
526	DNA variants affecting the expression of numerous genes in trans have diverse mechanisms of action and evolutionary histories. <i>PLoS Genetics</i> , 2019, 15, e1008375.	3.5	34
527	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. <i>Genome Biology</i> , 2019, 20, 235.	8.8	26
528	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019, 10, 5175.	12.8	69
529	Identification of loci of functional relevance to Barrett's esophagus and esophageal adenocarcinoma: Cross-referencing of expression quantitative trait loci data from disease-relevant tissues with genetic association data. <i>PLoS ONE</i> , 2019, 14, e0227072.	2.5	5
530	Profiling of the plasma proteome across different stages of human heart failure. <i>Nature Communications</i> , 2019, 10, 5830.	12.8	53
531	RSAT variation-tools: An accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1415-1428.	4.1	9

#	ARTICLE	IF	CITATIONS
532	De novo variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 4127-4136.	7.9	18
533	Brain age prediction using deep learning uncovers associated sequence variants. <i>Nature Communications</i> , 2019, 10, 5409.	12.8	238
534	No Effect of Genome-Wide Significant Schizophrenia Risk Variation at the <i>DRD2</i> Locus on the Allelic Expression of <i>DRD2</i> in Postmortem Striatum. <i>Molecular Neuropsychiatry</i> , 2019, 5, 212-217.	2.9	4
535	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. <i>BMC Bioinformatics</i> , 2019, 20, 572.	2.6	7
536	Identification of novel common variants associated with chronic pain using conditional false discovery rate analysis with major depressive disorder and assessment of pleiotropic effects of LRFN5. <i>Translational Psychiatry</i> , 2019, 9, 310.	4.8	16
537	Model-based clustering of multi-tissue gene expression data. <i>Bioinformatics</i> , 2020, 36, 1807-1813.	4.1	13
538	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. <i>Npj Genomic Medicine</i> , 2019, 4, 29.	3.8	8
539	Scaling computational genomics to millions of individuals with GPUs. <i>Genome Biology</i> , 2019, 20, 228.	8.8	108
540	Fine-Mapping Array Design for Multi-Ethnic Studies of Multiple Sclerosis. <i>Genes</i> , 2019, 10, 903.	2.4	3
541	I3: A Self-organising Learning Workflow for Intuitive Integrative Interpretation of Complex Genetic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 503-510.	6.9	2
542	PALMD as a novel target for calcific aortic valve stenosis. <i>Current Opinion in Cardiology</i> , 2019, 34, 105-111.	1.8	6
543	The somatic mutation landscape of the human body. <i>Genome Biology</i> , 2019, 20, 298.	8.8	84
544	Brain Banks Spur New Frontiers in Neuropsychiatric Research and Strategies for Analysis and Validation. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 402-414.	6.9	12
545	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. <i>Nature Communications</i> , 2019, 10, 5741.	12.8	110
547	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. <i>Pain</i> , 2019, 160, 2328-2337.	4.2	19
548	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. <i>PLoS Genetics</i> , 2019, 15, e1008481.	3.5	20
549	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. <i>Nature</i> , 2019, 574, 538-542.	27.8	251
550	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. <i>Nature Genetics</i> , 2019, 51, 1506-1517.	21.4	35

#	ARTICLE	IF	CITATIONS
551	The kidney transcriptome, from single cells to whole organs and back. <i>Current Opinion in Nephrology and Hypertension</i> , 2019, 28, 219-226.	2.0	11
552	Three DNA Polymorphisms Previously Identified as Markers for Handgrip Strength Are Associated With Strength in Weightlifters and Muscle Fiber Hypertrophy. <i>Journal of Strength and Conditioning Research</i> , 2019, 33, 2602-2607.	2.1	14
553	Ten years in. <i>Current Opinion in Nephrology and Hypertension</i> , 2019, 28, 375-382.	2.0	1
554	An AGTR1 Variant Worsens Nonalcoholic Fatty Liver Disease and the Metabolic Syndrome. <i>American Journal of Gastroenterology</i> , 2019, 114, 556-559.	0.4	5
555	A Genome-Wide Association Study of Sprint Performance in Elite Youth Football Players. <i>Journal of Strength and Conditioning Research</i> , 2019, 33, 2344-2351.	2.1	47
556	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	28.9	81
557	A multiple coefficient of determination-based method for parsing SNPs that correlate with mRNA expression. <i>Scientific Reports</i> , 2019, 9, 20110.	3.3	0
558	PolyQTL: Bayesian multiple eQTL detection with control for population structure and sample relatedness. <i>Bioinformatics</i> , 2019, 35, 1061-1063.	4.1	6
559	Long intergenic noncoding RNA 299 methylation in peripheral blood is a biomarker for triple-negative breast cancer. <i>Epigenomics</i> , 2019, 11, 81-93.	2.1	32
560	Screening the full leucocyte receptor complex genomic region revealed associations with pemphigus that might be explained by gene regulation. <i>Immunology</i> , 2019, 156, 86-93.	4.4	12
561	Coordinated Tcf7l2 regulation in a mouse model implicates Wnt signaling in fetal alcohol spectrum disorders. <i>Biochemistry and Cell Biology</i> , 2019, 97, 375-379.	2.0	5
562	The role of sex in the genomics of human complex traits. <i>Nature Reviews Genetics</i> , 2019, 20, 173-190.	16.3	203
563	Evidence for Weak Selective Constraint on Human Gene Expression. <i>Genetics</i> , 2019, 211, 757-772.	2.9	48
564	Gene expression models based on transcription factor binding events confer insight into functional cis-regulatory variants. <i>Bioinformatics</i> , 2019, 35, 2610-2617.	4.1	19
565	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. <i>Nature Genetics</i> , 2019, 51, 335-342.	21.4	33
566	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.	6.2	106
567	Quantifying promoter-specific Insulin-like Growth Factor 1 gene expression by interrogating public databases. <i>Physiological Reports</i> , 2019, 7, e13970.	1.7	7
568	Cell Specificity of Human Regulatory Annotations and Their Genetic Effects on Gene Expression. <i>Genetics</i> , 2019, 211, 549-562.	2.9	16

#	ARTICLE	IF	CITATIONS
569	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, 29.	12.8	113
570	Exploring the underlying biology of intrinsic cardiorespiratory fitness through integrative analysis of genomic variants and muscle gene expression profiling. <i>Journal of Applied Physiology</i> , 2019, 126, 1292-1314.	2.5	18
571	High-resolution genetic mapping of putative causal interactions between regions of open chromatin. <i>Nature Genetics</i> , 2019, 51, 128-137.	21.4	80
572	Sphingolipid dysregulation due to lack of functional KDSR impairs proplatelet formation causing thrombocytopenia. <i>Haematologica</i> , 2019, 104, 1036-1045.	3.5	28
573	A Multiplexed Assay for Exon Recognition Reveals that an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Splicing Disruptions. <i>Molecular Cell</i> , 2019, 73, 183-194.e8.	9.7	88
574	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	14.5	699
575	Genome-wide association study of cervical cancer suggests a role for <i>ARRDC3</i> gene in human papillomavirus infection. <i>Human Molecular Genetics</i> , 2019, 28, 341-348.	2.9	33
576	Sex differences in the genetic architecture of obsessive-compulsive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 351-364.	1.7	41
577	A powerful and data-adaptive test for rare-variant-based gene-environment interaction analysis. <i>Statistics in Medicine</i> , 2019, 38, 1230-1244.	1.6	15
578	Dissecting the Genetics of Osteoporosis using Systems Approaches. <i>Trends in Genetics</i> , 2019, 35, 55-67.	6.7	43
579	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. <i>Cell</i> , 2019, 176, 549-563.e23.	28.9	87
580	Most chromatin interactions are not in linkage disequilibrium. <i>Genome Research</i> , 2019, 29, 334-343.	5.5	29
581	Anastrozole Aromatase Inhibitor Plasma Drug Concentration Genome-Wide Association Study: Functional Epistatic Interaction Between <i>SLC38A7</i> and <i>ALPPL2</i> . <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 219-227.	4.7	10
582	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	21.4	1,307
583	Genetic polymorphisms in genes of class switch recombination and multiple myeloma risk and survival: an IMMENSE study. <i>Leukemia and Lymphoma</i> , 2019, 60, 1803-1811.	1.3	11
584	Polyploidy, the Nucleotype, and Novelty: The Impact of Genome Doubling on the Biology of the Cell. <i>International Journal of Plant Sciences</i> , 2019, 180, 1-52.	1.3	222
585	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	2.9	12
586	C57BL/6 substrain differences in inflammatory and neuropathic nociception and genetic mapping of a major quantitative trait locus underlying acute thermal nociception. <i>Molecular Pain</i> , 2019, 15, 174480691882504.	2.1	25

#	ARTICLE	IF	CITATIONS
587	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
588	Systems-Wide Approaches in Induced Pluripotent Stem Cell Models. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2019, 14, 395-419.	22.4	24
589	On the Regulatory Evolution of New Genes Throughout Their Life History. <i>Molecular Biology and Evolution</i> , 2019, 36, 15-27.	8.9	24
590	Association of <i>MCPA</i> promoter polymorphism with susceptibility to nasopharyngeal carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6661-6670.	2.6	7
591	A QTL on chromosome 3q23 influences processing speed in humans. <i>Genes, Brain and Behavior</i> , 2019, 18, e12530.	2.2	1
592	eQTL of <i>KCNK2</i> regionally influences the brain sulcal widening: evidence from 15,597 UK Biobank participants with neuroimaging data. <i>Brain Structure and Function</i> , 2019, 224, 847-857.	2.3	21
593	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019, 29, 120-127.e5.	3.9	86
594	Harnessing genomic information for livestock improvement. <i>Nature Reviews Genetics</i> , 2019, 20, 135-156.	16.3	262
595	Glomerular and tubulointerstitial eQTLs for genomic discovery. <i>Nature Reviews Nephrology</i> , 2019, 15, 3-4.	9.6	0
596	Atherosclerosis-associated differentially methylated regions can reflect the disease phenotype and are often at enhancers. <i>Atherosclerosis</i> , 2019, 280, 183-191.	0.8	29
597	Systems, variation, individuality and plant hormones. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 146, 3-22.	2.9	2
598	Genetics and Genomics of Endometriosis. , 2019, , 399-426.		2
599	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. <i>Bioinformatics</i> , 2019, 35, 1644-1652.	4.1	36
600	<i>Taq1a</i> polymorphism (rs1800497) is associated with obesity-related outcomes and dietary intake in a multi-ethnic sample of children. <i>Pediatric Obesity</i> , 2019, 14, e12470.	2.8	10
601	Genome-wide meta-analysis identifies <i>BARX1</i> and <i>EML4-MTA3</i> as new loci associated with infantile hypertrophic pyloric stenosis. <i>Human Molecular Genetics</i> , 2019, 28, 332-340.	2.9	18
602	Eleven loci with new reproducible genetic associations with allergic disease risk. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 691-699.	2.9	49
603	Genome-wide analysis reveals extensive genetic overlap between schizophrenia, bipolar disorder, and intelligence. <i>Molecular Psychiatry</i> , 2020, 25, 844-853.	7.9	156
604	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83

#	ARTICLE	IF	CITATIONS
605	Mapping Tumor-Specific Expression QTLs in Impure Tumor Samples. <i>Journal of the American Statistical Association</i> , 2020, 115, 79-89.	3.1	3
606	Latexin regulation by HMGB2 is required for hematopoietic stem cell maintenance. <i>Haematologica</i> , 2020, 105, 573-584.	3.5	19
607	Genetics of suicide attempts in individuals with and without mental disorders: a population-based genome-wide association study. <i>Molecular Psychiatry</i> , 2020, 25, 2410-2421.	7.9	124
608	Examination of the shared genetic basis of anorexia nervosa and obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2020, 25, 2036-2046.	7.9	83
609	Genetic testing of various eye disorders. , 2020, , 239-258.		0
610	Understanding the genetics of neuropsychiatric disorders: the potential role of genomic regulatory blocks. <i>Molecular Psychiatry</i> , 2020, 25, 6-18.	7.9	26
611	ReQTL: identifying correlations between expressed SNVs and gene expression using RNA-sequencing data. <i>Bioinformatics</i> , 2020, 36, 1351-1359.	4.1	13
612	QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, D983-D991.	14.5	82
613	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. <i>Human Molecular Genetics</i> , 2020, 29, 70-79.	2.9	17
614	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. <i>Bioinformatics</i> , 2020, 36, 782-788.	4.1	28
615	ncRNA-eQTL: a database to systematically evaluate the effects of SNPs on non-coding RNA expression across cancer types. <i>Nucleic Acids Research</i> , 2020, 48, D956-D963.	14.5	56
616	Identifying causal variants and genes using functional genomics in specialized cell types and contexts. <i>Human Genetics</i> , 2020, 139, 95-102.	3.8	16
617	Schizophrenia research in the era of Team Science and big data. <i>Schizophrenia Research</i> , 2020, 217, 13-16.	2.0	7
618	Stochastic imputation for integrated transcriptome association analysis of a longitudinally measured trait. <i>Statistical Methods in Medical Research</i> , 2020, 29, 1167-1180.	1.5	4
619	Repurposing antihypertensive drugs for the prevention of Alzheimer's disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2020, 49, 1132-1140.	1.9	55
620	The how and why of lncRNA function: An innate immune perspective. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194419.	1.9	196
621	The TMEM106B FTLD-protective variant, rs1990621, is also associated with increased neuronal proportion. <i>Acta Neuropathologica</i> , 2020, 139, 45-61.	7.7	51
622	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. <i>Bioinformatics</i> , 2020, 36, 690-697.	4.1	9

#	ARTICLE	IF	CITATIONS
623	CGIDLA:Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Bioinformatics, 2020, 17, 2148-2154.	3.0	17
624	Exploring lithiumâ€™s transcriptional mechanisms of action in bipolar disorder: a multi-step study. Neuropsychopharmacology, 2020, 45, 947-955.	5.4	24
625	Identification of relevant hub genes for early intervention at gene coexpression modules with altered predicted expression in schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2020, 98, 109815.	4.8	12
626	Kynurenic acid and cancer: facts and controversies. Cellular and Molecular Life Sciences, 2020, 77, 1531-1550.	5.4	65
627	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.	1.3	137
628	Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. Trends in Molecular Medicine, 2020, 26, 232-241.	6.7	31
629	Transcriptomeâ€™wide association study reveals candidate causal genes for lung cancer. International Journal of Cancer, 2020, 146, 1862-1878.	5.1	33
630	Mendelian randomization analysis revealed potential causal factors for systemic lupus erythematosus. Immunology, 2020, 159, 279-288.	4.4	18
631	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	5.6	208
632	Single-Cell RNA Sequencing Reveals Stromal Evolution into LRRC15+ Myofibroblasts as a Determinant of Patient Response to Cancer Immunotherapy. Cancer Discovery, 2020, 10, 232-253.	9.4	466
633	Performance comparison of dimensionality reduction methods on RNA-Seq data from the GTEx project. Genes and Genomics, 2020, 42, 225-234.	1.4	0
634	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
635	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	6.3	59
636	Transcriptomeâ€™wide association analysis offers novel opportunities for clinical translation of genetic discoveries on mental disorders. World Psychiatry, 2020, 19, 113-114.	10.4	4
637	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature Communications, 2020, 11, 185.	12.8	45
638	Shared Genetic Loci Between Body Mass Index and Major Psychiatric Disorders. JAMA Psychiatry, 2020, 77, 503.	11.0	82
639	The Role of the Stress Factor in Mediating the Genetic Predisposition to Stroke of the Background of Hypertensive Disease. Neuroscience and Behavioral Physiology, 2020, 50, 143-148.	0.4	3
640	Comparative and Functional Genomic Resource for Mechanistic Studies of Human Blood Pressureâ€™Associated Single Nucleotide Polymorphisms. Hypertension, 2020, 75, 859-868.	2.7	16

#	ARTICLE	IF	CITATIONS
641	Mechanisms of tissue and cell-type specificity in heritable traits and diseases. Nature Reviews Genetics, 2020, 21, 137-150.	16.3	105
642	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	27.8	441
643	Omics in Neurodegenerative Disease: Hope or Hype?. Trends in Genetics, 2020, 36, 152-159.	6.7	38
644	Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases. PLoS Genetics, 2020, 16, e1008538.	3.5	40
645	ASCOT identifies key regulators of neuronal subtype-specific splicing. Nature Communications, 2020, 11, 137.	12.8	50
646	Expression quantitative trait loci in ABC transporters are associated with survival in 5-FU treated colorectal cancer patients. Mutagenesis, 2020, 35, 273-281.	2.6	2
647	A New Liver Expression Quantitative Trait Locus Map From 1,183 Individuals Provides Evidence for Novel Expression Quantitative Trait Loci of Drug Response, Metabolic, and Sex-Biased Phenotypes. Clinical Pharmacology and Therapeutics, 2020, 107, 1383-1393.	4.7	20
648	Multiple testing approaches for hypotheses in integrative genomics. Wiley Interdisciplinary Reviews: Computational Statistics, 2020, 12, e1493.	3.9	0
649	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. Lancet Rheumatology, The, 2020, 2, e50-e62.	3.9	17
650	Epilepsy and developmental disorders: Next generation sequencing in the clinic. European Journal of Paediatric Neurology, 2020, 24, 15-23.	1.6	98
651	A Comprehensive Sequencing-Based Analysis of Allelic Methylation Patterns in Hemostatic Genes in Human Liver. Thrombosis and Haemostasis, 2020, 120, 229-242.	3.4	2
652	Organic Cation Transporters in Health and Disease. Pharmacological Reviews, 2020, 72, 253-319.	16.0	180
653	eQTL Analysis. Methods in Molecular Biology, 2020, , .	0.9	4
654	Geneticsâ€™ Piece of the PI: Inferring the Origin of Complex Traits and Diseases from Proteome-Wide Protein-Protein Interaction Dynamics. BioEssays, 2020, 42, 1900169.	2.5	0
655	Longitudinal DNA methylation changes at MET may alter HGF/c-MET signalling in adolescents at risk for depression. Epigenetics, 2020, 15, 646-663.	2.7	12
656	Quantile regression for challenging cases of eQTL mapping. Briefings in Bioinformatics, 2020, 21, 1756-1765.	6.5	3
657	A Robust Method Uncovers Significant Context-Specific Heritability in Diverse Complex Traits. American Journal of Human Genetics, 2020, 106, 71-91.	6.2	54
658	VarGen: an R package for disease-associated variant discovery and annotation. Bioinformatics, 2020, 36, 2626-2627.	4.1	0

#	ARTICLE	IF	CITATIONS
659	A powerful fine-mapping method for transcriptome-wide association studies. <i>Human Genetics</i> , 2020, 139, 199-213.	3.8	32
660	Design and synthesis of novel spirooxindole-indenoquinoxaline derivatives as novel tryptophanyl-tRNA synthetase inhibitors. <i>Molecular Diversity</i> , 2020, 24, 1043-1063.	3.9	13
661	Overcoming challenges and dogmas to understand the functions of pseudogenes. <i>Nature Reviews Genetics</i> , 2020, 21, 191-201.	16.3	151
662	Overlapping genetic architecture between Parkinson disease and melanoma. <i>Acta Neuropathologica</i> , 2020, 139, 347-364.	7.7	23
663	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. <i>European Journal of Human Genetics</i> , 2020, 28, 253-263.	2.8	29
664	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020, 126, 350-360.	4.5	41
665	Deep learning of pharmacogenomics resources: moving towards precision oncology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2066-2083.	6.5	43
666	PBX-WNT-PCP6-RF6 pathway in nonsyndromic cleft lip and palate. <i>Birth Defects Research</i> , 2020, 112, 234-244.	1.5	18
667	Explaining Gene Expression Using Twenty-One MicroRNAs. <i>Journal of Computational Biology</i> , 2020, 27, 1157-1170.	1.6	5
668	Striated muscle-specific serine/threonine-protein kinase beta segregates with high versus low responsiveness to endurance exercise training. <i>Physiological Genomics</i> , 2020, 52, 35-46.	2.3	17
669	Identification and functional validation of genetic variants in potential miRNA target sites of established BMI genes. <i>International Journal of Obesity</i> , 2020, 44, 1191-1195.	3.4	5
670	An integrative approach for fine-mapping chromatin interactions. <i>Bioinformatics</i> , 2020, 36, 1704-1711.	4.1	5
671	Genetic Susceptibility to Hepatic Sinusoidal Obstruction Syndrome in Pediatric Patients Undergoing Hematopoietic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, 920-927.	2.0	11
672	Comparison with randomized controlled trials as a strategy for evaluating instruments in Mendelian randomization. <i>International Journal of Epidemiology</i> , 2020, 49, 1404-1406.	1.9	18
673	Operating characteristics of the rank-based inverse normal transformation for quantitative trait analysis in genome-wide association studies. <i>Biometrics</i> , 2020, 76, 1262-1272.	1.4	120
674	Evaluation of polymorphisms in microRNA-binding sites and pancreatic cancer risk in Chinese population. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 2252-2259.	3.6	6
675	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. <i>Nature Communications</i> , 2020, 11, 45.	12.8	69
676	Landscape of DNA binding signatures of myocyte enhancer factor-2B reveals a unique interplay of base and shape readout. <i>Nucleic Acids Research</i> , 2020, 48, 8529-8544.	14.5	17

#	ARTICLE	IF	CITATIONS
677	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. <i>Nucleic Acids Research</i> , 2020, 48, e109-e109.	14.5	15
678	Identification and analysis of RNA structural disruptions induced by single nucleotide variants using Riprap and RiboSNitchDB. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa057.	3.2	10
679	Single-Cell Transcriptome Analysis Reveals Dynamic Cell Populations and Differential Gene Expression Patterns in Control and Aneurysmal Human Aortic Tissue. <i>Circulation</i> , 2020, 142, 1374-1388.	1.6	145
680	Genetically-regulated transcriptomics & copy number variation of proctitis points to altered mitochondrial and DNA repair mechanisms in individuals of European ancestry. <i>BMC Cancer</i> , 2020, 20, 954.	2.6	7
681	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , 2020, 7, 326.	5.3	40
682	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	11.9	327
683	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020, 44, 854-867.	1.3	28
684	Bayesian Genome-wide TWAS Method to Leverage both cis- and trans-eQTL Information through Summary Statistics. <i>American Journal of Human Genetics</i> , 2020, 107, 714-726.	6.2	53
685	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. <i>Cell Systems</i> , 2020, 11, 215-228.e5.	6.2	52
686	Transcriptomics and solid tumors: The next frontier in precision cancer medicine. <i>Seminars in Cancer Biology</i> , 2022, 84, 50-59.	9.6	36
687	Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. <i>Genome Research</i> , 2020, 30, 1379-1392.	5.5	35
688	A Single-Cell RNA Expression Map of Human Coronavirus Entry Factors. <i>Cell Reports</i> , 2020, 32, 108175.	6.4	215
689	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. <i>PLoS Genetics</i> , 2020, 16, e1009025.	3.5	42
690	Identification of a Core Module for Bone Mineral Density through the Integration of a Co-expression Network and GWAS Data. <i>Cell Reports</i> , 2020, 32, 108145.	6.4	21
691	Understand variability of COVID-19 through population and tissue variations in expression of SARS-CoV-2 host genes. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100443.	3.4	24
692	Wnt-regulated lncRNA discovery enhanced by in vivo identification and CRISPRi functional validation. <i>Genome Medicine</i> , 2020, 12, 89.	8.2	12
693	Varmole: a biologically drop-connect deep neural network model for prioritizing disease risk variants and genes. <i>Bioinformatics</i> , 2021, 37, 1772-1775.	4.1	12
694	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. <i>Cell Reports</i> , 2020, 32, 108029.	6.4	28

#	ARTICLE	IF	CITATIONS
695	An era of single-cell genomics consortia. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1409-1418.	7.7	12
696	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. <i>Nature Communications</i> , 2020, 11, 5139.	12.8	131
697	Data integration for inferring context-specific gene regulatory networks. <i>Current Opinion in Systems Biology</i> , 2020, 23, 38-46.	2.6	6
698	Prostaglandin E2-EP4 Axis Promotes Lipolysis and Fibrosis in Adipose Tissue Leading to Ectopic Fat Deposition and Insulin Resistance. <i>Cell Reports</i> , 2020, 33, 108265.	6.4	30
699	The support of genetic evidence for cardiovascular risk induced by antineoplastic drugs. <i>Science Advances</i> , 2020, 6, .	10.3	7
700	Systems biology and bioinformatics approach to identify gene signatures, pathways and therapeutic targets of Alzheimer's disease. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100439.	3.4	5
701	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
702	A survey of genetic variants in SARS-CoV-2 interacting domains of ACE2, TMPRSS2 and TLR3/7/8 across populations. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104507.	2.3	31
703	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <i>Nature Communications</i> , 2020, 11, 4930.	12.8	20
704	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <i>Nature Genetics</i> , 2020, 52, 1169-1177.	21.4	206
705	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. <i>Nature Genetics</i> , 2020, 52, 1239-1246.	21.4	134
706	Combinatorial and statistical prediction of gene expression from haplotype sequence. <i>Bioinformatics</i> , 2020, 36, i194-i202.	4.1	2
707	Cross-species regulatory sequence activity prediction. <i>PLoS Computational Biology</i> , 2020, 16, e1008050.	3.2	116
708	LncRNA PCAT18/miR-301a/TP53INP1 axis is involved in gastric cancer cell viability, migration and invasion. <i>Journal of Biochemistry</i> , 2020, 168, 547-555.	1.7	6
709	Genomic mechanisms in Alzheimer's disease. <i>Brain Pathology</i> , 2020, 30, 966-977.	4.1	29
710	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. <i>New Phytologist</i> , 2020, 226, 1738-1752.	7.3	74
711	A Simple New Approach to Variable Selection in Regression, with Application to Genetic Fine Mapping. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2020, 82, 1273-1300.	2.2	431
712	Multi-omics Data Integration for Identifying Osteoporosis Biomarkers and Their Biological Interaction and Causal Mechanisms. <i>IScience</i> , 2020, 23, 100847.	4.1	48

#	ARTICLE	IF	CITATIONS
713	Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. Nature Communications, 2020, 11, 3570.	12.8	84
714	Translating GWAS-identified loci for cardiac rhythm and rate using an in vivo image- and CRISPR/Cas9-based approach. Scientific Reports, 2020, 10, 11831.	3.3	12
715	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. Haematologica, 2021, 106, 2233-2241.	3.5	4
716	Genomic databases. , 2020, , 47-62.		2
717	Functional Specialization of Human Salivary Glands and Origins of Proteins Intrinsic to Human Saliva. Cell Reports, 2020, 33, 108402.	6.4	54
718	Methods for correcting inference based on outcomes predicted by machine learning. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30266-30275.	7.1	28
719	<p>Identification of Genetic Variants for Female Obesity and Evaluation of the Causal Role of Genetically Defined Obesity in Polycystic Ovarian Syndrome</p>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2020, Volume 13, 4311-4322.	2.4	7
720	Multiple-Tissue Integrative Transcriptome-Wide Association Studies Discovered New Genes Associated With Amyotrophic Lateral Sclerosis. Frontiers in Genetics, 2020, 11, 587243.	2.3	15
721	Characterization of the dual functional effects of heat shock proteins (HSPs) in cancer hallmarks to aid development of HSP inhibitors. Genome Medicine, 2020, 12, 101.	8.2	31
722	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	12.8	52
723	Natural variation of the cardiac transcriptome in humans. RNA Biology, 2020, 18, 1-8.	3.1	1
724	Exploring Additional Valuable Information From Single-Cell RNA-Seq Data. Frontiers in Cell and Developmental Biology, 2020, 8, 593007.	3.7	12
725	Genomic and transcriptomic alterations associated with drug vulnerabilities and prognosis in adenocarcinoma at the gastroesophageal junction. Nature Communications, 2020, 11, 6091.	12.8	21
726	Robust inference of positive selection on regulatory sequences in the human brain. Science Advances, 2020, 6, .	10.3	20
727	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. Science Advances, 2020, 6, .	10.3	31
728	WWOX Loss of Function in Neurodevelopmental and Neurodegenerative Disorders. International Journal of Molecular Sciences, 2020, 21, 8922.	4.1	30
729	An Imperative Need for Further Genetic Studies of Alopecia Areata. Journal of Investigative Dermatology Symposium Proceedings, 2020, 20, S22-S27.	0.8	8
730	Rare genetic variants in the gene encoding histone lysine demethylase 4C (KDM4C) and their contributions to susceptibility to schizophrenia and autism spectrum disorder. Translational Psychiatry, 2020, 10, 421.	4.8	11

#	ARTICLE	IF	CITATIONS
731	The Intersection between COVID-19, the Gene Family of ACE2 and Alzheimerâ€™s Disease. Neuroscience Insights, 2020, 15, 263310552097574.	1.6	8
732	A comparative genomics multitool for scientific discovery and conservation. Nature, 2020, 587, 240-245.	27.8	216
733	The Effect of Liraglutide on Î²-Blockade for Preventing Variceal Bleeding: A Case Series. Annals of Internal Medicine, 2020, 173, 404-405.	3.9	13
734	rs34331204 regulates <i>TSPAN13</i> expression and contributes to Alzheimerâ€™s disease with sex differences. Brain, 2020, 143, e95-e95.	7.6	48
735	Connective Tissue Growth Factor: From Molecular Understandings to Drug Discovery. Frontiers in Cell and Developmental Biology, 2020, 8, 593269.	3.7	75
736	The top 100 most-cited articles citing human brain banking from 1970 to 2020: a bibliometric analysis. Cell and Tissue Banking, 2020, 21, 685-697.	1.1	7
737	Genetic variability in the expression of the SARS-CoV-2 host cell entry factors across populations. Genes and Immunity, 2020, 21, 269-272.	4.1	40
738	Mendelian, non-Mendelian, multigenic inheritance, and epigenetics. , 2020, , 3-25.		0
739	Epigenomic and Transcriptomic Dynamics During Human Heart Organogenesis. Circulation Research, 2020, 127, e184-e209.	4.5	27
740	Complete Topological Mapping of a Cellular Protein Interactome Reveals Bow-Tie Motifs as Ubiquitous Connectors of Protein Complexes. Cell Reports, 2020, 31, 107763.	6.4	4
741	An enhanced machine learning tool for cis â€œQTL mapping with regularization and confounder adjustments. Genetic Epidemiology, 2020, 44, 798-810.	1.3	0
742	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. Blood, 2020, 136, 1956-1967.	1.4	34
743	Systemic lipid dysregulation is a risk factor for macular neurodegenerative disease. Scientific Reports, 2020, 10, 12165.	3.3	24
744	Independent evolution of transcript abundance and gene regulatory dynamics. Genome Research, 2020, 30, 1000-1011.	5.5	8
745	Integrative Genomic Analysis Predicts Regulatory Role of N6-Methyladenosine-Associated SNPs for Adiposity. Frontiers in Cell and Developmental Biology, 2020, 8, 551.	3.7	6
746	Polymorphic mobile element insertions contribute to gene expression and alternative splicing in human tissues. Genome Biology, 2020, 21, 185.	8.8	20
747	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. Nature Communications, 2020, 11, 3761.	12.8	22
748	Genome-Wide Association Analysis Identified ANXA1 Associated with Shoulder Impingement Syndrome in UK Biobank Samples. G3: Genes, Genomes, Genetics, 2020, 10, 3279-3284.	1.8	5

#	ARTICLE	IF	CITATIONS
749	Integrative Analysis Revealing Human Heart-Specific Genes and Consolidating Heart-Related Phenotypes. <i>Frontiers in Genetics</i> , 2020, 11, 777.	2.3	6
750	RADAR: annotation and prioritization of variants in the post-transcriptional regulome of RNA-binding proteins. <i>Genome Biology</i> , 2020, 21, 151.	8.8	9
751	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	6.4	44
752	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	5.5	32
753	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. <i>Translational Psychiatry</i> , 2020, 10, 265.	4.8	56
754	Large-scale comparative evaluation of user-friendly tools for predicting variant-induced alterations of splicing regulatory elements. <i>Human Mutation</i> , 2020, 41, 1811-1829.	2.5	29
755	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. <i>Stem Cell Reports</i> , 2020, 15, 214-225.	4.8	18
756	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. <i>Nature Medicine</i> , 2020, 26, 1609-1615.	30.7	255
757	Neanderthal introgression reintroduced functional ancestral alleles lost in Eurasian populations. <i>Nature Ecology and Evolution</i> , 2020, 4, 1332-1341.	7.8	33
758	Genome-wide pQTL analysis of protein expression regulatory networks in the human liver. <i>BMC Biology</i> , 2020, 18, 97.	3.8	49
759	Promoter CpG Density Predicts Downstream Gene Loss-of-Function Intolerance. <i>American Journal of Human Genetics</i> , 2020, 107, 487-498.	6.2	12
760	Using functional genomics to advance the understanding of psoriatic arthritis. <i>Rheumatology</i> , 2020, 59, 3137-3146.	1.9	8
761	Genome-wide association analysis of pulse wave velocity traits provide new insights into the causal relationship between arterial stiffness and blood pressure. <i>PLoS ONE</i> , 2020, 15, e0237237.	2.5	18
762	A meta-analysis and <i>in silico</i> analysis of polymorphic variants conferring breast cancer risk in the Indian subcontinent. <i>Future Oncology</i> , 2020, 16, 2121-2142.	2.4	5
763	Patient derived stem cells for discovery and validation of novel pathogenic variants in inherited retinal disease. <i>Progress in Retinal and Eye Research</i> , 2021, 83, 100918.	15.5	16
764	The Y Chromosome: A Complex Locus for Genetic Analyses of Complex Human Traits. <i>Genes</i> , 2020, 11, 1273.	2.4	12
765	Genome-wide association study of self-reported walking pace suggests beneficial effects of brisk walking on health and survival. <i>Communications Biology</i> , 2020, 3, 634.	4.4	21
766	Polymorphic Genetic Markers of the GABA Catabolism Pathway in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 301-311.	2.6	5

#	ARTICLE	IF	CITATIONS
767	Prediction of genome-wide effects of single nucleotide variants on transcription factor binding. <i>Scientific Reports</i> , 2020, 10, 17632.	3.3	11
768	rs1769793 variant reduces EGN1 expression in skeletal muscle and hippocampus and contributes to high aerobic capacity in hypoxia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29283-29285.	7.1	3
769	Genome-wide association studies of antidepressant class response and treatment-resistant depression. <i>Translational Psychiatry</i> , 2020, 10, 360.	4.8	33
770	Identification of 31 loci for mammographic density phenotypes and their associations with breast cancer risk. <i>Nature Communications</i> , 2020, 11, 5116.	12.8	29
771	Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. <i>BMC Bioinformatics</i> , 2020, 21, 469.	2.6	14
772	Translation-Focused Approaches to GPCR Drug Discovery for Cognitive Impairments Associated with Schizophrenia. <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 1042-1062.	4.9	6
773	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. <i>Nature Communications</i> , 2020, 11, 5504.	12.8	39
774	Integration of Online Omics-Data Resources for Cancer Research. <i>Frontiers in Genetics</i> , 2020, 11, 578345.	2.3	50
775	Detection and characterisation of novel alternative splicing variants of the mitochondrial folate enzyme MTHFD2. <i>Molecular Biology Reports</i> , 2020, 47, 7089-7096.	2.3	2
776	Canalization and Robustness in Human Genetics and Disease. <i>Annual Review of Genetics</i> , 2020, 54, 189-211.	7.6	22
777	Integrative genomics analysis of various omics data and networks identify risk genes and variants vulnerable to childhood-onset asthma. <i>BMC Medical Genomics</i> , 2020, 13, 123.	1.5	15
778	Genome-Wide Association Study of Susceptibility Loci for <i>TCF3-PBX1</i> Acute Lymphoblastic Leukemia in Children. <i>Journal of the National Cancer Institute</i> , 2021, 113, 933-937.	6.3	9
779	Pharmacologically reversible zonation-dependent endothelial cell transcriptomic changes with neurodegenerative disease associations in the aged brain. <i>Nature Communications</i> , 2020, 11, 4413.	12.8	59
780	ZMAT2 in Humans and Other Primates: A Highly Conserved and Understudied Gene. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432094150.	1.2	3
781	Epigenetic fine-mapping: identification of causal mechanisms for autoimmunity. <i>Current Opinion in Immunology</i> , 2020, 67, 50-56.	5.5	1
782	The statistical practice of the GTEx Project: from single to multiple tissues. <i>Quantitative Biology</i> , 2021, 9, 151-167.	0.5	1
783	“Moving genes”: how dystonia genes functionally converge on the transcriptome. <i>Brain</i> , 2020, 143, 2631-2634.	7.6	0
784	Transcriptomic Heterogeneity of Alzheimer’s Disease Associated with Lipid Genetic Risk. <i>NeuroMolecular Medicine</i> , 2020, 22, 534-541.	3.4	4

#	ARTICLE	IF	CITATIONS
785	Integrative analysis identifies the association between CASZ1 methylation and ischemic stroke. <i>Neurology: Genetics</i> , 2020, 6, e509.	1.9	11
786	N-Terminal Acetyltransferases Are Cancer-Essential Genes Prevalently Upregulated in Tumours. <i>Cancers</i> , 2020, 12, 2631.	3.7	20
787	GBAT: a gene-based association test for robust detection of trans-gene regulation. <i>Genome Biology</i> , 2020, 21, 211.	8.8	12
788	A second X chromosome contributes to resilience in a mouse model of Alzheimer's disease. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	107
789	Genome-wide association meta-analysis for early age-related macular degeneration highlights novel loci and insights for advanced disease. <i>BMC Medical Genomics</i> , 2020, 13, 120.	1.5	56
790	Phenome-wide analyses establish a specific association between aortic valve PALMD expression and calcific aortic valve stenosis. <i>Communications Biology</i> , 2020, 3, 477.	4.4	12
791	Low tolerance for transcriptional variation at cohesin genes is accompanied by functional links to disease-relevant pathways. <i>Journal of Medical Genetics</i> , 2021, 58, 534-542.	3.2	3
792	Gene expression profiles complement the analysis of genomic modifiers of the clinical onset of Huntington disease. <i>Human Molecular Genetics</i> , 2020, 29, 2788-2802.	2.9	17
793	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. <i>Science Advances</i> , 2020, 6, .	10.3	33
794	Low Baseline Pulmonary Levels of Cytotoxic Lymphocytes as a Predisposing Risk Factor for Severe COVID-19. <i>MSystems</i> , 2020, 5, .	3.8	9
795	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. <i>PLoS Genetics</i> , 2020, 16, e1008780.	3.5	10
796	SparkINFERNO: a scalable high-throughput pipeline for inferring molecular mechanisms of non-coding genetic variants. <i>Bioinformatics</i> , 2020, 36, 3879-3881.	4.1	7
797	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. <i>Journal of Nutrition</i> , 2020, 150, 2635-2645.	2.9	4
798	Genetic variants modulate gene expression statin response in human lymphoblastoid cell lines. <i>BMC Genomics</i> , 2020, 21, 555.	2.8	15
799	Whole genome sequencing of elite athletes. <i>Biology of Sport</i> , 2020, 37, 295-304.	3.2	22
800	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. <i>Nature Genetics</i> , 2020, 52, 1122-1131.	21.4	298
801	What Has a Century of Quantitative Genetics Taught Us About Nature's Genetic Tool Kit?. <i>Annual Review of Genetics</i> , 2020, 54, 439-464.	7.6	11
802	Genome-wide detection of tandem DNA repeats that are expanded in autism. <i>Nature</i> , 2020, 586, 80-86.	27.8	155

#	ARTICLE	IF	CITATIONS
803	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020, 369, 1318-1330.	12.6	2,385
804	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. <i>Cancer Research</i> , 2020, 80, 4346-4354.	0.9	28
805	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232.	8.8	46
806	A polyclonal allelic expression assay for detecting regulatory effects of transcript variants. <i>Genome Medicine</i> , 2020, 12, 79.	8.2	5
807	Primo: integration of multiple GWAS and omics QTL summary statistics for elucidation of molecular mechanisms of trait-associated SNPs and detection of pleiotropy in complex traits. <i>Genome Biology</i> , 2020, 21, 236.	8.8	26
808	Cytokines mapping for tissue-specific expression, eQTLs and GWAS traits. <i>Scientific Reports</i> , 2020, 10, 14740.	3.3	4
809	Prevention of adverse drug effects: a pharmacogenomic approach. <i>Current Opinion in Pediatrics</i> , 2020, 32, 646-653.	2.0	1
810	ILRUN, a Human Plasma Lipid GWAS Locus, Regulates Lipoprotein Metabolism in Mice. <i>Circulation Research</i> , 2020, 127, 1347-1361.	4.5	11
811	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020, 21, 233.	8.8	64
812	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	8.8	68
813	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. <i>Genome Biology</i> , 2020, 21, 235.	8.8	18
814	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. <i>PLoS Medicine</i> , 2020, 17, e1003302.	8.4	63
815	Deconvolving the contributions of cell-type heterogeneity on cortical gene expression. <i>PLoS Computational Biology</i> , 2020, 16, e1008120.	3.2	66
816	Systematic identification of functional SNPs interrupting 3'UTR polyadenylation signals. <i>PLoS Genetics</i> , 2020, 16, e1008977.	3.5	30
817	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21813-21820.	7.1	22
818	Partitioning gene-based variance of complex traits by gene score regression. <i>PLoS ONE</i> , 2020, 15, e0237657.	2.5	2
819	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 387-395.	3.6	16
820	On the cross-population generalizability of gene expression prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008927.	3.5	41

#	ARTICLE	IF	CITATIONS
821	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. Nature Communications, 2020, 11, 6258.	12.8	8
822	Qtlizer: comprehensive QTL annotation of GWAS results. Scientific Reports, 2020, 10, 20417.	3.3	23
823	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	4.4	10
824	Fine-mapping and cell-specific enrichment at corneal resistance factor loci prioritize candidate causal regulatory variants. Communications Biology, 2020, 3, 762.	4.4	6
825	Dosage-sensitive molecular mechanisms are associated with the tissue-specificity of traits and diseases. Computational and Structural Biotechnology Journal, 2020, 18, 4024-4032.	4.1	6
826	nMAGMA: a network-enhanced method for inferring risk genes from GWAS summary statistics and its application to schizophrenia. Briefings in Bioinformatics, 2021, 22, .	6.5	4
827	Covariate adaptive familywise error rate control for genome-wide association studies. Biometrika, 2021, 108, 915-931.	2.4	3
828	Associations of Observational and Genetically Determined Caffeine Intake With Coronary Artery Disease and Diabetes Mellitus. Journal of the American Heart Association, 2020, 9, e016808.	3.7	21
829	Differential transcriptomics in sarcoidosis lung and lymph node granulomas with comparisons to pathogen-specific granulomas. Respiratory Research, 2020, 21, 321.	3.6	17
830	Integrative Analysis of Transcriptome-Wide Association Study and mRNA Expression Profiles Identifies Candidate Genes Associated With Idiopathic Pulmonary Fibrosis. Frontiers in Genetics, 2020, 11, 604324.	2.3	6
831	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	12.8	53
832	Learning from Fifteen Years of Genome-Wide Association Studies in Age-Related Macular Degeneration. Cells, 2020, 9, 2267.	4.1	18
833	Identification of Functional Genetic Variants Associated With Alcohol Dependence and Related Phenotypes Using a High-Throughput Assay. Alcoholism: Clinical and Experimental Research, 2020, 44, 2494-2518.	2.4	7
834	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. Nature Communications, 2020, 11, 5562.	12.8	80
835	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, e003085.	3.6	14
836	Leveraging Multiple Layers of Data To Predict <i>Drosophila</i> Complex Traits. G3: Genes, Genomes, Genetics, 2020, 10, 4599-4613.	1.8	21
837	Expression quantitative trait locus fine mapping of the 17q12-21 asthma locus in African American children: a genetic association and gene expression study. Lancet Respiratory Medicine, the, 2020, 8, 482-492.	10.7	47
838	Genome-wide association study of MRI markers of cerebral small vessel disease in 42,310 participants. Nature Communications, 2020, 11, 2175.	12.8	93

#	ARTICLE	IF	CITATIONS
839	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand <i>KITLG/SCF</i> and Gene-By-Air-Pollution Interaction. <i>Genetics</i> , 2020, 215, 869-886.	2.9	11
840	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
841	Quantifying genetic effects on disease mediated by assayed gene expression levels. <i>Nature Genetics</i> , 2020, 52, 626-633.	21.4	191
842	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020, 30, 790-801.	5.5	97
843	Summary-Based Methylome-Wide Association Analyses Suggest Potential Genetically Driven Epigenetic Heterogeneity of Alzheimer's Disease. <i>Journal of Clinical Medicine</i> , 2020, 9, 1489.	2.4	10
844	Demographic and genetic factors influence the abundance of infiltrating immune cells in human tissues. <i>Nature Communications</i> , 2020, 11, 2213.	12.8	23
845	Genetic perspective on the synergistic connection between vesicular transport, lysosomal and mitochondrial pathways associated with Parkinson's disease pathogenesis. <i>Acta Neuropathologica Communications</i> , 2020, 8, 63.	5.2	45
846	Complement genes contribute sex-biased vulnerability in diverse disorders. <i>Nature</i> , 2020, 582, 577-581.	27.8	158
847	ASEP: Gene-based detection of allele-specific expression across individuals in a population by RNA sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008786.	3.5	42
848	Recent Advances in Understanding the Genetic Architecture of Autism. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 289-304.	6.2	30
849	Flexible Mixture Model Approaches That Accommodate Footprint Size Variability for Robust Detection of Balancing Selection. <i>Molecular Biology and Evolution</i> , 2020, 37, 3267-3291.	8.9	23
850	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. <i>Nature Metabolism</i> , 2020, 2, 487-498.	11.9	32
851	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. <i>Nature Communications</i> , 2020, 11, 2695.	12.8	29
852	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. <i>Nature Communications</i> , 2020, 11, 2718.	12.8	53
853	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. <i>Nature Communications</i> , 2020, 11, 2797.	12.8	34
854	Pairwise common variant meta-analyses of schizophrenia with other psychiatric disorders reveals shared and distinct gene and gene-set associations. <i>Translational Psychiatry</i> , 2020, 10, 134.	4.8	37
855	Transcriptional and Cellular Diversity of the Human Heart. <i>Circulation</i> , 2020, 142, 466-482.	1.6	326
856	Identifying Shared Risk Genes for Asthma, Hay Fever, and Eczema by Multi-Trait and Multiomic Association Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 270.	2.3	15

#	ARTICLE	IF	CITATIONS
857	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohn's Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. <i>Frontiers in Genetics</i> , 2020, 11, 486.	2.3	15
858	Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. <i>American Journal of Human Genetics</i> , 2020, 106, 885-892.	6.2	51
859	A Multiple-Testing Procedure for High-Dimensional Mediation Hypotheses. <i>Journal of the American Statistical Association</i> , 2022, 117, 198-213.	3.1	30
860	Assessing established BMI variants for a role in nighttime eating behavior in robustly phenotyped Southwestern American Indians. <i>European Journal of Clinical Nutrition</i> , 2020, 74, 1718-1724.	2.9	3
861	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020, 581, 459-464.	27.8	115
862	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	27.8	6,140
863	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002670.	3.6	44
864	Data-based RNA-seq simulations by binomial thinning. <i>BMC Bioinformatics</i> , 2020, 21, 206.	2.6	20
865	Genome-wide analysis of carotid plaque burden suggests a role of IL5 in men. <i>PLoS ONE</i> , 2020, 15, e0233728.	2.5	7
866	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
867	Significance of Single-Nucleotide Variants in Long Intergenic Non-protein Coding RNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 347.	3.7	30
868	Analysis of putative cis-regulatory elements regulating blood pressure variation. <i>Human Molecular Genetics</i> , 2020, 29, 1922-1932.	2.9	7
869	Structure and expression of the long noncoding RNA gene MIR503 in humans and non-human primates. <i>Molecular and Cellular Endocrinology</i> , 2020, 510, 110819.	3.2	6
870	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020, 581, 444-451.	27.8	614
871	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	27.8	142
872	Quantitative analysis of Y-Chromosome gene expression across 36 human tissues. <i>Genome Research</i> , 2020, 30, 860-873.	5.5	56
873	Altered glucocorticoid metabolism represents a feature of macrophage aging. <i>Aging Cell</i> , 2020, 19, e13156.	6.7	24
874	Virus-induced genetics revealed by multidimensional precision medicine transcriptional workflow applicable to COVID-19. <i>Physiological Genomics</i> , 2020, 52, 255-268.	2.3	21

#	ARTICLE	IF	CITATIONS
875	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 962-972.	5.6	11
876	The Zmat2 gene in non-mammalian vertebrates: Organizational simplicity within a divergent locus in fish. <i>PLoS ONE</i> , 2020, 15, e0233081.	2.5	0
877	The polygenic architecture of schizophrenia “rethinking pathogenesis and nosology. <i>Nature Reviews Neurology</i> , 2020, 16, 366-379.	10.1	122
878	Epigenomes of Human Hearts Reveal New Genetic Variants Relevant for Cardiac Disease and Phenotype. <i>Circulation Research</i> , 2020, 127, 761-777.	4.5	29
879	Functional annotation of rare structural variation in the human brain. <i>Nature Communications</i> , 2020, 11, 2990.	12.8	32
880	Genetic Basis and Prognostic Value of Exercise QT Dynamics. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002774.	3.6	12
881	Broadening primate genomics: new insights into the ecology and evolution of primate gene regulation. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 16-22.	3.3	10
882	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , 2020, 31, 107795.	6.4	207
883	Protein QTL analysis of IGF-I and its binding proteins provides insights into growth biology. <i>Human Molecular Genetics</i> , 2020, 29, 2625-2636.	2.9	2
884	Estimating and Accounting for Unobserved Covariates in High-Dimensional Correlated Data. <i>Journal of the American Statistical Association</i> , 2022, 117, 225-236.	3.1	5
885	Genetic Association Reveals Protection against Recurrence of <i>Clostridium difficile</i> Infection with Bezlotoxumab Treatment. <i>MSphere</i> , 2020, 5, .	2.9	13
886	Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. <i>PLoS Genetics</i> , 2020, 16, e1008855.	3.5	9
887	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. <i>Cell</i> , 2020, 182, 145-161.e23.	28.9	464
888	Common Variants Coregulate Expression of <i>GBA</i> and Modifier Genes to Delay Parkinson's Disease Onset. <i>Movement Disorders</i> , 2020, 35, 1346-1356.	3.9	30
889	Genome-wide association study identifies genetic susceptibility loci and pathways of radiation-induced acute oral mucositis. <i>Journal of Translational Medicine</i> , 2020, 18, 224.	4.4	29
890	MALAT1 Long Non-Coding RNA: Functional Implications. <i>Non-coding RNA</i> , 2020, 6, 22.	2.6	115
891	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020, 52, 669-679.	21.4	304
892	Identification of population-level differentially expressed genes in one-phenotype data. <i>Bioinformatics</i> , 2020, 36, 4283-4290.	4.1	7

#	ARTICLE	IF	CITATIONS
893	Unravelling the complex genetics of common kidney diseases: from variants to mechanisms. <i>Nature Reviews Nephrology</i> , 2020, 16, 628-640.	9.6	33
894	Transcription Factor KLF14 and Metabolic Syndrome. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 91.	2.4	23
895	Characterization of a Novel FLT3 BiTE Molecule for the Treatment of Acute Myeloid Leukemia. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1875-1888.	4.1	34
896	Molecular mechanisms of coronary disease revealed using quantitative trait loci for TCF21 binding, chromatin accessibility, and chromosomal looping. <i>Genome Biology</i> , 2020, 21, 135.	8.8	16
897	Complexities of Understanding Function from CKD-Associated DNA Variants. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2020, 15, 1028-1040.	4.5	1
898	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. <i>Neuron</i> , 2020, 107, 496-508.e6.	8.1	29
899	Genetic variants associated with alcohol dependence co-ordinate regulation of ADH genes in gastrointestinal and adipose tissues. <i>Scientific Reports</i> , 2020, 10, 9897.	3.3	1
900	Methylation map genes can be critical in determining the methylome of intracranial aneurysm patients. <i>Epigenomics</i> , 2020, 12, 859-871.	2.1	3
901	Further confirmation of netrin 1 receptor (DCC) as a depression risk gene via integrations of multi-omics data. <i>Translational Psychiatry</i> , 2020, 10, 98.	4.8	26
902	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. <i>Nature Neuroscience</i> , 2020, 23, 510-519.	14.8	67
903	Machine learning prediction of oncology drug targets based on protein and network properties. <i>BMC Bioinformatics</i> , 2020, 21, 104.	2.6	35
904	Shared genetic etiology underlying Alzheimer's disease and major depressive disorder. <i>Translational Psychiatry</i> , 2020, 10, 88.	4.8	45
905	Regulation of gene expression by growth hormone. <i>Molecular and Cellular Endocrinology</i> , 2020, 507, 110788.	3.2	21
906	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020, 367, .	12.6	517
907	Big data in digital healthcare: lessons learnt and recommendations for general practice. <i>Heredity</i> , 2020, 124, 525-534.	2.6	103
908	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	12.8	85
909	Dysregulated Antibody, Natural Killer Cell and Immune Mediator Profiles in Autoimmune Thyroid Diseases. <i>Cells</i> , 2020, 9, 665.	4.1	18
910	A genome-wide association study identifies <i>FSHR</i> rs2300441 associated with follicle-stimulating hormone levels. <i>Clinical Genetics</i> , 2020, 97, 869-877.	2.0	8

#	ARTICLE	IF	CITATIONS
911	Capturing functional epigenomes for insight into metabolic diseases. <i>Molecular Metabolism</i> , 2020, 38, 100936.	6.5	9
912	8q24 genetic variation and comprehensive haplotypes altering familial risk of prostate cancer. <i>Nature Communications</i> , 2020, 11, 1523.	12.8	10
913	Germline Polymorphisms and Length of Survival of Nasopharyngeal Carcinoma: An Exome-Wide Association Study in Multiple Cohorts. <i>Advanced Science</i> , 2020, 7, 1903727.	11.2	12
914	Identification of a functional human-unique 351-bp Alu insertion polymorphism associated with major depressive disorder in the 1p31.1 GWAS risk loci. <i>Neuropsychopharmacology</i> , 2020, 45, 1196-1206.	5.4	17
915	UGT1A1 Variants c.864+5G>T and c.996+2_996+5del of a Crigler-Najjar Patient Induce Aberrant Splicing in Minigene Assays. <i>Frontiers in Genetics</i> , 2020, 11, 169.	2.3	9
916	The genetic architecture of membranous nephropathy and its potential to improve non-invasive diagnosis. <i>Nature Communications</i> , 2020, 11, 1600.	12.8	120
917	Completing the ENCODE3 compendium yields accurate imputations across a variety of assays and human biosamples. <i>Genome Biology</i> , 2020, 21, 82.	8.8	22
918	DNA methylation and cis-regulation of gene expression by prostate cancer risk SNPs. <i>PLoS Genetics</i> , 2020, 16, e1008667.	3.5	15
919	HNF1A recruits KDM6A to activate differentiated acinar cell programs that suppress pancreatic cancer. <i>EMBO Journal</i> , 2020, 39, e102808.	7.8	44
920	Profiling haplotype specific CpG and CpH methylation within a schizophrenia GWAS locus on chromosome 14 in schizophrenia and healthy subjects. <i>Scientific Reports</i> , 2020, 10, 4704.	3.3	3
921	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 2137-2152.	8.9	14
922	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. <i>PLoS Genetics</i> , 2020, 16, e1008686.	3.5	8
923	Novel and Known Gene-Smoking Interactions With cIMT Identified as Potential Drivers for Atherosclerosis Risk in West-African Populations of the AWI-Gen Study. <i>Frontiers in Genetics</i> , 2019, 10, 1354.	2.3	10
924	epiCOLOC: Integrating Large-Scale and Context-Dependent Epigenomics Features for Comprehensive Colocalization Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 53.	2.3	13
925	Shared genetic etiology underlying late-onset Alzheimer's disease and posttraumatic stress syndrome. <i>Alzheimer's and Dementia</i> , 2020, 16, 1280-1292.	0.8	15
926	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. <i>Molecular Cell</i> , 2020, 79, 521-534.e15.	9.7	110
927	Gene constraint and genotype-phenotype correlations in neurodevelopmental disorders. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 69-75.	3.3	7
928	Integrative analysis highlighted susceptibility genes for rheumatoid arthritis. <i>International Immunopharmacology</i> , 2020, 86, 106716.	3.8	8

#	ARTICLE	IF	CITATIONS
929	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. <i>Nature Communications</i> , 2020, 11, 3126.	12.8	44
930	Archaic hominin genomics provides a window into gene expression evolution. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 44-49.	3.3	9
931	Genetic drug target validation using Mendelian randomisation. <i>Nature Communications</i> , 2020, 11, 3255.	12.8	175
932	Exposure to the Heavy-Metal Lead Induces DNA Copy Number Alterations in Zebrafish Cells. <i>Chemical Research in Toxicology</i> , 2020, 33, 2047-2053.	3.3	4
933	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163.	8.8	76
934	A Functional Variant of the miR-15 Family Is Associated with a Decreased Risk of Esophageal Squamous Cell Carcinoma. <i>DNA and Cell Biology</i> , 2020, 39, 1583-1594.	1.9	6
935	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	68
936	Regional Variation of Splicing QTLs in Human Brain. <i>American Journal of Human Genetics</i> , 2020, 107, 196-210.	6.2	26
937	Nonclinical cardiovascular safety evaluation of romosozumab, an inhibitor of sclerostin for the treatment of osteoporosis in postmenopausal women at high risk of fracture. <i>Regulatory Toxicology and Pharmacology</i> , 2020, 115, 104697.	2.7	32
938	Suppression of adenosine-to-inosine (A-to-I) RNA editome by death associated protein 3 (DAP3) promotes cancer progression. <i>Science Advances</i> , 2020, 6, eaba5136.	10.3	29
939	The importance of including ethnically diverse populations in studies of quantitative trait evolution. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 30-35.	3.3	5
940	Selection Shapes Synonymous Stop Codon Use in Mammals. <i>Journal of Molecular Evolution</i> , 2020, 88, 549-561.	1.8	6
941	Functional genomics links genetic origins to pathophysiology in neurodegenerative and neuropsychiatric disease. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 117-125.	3.3	7
942	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020, 16, e1008785.	3.5	29
943	Zmat2 in mammals: conservation and diversification among genes and Pseudogenes. <i>BMC Genomics</i> , 2020, 21, 113.	2.8	2
944	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007616.	3.2	54
945	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. <i>Frontiers in Genetics</i> , 2019, 10, 1309.	2.3	17
946	Applications of Functional Genomics for Drug Discovery. <i>SLAS Discovery</i> , 2020, 25, 823-842.	2.7	6

#	ARTICLE	IF	CITATIONS
947	Determining sequencing depth in a single-cell RNA-seq experiment. Nature Communications, 2020, 11, 774.	12.8	74
948	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
949	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.9	43
950	Transcriptome analysis reveals the difference between "healthy" and "common" aging and their connection with age-related diseases. Aging Cell, 2020, 19, e13121.	6.7	22
951	IGREX for quantifying the impact of genetically regulated expression on phenotypes. NAR Genomics and Bioinformatics, 2020, 2, lqaa010.	3.2	15
952	Integrative comparison of the genomic and transcriptomic landscape between prostate cancer patients of predominantly African or European genetic ancestry. PLoS Genetics, 2020, 16, e1008641.	3.5	78
953	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	21.4	85
954	Contribution of unfixed transposable element insertions to human regulatory variation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190331.	4.0	32
955	Cellular deconvolution of GTEx tissues powers discovery of disease and cell-type associated regulatory variants. Nature Communications, 2020, 11, 955.	12.8	96
956	Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. Cell Systems, 2020, 10, 193-203.e4.	6.2	15
957	A Multi-Omics Perspective of Quantitative Trait Loci in Precision Medicine. Trends in Genetics, 2020, 36, 318-336.	6.7	41
958	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. Molecular Psychiatry, 2020, 25, 1673-1687.	7.9	82
959	The behavioral, cellular and immune mediators of HIV-1 acquisition: New insights from population genetics. Scientific Reports, 2020, 10, 3304.	3.3	8
960	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
961	Club Cell TRPV4 Serves as a Damage Sensor Driving Lung Allergic Inflammation. Cell Host and Microbe, 2020, 27, 614-628.e6.	11.0	47
962	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	12.8	235
963	Genomic dissection of 43 serum urate-associated loci provides multiple insights into molecular mechanisms of urate control. Human Molecular Genetics, 2020, 29, 923-943.	2.9	40
964	Integrating Multi-Omics Data to Identify Novel Disease Genes and Single-Nucleotide Polymorphisms. Frontiers in Genetics, 2019, 10, 1336.	2.3	7

#	ARTICLE	IF	CITATIONS
965	Variations and expression features of CYP2D6 contribute to schizophrenia risk. <i>Molecular Psychiatry</i> , 2021, 26, 2605-2615.	7.9	8
966	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. <i>Nature Medicine</i> , 2020, 26, 98-109.	30.7	32
967	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	28.9	1,422
968	Differential network analysis of multiple human tissue interactomes highlights tissue-selective processes and genetic disorder genes. <i>Bioinformatics</i> , 2020, 36, 2821-2828.	4.1	28
969	A Multi-tissue Transcriptome Analysis of Human Metabolites Guides Interpretability of Associations Based on Multi-SNP Models for Gene Expression. <i>American Journal of Human Genetics</i> , 2020, 106, 188-201.	6.2	26
970	rs953413 Regulates Polyunsaturated Fatty Acid Metabolism by Modulating ELOVL2 Expression. <i>IScience</i> , 2020, 23, 100808.	4.1	19
971	From Genetic Association to Molecular Mechanisms for Islet-cell Dysfunction in Type 2 Diabetes. <i>Journal of Molecular Biology</i> , 2020, 432, 1551-1578.	4.2	27
972	Transcript specific regulation of expression influences susceptibility to multiple sclerosis. <i>European Journal of Human Genetics</i> , 2020, 28, 826-834.	2.8	10
973	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. <i>Human Molecular Genetics</i> , 2020, 29, 515-526.	2.9	7
974	Towards a comprehensive catalogue of validated and target-linked human enhancers. <i>Nature Reviews Genetics</i> , 2020, 21, 292-310.	16.3	229
975	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
976	A comparison of gene expression and DNA methylation patterns across tissues and species. <i>Genome Research</i> , 2020, 30, 250-262.	5.5	91
977	Novel Approaches for Identifying the Molecular Background of Schizophrenia. <i>Cells</i> , 2020, 9, 246.	4.1	13
978	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020, 1, 235-248.	13.2	430
979	The open targets post-GWAS analysis pipeline. <i>Bioinformatics</i> , 2020, 36, 2936-2937.	4.1	24
980	Allele-Specific QTL Fine Mapping with PLASMA. <i>American Journal of Human Genetics</i> , 2020, 106, 170-187.	6.2	14
981	LncRNA-AC006129.1 reactivates a SOCS3-mediated anti-inflammatory response through DNA methylation-mediated CIC downregulation in schizophrenia. <i>Molecular Psychiatry</i> , 2021, 26, 4511-4528.	7.9	26
982	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	27.8	280

#	ARTICLE	IF	CITATIONS
983	A combined RNA-seq and whole genome sequencing approach for identification of non-coding pathogenic variants in single families. <i>Human Molecular Genetics</i> , 2020, 29, 967-979.	2.9	12
984	An integrated analysis of public genomic data unveils a possible functional mechanism of psoriasis risk via a long-range ERRFI1 enhancer. <i>BMC Medical Genomics</i> , 2020, 13, 8.	1.5	9
985	Focus on Causality in ESC/iPSC-Based Modeling of Psychiatric Disorders. <i>Cells</i> , 2020, 9, 366.	4.1	12
986	Enhancer Domains Predict Gene Pathogenicity and Inform Gene Discovery in Complex Disease. <i>American Journal of Human Genetics</i> , 2020, 106, 215-233.	6.2	72
987	Statistical Methods in Genome-Wide Association Studies. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 265-288.	6.5	6
988	Diverse types of genomic evidence converge on alcohol use disorder risk genes. <i>Journal of Medical Genetics</i> , 2020, 57, 733-743.	3.2	10
989	A genome-wide analysis of DNA methylation identifies a novel association signal for Lp(a) concentrations in the LPA promoter. <i>PLoS ONE</i> , 2020, 15, e0232073.	2.5	8
990	Reconstructing the blood metabolome and genotype using long-range chromatin interactions. <i>Metabolism Open</i> , 2020, 6, 100035.	2.9	6
991	Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. <i>American Journal of Human Genetics</i> , 2020, 106, 496-512.	6.2	56
992	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. <i>Cell Reports</i> , 2020, 31, 107489.	6.4	91
993	The contribution of rare genetic variants to the pathogenesis of polycystic ovary syndrome. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2020, 12, 26-32.	1.4	21
994	Whole exome sequencing in ADHD trios from single and multi-incident families implicates new candidate genes and highlights polygenic transmission. <i>European Journal of Human Genetics</i> , 2020, 28, 1098-1110.	2.8	13
995	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	12.8	211
996	Genetic basis for divergence in developmental gene expression in two closely related sea urchins. <i>Nature Ecology and Evolution</i> , 2020, 4, 831-840.	7.8	18
997	Structural basis for substrate and product recognition in human phosphoglucomutase-1 (PGM1) isoform 2, a member of the Î±-d-phosphohexomutase superfamily. <i>Scientific Reports</i> , 2020, 10, 5656.	3.3	9
998	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 646-653.	1.3	5
999	Tumor Necrosis Factor Alpha Regulates Skeletal Myogenesis by Inhibiting SP1 Interaction with cis-Acting Regulatory Elements within the Fbxl2 Gene Promoter. <i>Molecular and Cellular Biology</i> , 2020, 40, .	2.3	6
1000	The Role of Genetic Variation of BMI, Body Composition, and Fat Distribution for Mental Traits and Disorders: A Look-Up and Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2020, 11, 373.	2.3	20

#	ARTICLE	IF	CITATIONS
1001	Integrated Analysis of Summary Statistics to Identify Pleiotropic Genes and Pathways for the Comorbidity of Schizophrenia and Cardiometabolic Disease. <i>Frontiers in Psychiatry</i> , 2020, 11, 256.	2.6	24
1002	Clinical impact of splicing in neurodevelopmental disorders. <i>Genome Medicine</i> , 2020, 12, 36.	8.2	15
1003	Predicting target genes of non-coding regulatory variants with IRT. <i>Bioinformatics</i> , 2020, 36, 4440-4448.	4.1	6
1004	Effective study design for comparative functional genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 385-386.	16.3	9
1005	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson's disease. <i>Nature Genetics</i> , 2020, 52, 482-493.	21.4	216
1006	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. <i>PLoS Genetics</i> , 2020, 16, e1008720.	3.5	180
1007	Consistent RNA sequencing contamination in GTEx and other data sets. <i>Nature Communications</i> , 2020, 11, 1933.	12.8	43
1008	APalyzer: a bioinformatics package for analysis of alternative polyadenylation isoforms. <i>Bioinformatics</i> , 2020, 36, 3907-3909.	4.1	44
1009	The Evolutionary Forces Shaping Cis- and Trans-Regulation of Gene Expression within a Population of Outcrossing Plants. <i>Molecular Biology and Evolution</i> , 2020, 37, 2386-2393.	8.9	13
1010	Effective SNP ranking improves the performance of eQTL mapping. <i>Genetic Epidemiology</i> , 2020, 44, 611-619.	1.3	2
1011	Genome-wide association studies and Mendelian randomization analyses for leisure sedentary behaviours. <i>Nature Communications</i> , 2020, 11, 1770.	12.8	66
1012	An analysis of genetically regulated gene expression across multiple tissues implicates novel gene candidates in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 43.	6.2	20
1013	Discovery of novel hepatocyte eQTLs in African Americans. <i>PLoS Genetics</i> , 2020, 16, e1008662.	3.5	21
1014	Leveraging gene co-expression patterns to infer trait-relevant tissues in genome-wide association studies. <i>PLoS Genetics</i> , 2020, 16, e1008734.	3.5	25
1015	Fast Algorithms for Conducting Large-Scale GWAS of Age-at-Onset Traits Using Cox Mixed-Effects Models. <i>Genetics</i> , 2020, 215, 41-58.	2.9	29
1016	Convolutional neural network models for cancer type prediction based on gene expression. <i>BMC Medical Genomics</i> , 2020, 13, 44.	1.5	103
1017	Characterisation of genetic regulatory effects for osteoporosis risk variants in human osteoclasts. <i>Genome Biology</i> , 2020, 21, 80.	8.8	36
1018	Integrating GWAS with bulk and single-cell RNA-sequencing reveals a role for LY86 in the anti-Candida host response. <i>PLoS Pathogens</i> , 2020, 16, e1008408.	4.7	18

#	ARTICLE	IF	CITATIONS
1019	Comprehensive Analysis of the Genetic and Epigenetic Mechanisms of Osteoporosis and Bone Mineral Density. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 194.	3.7	10
1020	Resources for functional genomic studies of health and development in nonhuman primates. <i>American Journal of Physical Anthropology</i> , 2020, 171, 174-194.	2.1	7
1021	The application of "omics"™ to pulmonary arterial hypertension. <i>British Journal of Pharmacology</i> , 2021, 178, 108-120.	5.4	18
1022	Splicing mutations in inherited retinal diseases. <i>Progress in Retinal and Eye Research</i> , 2021, 80, 100874.	15.5	22
1023	Genome-wide Association Analysis of Parkinson's Disease and Schizophrenia Reveals Shared Genetic Architecture and Identifies Novel Risk Loci. <i>Biological Psychiatry</i> , 2021, 89, 227-235.	1.3	53
1024	CpG-island-based annotation and analysis of human housekeeping genes. <i>Briefings in Bioinformatics</i> , 2021, 22, 515-525.	6.5	31
1025	An absolute human stemness index associated with oncogenic dedifferentiation. <i>Briefings in Bioinformatics</i> , 2021, 22, 2151-2160.	6.5	22
1026	Cognitive disorders associated with hospitalization of COVID-19: Results from an observational cohort study. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 383-392.	4.1	44
1027	GRNdb: decoding the gene regulatory networks in diverse human and mouse conditions. <i>Nucleic Acids Research</i> , 2021, 49, D97-D103.	14.5	58
1028	TreeMap: a structured approach to fine mapping of eQTL variants. <i>Bioinformatics</i> , 2021, 37, 1125-1134.	4.1	6
1029	Massively Parallel Reporter Assays: Defining Functional Psychiatric Genetic Variants Across Biological Contexts. <i>Biological Psychiatry</i> , 2021, 89, 76-89.	1.3	34
1030	Genomic, transcriptomic, and protein landscape profile of CFTR and cystic fibrosis. <i>Human Genetics</i> , 2021, 140, 423-439.	3.8	3
1031	Transcriptomic Insight Into the Polygenic Mechanisms Underlying Psychiatric Disorders. <i>Biological Psychiatry</i> , 2021, 89, 54-64.	1.3	36
1032	Cross-disease analysis of depression, ataxia and dystonia highlights a role for synaptic plasticity and the cerebellum in the pathophysiology of these comorbid diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 165976.	3.8	13
1033	Where Are the Disease-Associated eQTLs?. <i>Trends in Genetics</i> , 2021, 37, 109-124.	6.7	163
1034	Gene Teller: an extensible Alexa Skill for gene-relevant databases. <i>Bioinformatics</i> , 2021, 36, 5267-5268.	4.1	2
1035	Genome-Wide Association Analysis of Neonatal White Matter Microstructure. <i>Cerebral Cortex</i> , 2021, 31, 933-948.	2.9	3
1036	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. <i>Biological Psychiatry</i> , 2021, 89, 246-255.	1.3	20

#	ARTICLE	IF	CITATIONS
1037	Molecular and evolutionary processes generating variation in gene expression. <i>Nature Reviews Genetics</i> , 2021, 22, 203-215.	16.3	154
1038	Genome-wide association study identifies a role for the progesterone receptor in benign prostatic hyperplasia risk. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 492-498.	3.9	5
1039	Exome Sequencing Identifies Abnormalities in Glycosylation and ANKRD36C in Patients with Immune-Mediated Thrombotic Thrombocytopenic Purpura. <i>Thrombosis and Haemostasis</i> , 2021, 121, 506-517.	3.4	4
1040	Genome-wide association study of individual differences of human lymphocyte profiles using large-scale cytometry data. <i>Journal of Human Genetics</i> , 2021, 66, 557-567.	2.3	9
1041	Discover novel disease-associated genes based on regulatory networks of long-range chromatin interactions. <i>Methods</i> , 2021, 189, 22-33.	3.8	8
1042	Mendelian randomization analysis identified genes pleiotropically associated with the risk and prognosis of COVID-19. <i>Journal of Infection</i> , 2021, 82, 126-132.	3.3	37
1043	Association of Genetic Variation With Cirrhosis: A Multi-Trait Genome-Wide Association and Gene-Environment Interaction Study. <i>Gastroenterology</i> , 2021, 160, 1620-1633.e13.	1.3	68
1044	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. <i>Cancer Research</i> , 2021, 81, 2556-2565.	0.9	24
1045	Elevated Blood Pressure Increases Pneumonia Risk: Epidemiological Association and Mendelian Randomization in the UK Biobank. <i>Med</i> , 2021, 2, 137-148.e4.	4.4	21
1046	Systems biology in cardiovascular disease: a multiomics approach. <i>Nature Reviews Cardiology</i> , 2021, 18, 313-330.	13.7	134
1047	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. <i>Nature Genetics</i> , 2021, 53, 110-119.	21.4	62
1048	Predicting regulatory variants using a dense epigenomic mapped CNN model elucidated the molecular basis of trait-tissue associations. <i>Nucleic Acids Research</i> , 2021, 49, 53-66.	14.5	17
1049	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome. <i>Nature Human Behaviour</i> , 2021, 5, 482-496.	12.0	30
1050	CSEA-DB: an omnibus for human complex trait and cell type associations. <i>Nucleic Acids Research</i> , 2021, 49, D862-D870.	14.5	21
1051	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 372-387.	3.6	12
1052	Delineating the Genetic Component of Gene Expression in Major Depression. <i>Biological Psychiatry</i> , 2021, 89, 627-636.	1.3	63
1053	Inverse association of FCER1A allergy variant in monocytes and plasmacytoid dendritic cells. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1510-1513.e8.	2.9	4
1054	Leveraging phenotypic variability to identify genetic interactions in human phenotypes. <i>American Journal of Human Genetics</i> , 2021, 108, 49-67.	6.2	36

#	ARTICLE	IF	CITATIONS
1055	HeRA: an atlas of enhancer RNAs across human tissues. <i>Nucleic Acids Research</i> , 2021, 49, D932-D938.	14.5	27
1056	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. <i>Movement Disorders</i> , 2021, 36, 449-459.	3.9	16
1057	Investigating an in silico approach for prioritizing antidepressant drug prescription based on drug-induced expression profiles and predicted gene expression. <i>Pharmacogenomics Journal</i> , 2021, 21, 85-93.	2.0	1
1058	Parsing multiomics landscape of activated synovial fibroblasts highlights drug targets linked to genetic risk of rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 440-450.	0.9	29
1059	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	5.2	42
1060	Genetically Determined Levels of Serum Metabolites and Risk of Neuroticism: A Mendelian Randomization Study. <i>International Journal of Neuropsychopharmacology</i> , 2021, 24, 32-39.	2.1	5
1061	An approach for normalization and quality control for NanoString RNA expression data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	67
1062	Independent replications and integrative analyses confirm TRANK1 as a susceptibility gene for bipolar disorder. <i>Neuropsychopharmacology</i> , 2021, 46, 1103-1112.	5.4	20
1063	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 80-90.	3.6	5
1064	DNA methylation profiles unique to Kalahari KhoeSan individuals. <i>Epigenetics</i> , 2021, 16, 537-553.	2.7	2
1065	Dream: powerful differential expression analysis for repeated measures designs. <i>Bioinformatics</i> , 2021, 37, 192-201.	4.1	138
1066	Virtual Histology of Cortical Thickness and Shared Neurobiology in 6 Psychiatric Disorders. <i>JAMA Psychiatry</i> , 2021, 78, 47.	11.0	136
1067	Allele-specific expression and high-throughput reporter assay reveal functional genetic variants associated with alcohol use disorders. <i>Molecular Psychiatry</i> , 2021, 26, 1142-1151.	7.9	26
1068	An Empirical Bayes approach for the identification of long-range chromosomal interaction from Hi-C data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2021, 20, 1-15.	0.6	0
1070	Advances in Lung Cancer Driver Genes Associated With Brain Metastasis. <i>Frontiers in Oncology</i> , 2020, 10, 606300.	2.8	12
1071	A broad introduction to RNA-Seq. <i>WikiJournal of Science</i> , 2021, 4, 4.	0.1	0
1072	Population-scale genetic control of alternative polyadenylation and its association with human diseases. <i>Quantitative Biology</i> , 2022, 10, 44-54.	0.5	2
1073	The pleiotropic functions of autophagy in metastasis. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	23

#	ARTICLE	IF	CITATIONS
1074	Multi-environment gene interactions linked to the interplay between polysubstance dependence and suicidality. <i>Translational Psychiatry</i> , 2021, 11, 34.	4.8	20
1075	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. <i>PLoS Genetics</i> , 2021, 17, e1009224.	3.5	43
1076	Making a family decision to donate the brain for genomic research: lessons from the genotype-tissue expression project (GTEx). <i>Cell and Tissue Banking</i> , 2021, 22, 431-441.	1.1	5
1079	Gene expression in major depressive disorder: Peripheral tissue and brain-based studies. , 2021, , 515-526.		0
1080	Proinflammatory Signaling Pathways and Genomic Signatures in Head and Neck Cancers. , 2021, , 143-184.		2
1082	Patterns of de novo tandem repeat mutations and their role in autism. <i>Nature</i> , 2021, 589, 246-250.	27.8	114
1083	Novel directions in data pre-processing and genome-wide association study (GWAS) methodologies to overcome ongoing challenges. <i>Informatics in Medicine Unlocked</i> , 2021, 24, 100586.	3.4	2
1084	Strategies for diseases prevention: the role of the general practitioner and primary health care. <i>Profilakticheskaya Meditsina</i> , 2021, 24, 7.	0.6	5
1085	Functional variants fine-mapping and gene function characterization provide insights into the role of ZNF323 in schizophrenia pathogenesis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 28-39.	1.7	8
1087	Genetic analysis of amyotrophic lateral sclerosis identifies contributing pathways and cell types. <i>Science Advances</i> , 2021, 7, .	10.3	59
1088	Using iPSC Models to Understand the Role of Estrogen in Neuron-Glia Interactions in Schizophrenia and Bipolar Disorder. <i>Cells</i> , 2021, 10, 209.	4.1	7
1089	Causal network inference from gene transcriptional time-series response to glucocorticoids. <i>PLoS Computational Biology</i> , 2021, 17, e1008223.	3.2	20
1090	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, 49.	8.8	150
1092	Selective Serotonin Reuptake Inhibitor Pharmacogenomics: Mechanisms and Prediction. <i>Frontiers in Pharmacology</i> , 2020, 11, 614048.	3.5	10
1094	Transcriptome wide association studies: general framework and methods. <i>Quantitative Biology</i> , 2021, 9, 141-150.	0.5	2
1095	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021, 6, 16.	1.8	90
1096	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. <i>Nature Neuroscience</i> , 2021, 24, 176-185.	14.8	73
1097	Efficient phasing and imputation of low-coverage sequencing data using large reference panels. <i>Nature Genetics</i> , 2021, 53, 120-126.	21.4	184

#	ARTICLE	IF	CITATIONS
1098	Water as a reactant in the differential expression of proteins in cancer. Computational and Systems Oncology, 2021, 1, e1007.	1.5	6
1099	New novel non-MHC genes were identified for cervical cancer with an integrative analysis approach of transcriptome-wide association study. Journal of Cancer, 2021, 12, 840-848.	2.5	7
1100	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. Journal of Clinical Investigation, 2021, 131, .	8.2	23
1101	SARS-CoV-2 infection susceptibility influenced by ACE2 genetic polymorphisms: insights from Tehran Cardio-Metabolic Genetic Study. Scientific Reports, 2021, 11, 1529.	3.3	25
1102	rs1990622 variant associates with Alzheimer's disease and regulates TMEM106B expression in human brain tissues. BMC Medicine, 2021, 19, 11.	5.5	57
1103	Detection of aberrant gene expression events in RNA sequencing data. Nature Protocols, 2021, 16, 1276-1296.	12.0	58
1104	The association between hypertension and nonalcoholic fatty liver disease (NAFLD): literature evidence and systems biology analysis. Bioengineered, 2021, 12, 2187-2202.	3.2	18
1105	Genetic loci shared between major depression and intelligence with mixed directions of effect. Nature Human Behaviour, 2021, 5, 795-801.	12.0	23
1106	Multi-omics analysis to identify susceptibility genes for colorectal cancer. Human Molecular Genetics, 2021, 30, 321-330.	2.9	13
1111	Evolutionary conservation and divergence of the human brain transcriptome. Genome Biology, 2021, 22, 52.	8.8	28
1112	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. Nature Communications, 2021, 12, 266.	12.8	87
1113	Statistical methods for mediation analysis in the era of high-throughput genomics: Current successes and future challenges. Computational and Structural Biotechnology Journal, 2021, 19, 3209-3224.	4.1	40
1114	Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. Nature Genetics, 2021, 53, 166-173.	21.4	49
1115	Chromatin information content landscapes inform transcription factor and DNA interactions. Nature Communications, 2021, 12, 1307.	12.8	19
1116	Identifying Thyroid Carcinoma-Related Genes by Integrating GWAS and eQTL Data. Frontiers in Cell and Developmental Biology, 2021, 9, 645275.	3.7	3
1117	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease. Translational Psychiatry, 2021, 11, 146.	4.8	13
1118	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	12.8	68
1122	Genetic Architecture Underlying the Metabolites of Chlorogenic Acid Biosynthesis in Populus tomentosa. International Journal of Molecular Sciences, 2021, 22, 2386.	4.1	7

#	ARTICLE	IF	CITATIONS
1123	Hippocampal transcriptome-wide association study and neurobiological pathway analysis for Alzheimer's disease. <i>PLoS Genetics</i> , 2021, 17, e1009363.	3.5	18
1125	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. <i>Human Molecular Genetics</i> , 2021, 30, 603-618.	2.9	5
1126	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	38
1127	Imputed gene expression risk scores: a functionally informed component of polygenic risk. <i>Human Molecular Genetics</i> , 2021, 30, 727-738.	2.9	11
1128	Genetically Predicted Blood Pressure and Risk of Atrial Fibrillation. <i>Hypertension</i> , 2021, 77, 376-382.	2.7	16
1129	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. <i>Nature Communications</i> , 2021, 12, 730.	12.8	9
1130	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021, 7, .	10.3	78
1131	Rare genetic variants affecting urine metabolite levels link population variation to inborn errors of metabolism. <i>Nature Communications</i> , 2021, 12, 964.	12.8	20
1132	A molecular quantitative trait locus map for osteoarthritis. <i>Nature Communications</i> , 2021, 12, 1309.	12.8	53
1133	SNPs associated with colorectal cancer at 15q13.3 affect risk enhancers that modulate <i>GREM1</i> gene expression. <i>Human Mutation</i> , 2021, 42, 237-245.	2.5	9
1134	Genetic contributions to autism spectrum disorder. <i>Psychological Medicine</i> , 2021, 51, 2260-2273.	4.5	67
1135	PICS2: next-generation fine mapping via probabilistic identification of causal SNPs. <i>Bioinformatics</i> , 2021, 37, 3004-3007.	4.1	21
1136	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. <i>PLoS Genetics</i> , 2021, 17, e1009309.	3.5	14
1137	Association of Genetic Variants With Migraine Subclassified by Clinical Symptoms in Adult Females. <i>Frontiers in Neurology</i> , 2020, 11, 617472.	2.4	5
1138	Potential biomarkers and lncRNA-mRNA regulatory networks in invasive growth hormone-secreting pituitary adenomas. <i>Journal of Endocrinological Investigation</i> , 2021, 44, 1947-1959.	3.3	9
1139	Altered Blood Cell Traits Underlie a Major Genetic Locus of Severe COVID-19. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, e147-e154.	3.6	12
1140	Genetic determinants of daytime napping and effects on cardiometabolic health. <i>Nature Communications</i> , 2021, 12, 900.	12.8	136
1141	Inherited Kidney Complement Diseases. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2021, 16, 942-956.	4.5	34

#	ARTICLE	IF	CITATIONS
1142	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. <i>ELife</i> , 2021, 10, .	6.0	41
1143	Inflammation status modulates the effect of host genetic variation on intestinal gene expression in inflammatory bowel disease. <i>Nature Communications</i> , 2021, 12, 1122.	12.8	16
1144	A Systems Biology Approach to Investigating the Interaction between Serotonin Synthesis by Tryptophan Hydroxylase and the Metabolic Homeostasis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2452.	4.1	12
1145	Elucidation of disease etiology by trans-layer omics analysis. <i>Inflammation and Regeneration</i> , 2021, 41, 6.	3.7	2
1147	<i>Trans</i>-acting genetic variation affects the expression of adjacent genes. <i>Genetics</i> , 2021, 217, .	2.9	4
1149	Elevation in viral entry genes and innate immunity compromise underlying increased infectivity and severity of COVID-19 in cancer patients. <i>Scientific Reports</i> , 2021, 11, 4533.	3.3	6
1150	Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. <i>Human Molecular Genetics</i> , 2021, 30, 294-304.	2.9	17
1151	A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity. <i>Nature Medicine</i> , 2021, 27, 659-667.	30.7	188
1153	Evolution, structure and emerging roles of C1ORF112 in DNA replication, DNA damage responses, and cancer. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4365-4376.	5.4	14
1154	Integrative Analysis of Omics Data Reveals Regulatory Network of CDK10 in Vitiligo Risk. <i>Frontiers in Genetics</i> , 2021, 12, 634553.	2.3	5
1155	Topologically associating domain boundaries that are stable across diverse cell types are evolutionarily constrained and enriched for heritability. <i>American Journal of Human Genetics</i> , 2021, 108, 269-283.	6.2	117
1156	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. <i>Nature Communications</i> , 2021, 12, 727.	12.8	83
1157	A fast and efficient colocalization algorithm for identifying shared genetic risk factors across multiple traits. <i>Nature Communications</i> , 2021, 12, 764.	12.8	195
1158	Sexual dimorphism in cancer: insights from transcriptional signatures in kidney tissue and renal cell carcinoma. <i>Human Molecular Genetics</i> , 2021, 30, 343-355.	2.9	14
1159	CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. <i>Bioinformatics</i> , 2021, 37, 2513-2520.	4.1	4
1160	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021, 6, 16.	1.8	48
1161	Integrative analysis identifies potential causal methylation-mRNA regulation chains for rheumatoid arthritis. <i>Molecular Immunology</i> , 2021, 131, 89-96.	2.2	6
1162	Integrating genomics with biomarkers and therapeutic targets to invigorate cardiovascular drug development. <i>Nature Reviews Cardiology</i> , 2021, 18, 435-453.	13.7	88

#	ARTICLE	IF	CITATIONS
1167	Global proteomic analysis of extracellular matrix in mouse and human brain highlights relevance to cerebrovascular disease. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2021, 41, 2423-2438.	4.3	14
1168	Hyperbolic geometry of gene expression. <i>IScience</i> , 2021, 24, 102225.	4.1	15
1170	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. <i>Nature Genetics</i> , 2021, 53, 313-321.	21.4	42
1171	Single cell eQTL analysis identifies cell type-specific genetic control of gene expression in fibroblasts and reprogrammed induced pluripotent stem cells. <i>Genome Biology</i> , 2021, 22, 76.	8.8	58
1173	Single nucleotide variations in <i>ZBTB46</i> are associated with post-thrombolytic parenchymal haematoma. <i>Brain</i> , 2021, 144, 2416-2426.	7.6	10
1174	Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	31
1175	Genetic variation and microRNA targeting of A-to-I RNA editing fine tune human tissue transcriptomes. <i>Genome Biology</i> , 2021, 22, 77.	8.8	26
1176	Common Genetic Variation in Humans Impacts In Vitro Susceptibility to SARS-CoV-2 Infection. <i>Stem Cell Reports</i> , 2021, 16, 505-518.	4.8	39
1177	Genome-wide association study of fish oil supplementation on lipid traits in 81,246 individuals reveals new gene-diet interaction loci. <i>PLoS Genetics</i> , 2021, 17, e1009431.	3.5	24
1178	Genetic architecture of four smoking behaviors using partitioned SNP heritability. <i>Addiction</i> , 2021, 116, 2498-2508.	3.3	14
1179	Identification of genetic factors influencing metabolic dysregulation and retinal support for MacTel, a retinal disorder. <i>Communications Biology</i> , 2021, 4, 274.	4.4	26
1180	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , 2021, 53, 304-312.	21.4	146
1182	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	8.9	14
1184	Ethnic and trans-ethnic genome-wide association studies identify new loci influencing Japanese Alzheimer's disease risk. <i>Translational Psychiatry</i> , 2021, 11, 151.	4.8	34
1187	The case for using mapped exonic non-duplicate reads when reporting RNA-sequencing depth: examples from pediatric cancer datasets. <i>GigaScience</i> , 2021, 10, .	6.4	2
1188	An Integrative Transcriptome-Wide Analysis of Amyotrophic Lateral Sclerosis for the Identification of Potential Genetic Markers and Drug Candidates. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3216.	4.1	12
1189	Genetic control of the human brain proteome. <i>American Journal of Human Genetics</i> , 2021, 108, 400-410.	6.2	52
1190	Systematic characterization of mutations altering protein degradation in human cancers. <i>Molecular Cell</i> , 2021, 81, 1292-1308.e11.	9.7	36

#	ARTICLE	IF	CITATIONS
1192	Nonlinear ridge regression improves cell-type-specific differential expression analysis. BMC Bioinformatics, 2021, 22, 141.	2.6	3
1193	Joint analysis of expression levels and histological images identifies genes associated with tissue morphology. Nature Communications, 2021, 12, 1609.	12.8	45
1195	Targeting androgen regulation of TMPRSS2 and ACE2 as a therapeutic strategy to combat COVID-19. IScience, 2021, 24, 102254.	4.1	72
1197	Common X-chromosome Variants Are Associated with Parkinson Disease Risk. Annals of Neurology, 2021, 90, 22-34.	5.3	28
1198	Polymorphisms of the matrix metalloproteinase genes are associated with essential hypertension in a Caucasian population of Central Russia. Scientific Reports, 2021, 11, 5224.	3.3	34
1199	Genetics of osteoarthritis. Osteoarthritis and Cartilage, 2022, 30, 636-649.	1.3	53
1200	Gene co-expression network analysis in human spinal cord highlights mechanisms underlying amyotrophic lateral sclerosis susceptibility. Scientific Reports, 2021, 11, 5748.	3.3	14
1202	Genome-wide association study of suicidal behaviour severity in mood disorders. World Journal of Biological Psychiatry, 2021, 22, 1-19.	2.6	3
1204	The origins and genetic interactions of KRAS mutations are allele- and tissue-specific. Nature Communications, 2021, 12, 1808.	12.8	90
1205	A first-generation pediatric cancer dependency map. Nature Genetics, 2021, 53, 529-538.	21.4	76
1206	Telomerase as a Therapeutic Target in Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1047-1061.	2.4	41
1207	Positive Controls in Adults and Children Support That Very Few, If Any, New Neurons Are Born in the Adult Human Hippocampus. Journal of Neuroscience, 2021, 41, 2554-2565.	3.6	90
1208	Variants in NEB and RIF1 genes on chr2q23 are associated with skeletal muscle index in Koreans: genome-wide association study. Scientific Reports, 2021, 11, 2333.	3.3	1
1209	Emerging Role of ODC1 in Neurodevelopmental Disorders and Brain Development. Genes, 2021, 12, 470.	2.4	15
1211	Shared associations identify causal relationships between gene expression and immune cell phenotypes. Communications Biology, 2021, 4, 279.	4.4	3
1212	Colocalization analysis of polycystic ovary syndrome to identify potential disease-mediating genes and proteins. European Journal of Human Genetics, 2021, 29, 1446-1454.	2.8	12
1213	A versatile platform for locus-scale genome rewriting and verification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
1214	Association of CSF proteins with tau and amyloid β^2 levels in asymptomatic 70-year-olds. Alzheimer's Research and Therapy, 2021, 13, 54.	6.2	9

#	ARTICLE	IF	CITATIONS
1215	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. <i>Nature Genetics</i> , 2021, 53, 445-454.	21.4	61
1216	Epigenetic and metabolic regulation of epidermal homeostasis. <i>Experimental Dermatology</i> , 2021, 30, 1009-1022.	2.9	11
1217	Editing GWAS: experimental approaches to dissect and exploit disease-associated genetic variation. <i>Genome Medicine</i> , 2021, 13, 41.	8.2	32
1220	Novel lincRNA Discovery and Tissue-Specific Gene Expression across 30 Normal Human Tissues. <i>Genes</i> , 2021, 12, 614.	2.4	4
1221	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. <i>PLoS Genetics</i> , 2021, 17, e1009455.	3.5	24
1224	eQTLHap: a tool for comprehensive eQTL analysis considering haplotypic and genotypic effects. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	0
1225	Tissue specificity-aware TWAS (TSA-TWAS) framework identifies novel associations with metabolic, immunologic, and virologic traits in HIV-positive adults. <i>PLoS Genetics</i> , 2021, 17, e1009464.	3.5	11
1226	The landscape of molecular chaperones across human tissues reveals a layered architecture of core and variable chaperones. <i>Nature Communications</i> , 2021, 12, 2180.	12.8	62
1227	Gene Expression Differences Between Young Adults Based on Trauma History and Post-traumatic Stress Disorder. <i>Frontiers in Psychiatry</i> , 2021, 12, 581093.	2.6	0
1228	Cell-type-specific expression quantitative trait loci associated with Alzheimer disease in blood and brain tissue. <i>Translational Psychiatry</i> , 2021, 11, 250.	4.8	29
1229	Identification of Three Novel Susceptibility Loci for Inflammatory Bowel Disease in Koreans in an Extended Genome-Wide Association Study. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 1898-1907.	1.3	13
1230	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. <i>American Journal of Human Genetics</i> , 2021, 108, 669-681.	6.2	8
1231	Using CRISPR to understand and manipulate gene regulation. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	9
1232	RNA Dysregulation: An Expanding Source of Cancer Immunotherapy Targets. <i>Trends in Pharmacological Sciences</i> , 2021, 42, 268-282.	8.7	39
1233	Novel Variance-Component TWAS method for studying complex human diseases with applications to Alzheimer's dementia. <i>PLoS Genetics</i> , 2021, 17, e1009482.	3.5	36
1234	Variable number tandem repeats mediate the expression of proximal genes. <i>Nature Communications</i> , 2021, 12, 2075.	12.8	47
1235	Association of Genetic Variants for Plasma LRG1 With Rapid Decline in Kidney Function in Patients With Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 2384-2394.	3.6	9
1237	Characterizing the Expression Patterns of Parkinson's Disease Associated Genes. <i>Frontiers in Neuroscience</i> , 2021, 15, 629156.	2.8	6

#	ARTICLE	IF	CITATIONS
1239	pyrpipe : a Python package for RNA-Seq workflows. NAR Genomics and Bioinformatics, 2021, 3, lqab049.	3.2	14
1240	Urine Metabolite Levels, Adverse Kidney Outcomes, and Mortality in CKD Patients: A Metabolome-wide Association Study. American Journal of Kidney Diseases, 2021, 78, 669-677.e1.	1.9	22
1241	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.7	14
1242	Whole-exome sequencing identifies genes associated with Tourette's disorder in multiplex families. Molecular Psychiatry, 2021, , .	7.9	16
1243	Spatial Expression Pattern of <i>ZNF391</i> Gene in the Brains of Patients With Schizophrenia, Bipolar Disorders or Major Depressive Disorder Identifies New Cross-Disorder Biotypes: A Trans-Diagnostic, Top-Down Approach. Schizophrenia Bulletin, 2021, 47, 1351-1363.	4.3	4
1244	Sex-stratified genome-wide association study of multisite chronic pain in UK Biobank. PLoS Genetics, 2021, 17, e1009428.	3.5	37
1245	Analysis of TERT Isoforms across TCGA, GTEx and CCLE Datasets. Cancers, 2021, 13, 1853.	3.7	5
1247	A cross-tissue transcriptome-wide association study identifies novel susceptibility genes for lung cancer in Chinese populations. Human Molecular Genetics, 2021, 30, 1666-1676.	2.9	9
1248	Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. Genome Research, 2021, 31, 1807-1818.	5.5	40
1249	Analysis of Brugada syndrome loci reveals that fine-mapping clustered GWAS hits enhances the annotation of disease-relevant variants. Cell Reports Medicine, 2021, 2, 100250.	6.5	4
1250	The functional polymorphisms linked with interleukin-1 β gene expression are associated with bipolar disorder. Psychiatric Genetics, 2021, 31, 72-78.	1.1	3
1251	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. Journal of Investigative Dermatology, 2021, 141, 2620-2629.	0.7	12
1252	Mendelian randomization integrating GWAS and eQTL data revealed genes pleiotropically associated with major depressive disorder. Translational Psychiatry, 2021, 11, 225.	4.8	19
1253	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	27.8	332
1254	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	8.8	2
1255	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.	1.3	10
1256	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. Frontiers in Genetics, 2021, 12, 624128.	2.3	14
1257	Combined epigenetic/genetic study identified an ALS age of onset modifier. Acta Neuropathologica Communications, 2021, 9, 75.	5.2	7

#	ARTICLE	IF	CITATIONS
1258	Association of polymorphisms in <i>ZFHX1B</i> , <i>KCNQ5</i> and <i>GJD2</i> with myopia progression and polygenic risk prediction in children. <i>British Journal of Ophthalmology</i> , 2021, 105, 1751-1757.	3.9	5
1260	Pleiotropic effects of telomere length loci with brain morphology and brain tissue expression. <i>Human Molecular Genetics</i> , 2021, 30, 1360-1370.	2.9	4
1261	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. <i>Diabetes</i> , 2021, 70, 1581-1591.	0.6	7
1262	Evolution of DNA methylation in the human brain. <i>Nature Communications</i> , 2021, 12, 2021.	12.8	53
1263	Predicting tissue-specific gene expression from whole blood transcriptome. <i>Science Advances</i> , 2021, 7, .	10.3	50
1266	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank. <i>Nature Neuroscience</i> , 2021, 24, 737-745.	14.8	212
1267	Beyond association: successes and challenges in linking non-coding genetic variation to functional consequences that modulate Alzheimer's disease risk. <i>Molecular Neurodegeneration</i> , 2021, 16, 27.	10.8	20
1268	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	12.8	32
1269	The impact of cell type and context-dependent regulatory variants on human immune traits. <i>Genome Biology</i> , 2021, 22, 122.	8.8	32
1270	A robust two-sample transcriptome-wide Mendelian randomization method integrating GWAS with multi-tissue eQTL summary statistics. <i>Genetic Epidemiology</i> , 2021, 45, 353-371.	1.3	11
1271	Bronchial gene expression signature associated with rate of subsequent FEV ₁ decline in individuals with and at risk of COPD. <i>Thorax</i> , 2022, 77, 31-39.	5.6	8
1272	Multi-omic analysis elucidates the genetic basis of hydrocephalus. <i>Cell Reports</i> , 2021, 35, 109085.	6.4	18
1274	A Novel Phenotype of Junctional Epidermolysis Bullosa with Transient Skin Fragility and Predominant Ocular Involvement Responsive to Human Amniotic Membrane Eyedrops. <i>Genes</i> , 2021, 12, 716.	2.4	5
1276	Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. <i>Npj Systems Biology and Applications</i> , 2021, 7, 24.	3.0	7
1277	High Resolution Haplotype Analyses of Classical HLA Genes in Families With Multiple Sclerosis Highlights the Role of HLA-DP Alleles in Disease Susceptibility. <i>Frontiers in Immunology</i> , 2021, 12, 644838.	4.8	5
1278	LRRK2 Gene Variants Associated With a Higher Risk for Alcohol Dependence in Multiethnic Populations. <i>Frontiers in Psychiatry</i> , 2021, 12, 665257.	2.6	3
1279	Genetic basis of lacunar stroke: a pooled analysis of individual patient data and genome-wide association studies. <i>Lancet Neurology</i> , The, 2021, 20, 351-361.	10.2	95
1280	Modeling the Evolutionary Architectures of Transcribed Human Enhancer Sequences Reveals Distinct Origins, Functions, and Associations with Human Trait Variation. <i>Molecular Biology and Evolution</i> , 2021, 38, 3681-3696.	8.9	7

#	ARTICLE	IF	CITATIONS
1281	Host Genome-Wide Association Study of Infant Susceptibility to <i>Shigella</i> -Associated Diarrhea. Infection and Immunity, 2021, 89, .	2.2	12
1282	Review of multi-omics data resources and integrative analysis for human brain disorders. Briefings in Functional Genomics, 2021, 20, 223-234.	2.7	19
1283	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.	21.4	629
1284	Ultraviolet light-induced collagen degradation inhibits melanoma invasion. Nature Communications, 2021, 12, 2742.	12.8	25
1286	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402.	27.8	170
1287	Chromatin accessibility in neuropsychiatric disorders. Neurobiology of Learning and Memory, 2021, 181, 107438.	1.9	2
1288	Integrative genomics analysis reveals a 21q22.11 locus contributing risk to COVID-19. Human Molecular Genetics, 2021, 30, 1247-1258.	2.9	28
1289	Identification of the conserved long non-coding RNAs in myogenesis. BMC Genomics, 2021, 22, 336.	2.8	0
1290	Modeling regulatory network topology improves genome-wide analyses of complex human traits. Nature Communications, 2021, 12, 2851.	12.8	17
1291	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. Nature Neuroscience, 2021, 24, 941-953.	14.8	47
1292	Cancer microenvironment and genomics: evolution in process. Clinical and Experimental Metastasis, 2022, 39, 85-99.	3.3	11
1293	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. Scientific Reports, 2021, 11, 10606.	3.3	4
1294	Single cell RNA-seq analysis of the flexor digitorum brevis mouse myofibers. Skeletal Muscle, 2021, 11, 13.	4.2	6
1296	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	21.4	37
1297	KIF18B is a Prognostic Biomarker and Correlates with Immune Infiltrates in Pan-Cancer. Frontiers in Molecular Biosciences, 2021, 8, 559800.	3.5	12
1298	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.	3.6	3
1300	Learning a genome-wide score of human-mouse conservation at the functional genomics level. Nature Communications, 2021, 12, 2495.	12.8	12
1302	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	5.4	12

#	ARTICLE	IF	CITATIONS
1303	Nuku, a family of primate retrocopies derived from <i>KU70</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
1304	Prostate cancer risk variants of the HOXB genetic locus. <i>Scientific Reports</i> , 2021, 11, 11385.	3.3	6
1305	Leveraging eQTLs to identify individual-level tissue of interest for a complex trait. <i>PLoS Computational Biology</i> , 2021, 17, e1008915.	3.2	3
1307	Genome-wide analysis identifies a novel LINC-PINT splice variant associated with vascular amyloid pathology in Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2021, 9, 93.	5.2	9
1309	Unveiling the neuroimaging-genetic intersections in the human brain. <i>Current Opinion in Neurology</i> , 2021, 34, 480-487.	3.6	13
1310	Connecting the epigenome, metabolome and proteome for a deeper understanding of disease. <i>Journal of Internal Medicine</i> , 2021, 290, 527-548.	6.0	5
1311	Integration of Immunome With Disease-Gene Network Reveals Common Cellular Mechanisms Between IMiDs and Drug Repurposing Strategies. <i>Frontiers in Immunology</i> , 2021, 12, 669400.	4.8	5
1312	Pervasive cis effects of variation in copy number of large tandem repeats on local DNA methylation and gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 809-824.	6.2	30
1313	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinson's disease. <i>Nature Genetics</i> , 2021, 53, 787-793.	21.4	82
1314	Enhancer release and retargeting activates disease-susceptibility genes. <i>Nature</i> , 2021, 595, 735-740.	27.8	76
1316	Integrative genomic analysis of blood pressure and related phenotypes in rats. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	2.4	6
1317	An Intronic Risk SNP rs12454712 for Central Obesity Acts As an Allele-Specific Enhancer To Regulate <i>BCL2</i> Expression. <i>Diabetes</i> , 2021, 70, 1679-1688.	0.6	10
1319	An atlas of alternative polyadenylation quantitative trait loci contributing to complex trait and disease heritability. <i>Nature Genetics</i> , 2021, 53, 994-1005.	21.4	85
1320	Tejaas: reverse regression increases power for detecting trans-eQTLs. <i>Genome Biology</i> , 2021, 22, 142.	8.8	4
1321	Schizophrenia: a classic battle ground of nature versus nurture debate. <i>Science Bulletin</i> , 2021, 66, 1037-1046.	9.0	4
1322	ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel. <i>Biostatistics</i> , 2023, 24, 388-405.	1.5	0
1323	Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. <i>Nature Communications</i> , 2021, 12, 3152.	12.8	17
1324	Tissue context determines the penetrance of regulatory DNA variation. <i>Nature Communications</i> , 2021, 12, 2850.	12.8	13

#	ARTICLE	IF	CITATIONS
1325	Transcriptome-wide association study uncovers the role of essential genes in anthracycline-induced cardiotoxicity. <i>Npj Genomic Medicine</i> , 2021, 6, 35.	3.8	7
1328	Dynamic landscape of immune cell-specific gene regulation in immune-mediated diseases. <i>Cell</i> , 2021, 184, 3006-3021.e17.	28.9	147
1330	Brain gene co-expression networks link complement signaling with convergent synaptic pathology in schizophrenia. <i>Nature Neuroscience</i> , 2021, 24, 799-809.	14.8	44
1331	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
1332	Introducing ADNP and SIRT1 as new partners regulating microtubules and histone methylation. <i>Molecular Psychiatry</i> , 2021, 26, 6550-6561.	7.9	25
1333	Epistatic interactions of genetic loci associated with age-related macular degeneration. <i>Scientific Reports</i> , 2021, 11, 13114.	3.3	4
1334	Genomics of Gulf War Illness in U.S. Veterans Who Served during the 1990â€“1991 Persian Gulf War: Methods and Rationale for Veterans Affairs Cooperative Study #2006. <i>Brain Sciences</i> , 2021, 11, 845.	2.3	7
1335	GSEApot: A Package for Customizing Gene Set Enrichment Analysis in R. <i>Journal of Computational Biology</i> , 2021, 28, 629-631.	1.6	12
1336	Assessment of prognostic prediction models for gastric cancer using genomic and transcriptomic profiles. <i>Meta Gene</i> , 2021, 28, 100890.	0.6	0
1337	Genetic architecture of 11 organ traits derived from abdominal MRI using deep learning. <i>ELife</i> , 2021, 10, .	6.0	102
1338	Rare variants regulate expression of nearby individual genes in multiple tissues. <i>PLoS Genetics</i> , 2021, 17, e1009596.	3.5	6
1341	Replicate sequencing libraries are important for quantification of allelic imbalance. <i>Nature Communications</i> , 2021, 12, 3370.	12.8	13
1342	A pig BodyMap transcriptome reveals diverse tissue physiologies and evolutionary dynamics of transcription. <i>Nature Communications</i> , 2021, 12, 3715.	12.8	60
1343	Stage 2 Registered Report: Variation in neurodevelopmental outcomes in children with sex chromosome trisomies: testing the double hit hypothesis. <i>Wellcome Open Research</i> , 2018, 3, 85.	1.8	7
1345	Shared genetic architecture between neuroticism, coronary artery disease and cardiovascular risk factors. <i>Translational Psychiatry</i> , 2021, 11, 368.	4.8	10
1346	Optimizing expression quantitative trait locus mapping workflows for single-cell studies. <i>Genome Biology</i> , 2021, 22, 188.	8.8	36
1349	Genetic underpinnings of affective temperaments: a pilot GWAS investigation identifies a new genome-wide significant SNP for anxious temperament in ADGRB3 gene. <i>Translational Psychiatry</i> , 2021, 11, 337.	4.8	9
1350	Multitrait transcriptome-wide association study (TWAS) tests. <i>Genetic Epidemiology</i> , 2021, 45, 563-576.	1.3	9

#	ARTICLE	IF	CITATIONS
1351	Chemical map-based prediction of nucleosome positioning using the Bioconductor package nuCpos. BMC Bioinformatics, 2021, 22, 322.	2.6	5
1353	Leveraging supervised learning for functionally informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	12.8	44
1354	Multi-Omics Approaches in Immunological Research. Frontiers in Immunology, 2021, 12, 668045.	4.8	22
1355	Functionally significant polymorphisms of the MMP-9 gene are associated with peptic ulcer disease in the Caucasian population of Central Russia. Scientific Reports, 2021, 11, 13515.	3.3	27
1357	Shared genetic study gives insights into the shared and distinct pathogenic immunity components of IgA nephropathy and SLE. Molecular Genetics and Genomics, 2021, 296, 1017-1026.	2.1	4
1358	Systematic analysis of exonic germline and postzygotic de novo mutations in bipolar disorder. Nature Communications, 2021, 12, 3750.	12.8	15
1361	Detection of quantitative trait loci from RNA-seq data with or without genotypes using BaseQTL. Nature Computational Science, 2021, 1, 421-432.	8.0	8
1363	A trans locus causes a ribosomopathy in hypertrophic hearts that affects mRNA translation in a protein length-dependent fashion. Genome Biology, 2021, 22, 191.	8.8	4
1364	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.	3.1	12
1365	Systems genetics in diversity outbred mice inform BMD GWAS and identify determinants of bone strength. Nature Communications, 2021, 12, 3408.	12.8	31
1367	A covariance-enhanced approach to multitissue joint eQTL mapping with application to transcriptome-wide association studies. Annals of Applied Statistics, 2021, 15, 998-1016.	1.1	0
1369	Brain-Specific Gene Expression and Quantitative Traits Association Analysis for Mild Cognitive Impairment. Biomedicine, 2021, 9, 658.	3.2	3
1370	Regulatory SNPs: Altered Transcription Factor Binding Sites Implicated in Complex Traits and Diseases. International Journal of Molecular Sciences, 2021, 22, 6454.	4.1	29
1371	Integrative approaches generate insights into the architecture of non-syndromic cleft lip \pm cleft palate. Human Genetics and Genomics Advances, 2021, 2, 100038.	1.7	8
1372	Grand Challenges in Bioinformatics Data Visualization. Frontiers in Bioinformatics, 2021, 1, .	2.1	18
1373	Prioritization of candidate causal genes for asthma in susceptibility loci derived from UK Biobank. Communications Biology, 2021, 4, 700.	4.4	77
1374	Stratifying Cumulus Cell Samples Based on Molecular Profiling to Help Resolve Biomarker Discrepancies and to Predict Oocyte Developmental Competence. International Journal of Molecular Sciences, 2021, 22, 6377.	4.1	2
1375	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. Frontiers in Molecular Biosciences, 2021, 8, 647277.	3.5	12

#	ARTICLE	IF	CITATIONS
1376	Multitomic analysis of the function of <i>SPOCK1</i> across cancers: an integrated bioinformatics approach. Journal of International Medical Research, 2021, 49, 030006052096265.	1.0	5
1377	Genetic mechanisms of COVID-19 and its association with smoking and alcohol consumption. Briefings in Bioinformatics, 2021, 22, .	6.5	31
1378	Editorial for the Special Issue on Micro/Nanofluidic Devices for Single Cell Analysis, Volume II. Micromachines, 2021, 12, 875.	2.9	2
1380	Tissue-specific expression of p73 and p63 isoforms in human tissues. Cell Death and Disease, 2021, 12, 745.	6.3	13
1381	An autoimmune disease risk variant: A trans master regulatory effect mediated by IRF1 under immune stimulation?. PLoS Genetics, 2021, 17, e1009684.	3.5	17
1382	Predicting pathogenic non-coding SVs disrupting the 3D genome in 1646 whole cancer genomes using multiple instance learning. Scientific Reports, 2021, 11, 14411.	3.3	1
1383	RBM20 Is a Candidate Gene for Hypertrophic Cardiomyopathy. Canadian Journal of Cardiology, 2021, 37, 1751-1759.	1.7	10
1384	VarSAn: associating pathways with a set of genomic variants using network analysis. Nucleic Acids Research, 2021, 49, 8471-8487.	14.5	1
1386	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. Nature Communications, 2021, 12, 4178.	12.8	20
1388	Genetic Variants Associated With Intraparenchymal Hemorrhage Progression After Traumatic Brain Injury. JAMA Network Open, 2021, 4, e2116839.	5.9	11
1390	Investigation of convergent and divergent genetic influences underlying schizophrenia and alcohol use disorder. Psychological Medicine, 2023, 53, 1196-1204.	4.5	7
1391	Mendelian randomization analysis identified genes potentially pleiotropically associated with periodontitis. Saudi Journal of Biological Sciences, 2021, 28, 4089-4095.	3.8	4
1392	Global Genetic Heterogeneity in Adaptive Traits. Molecular Biology and Evolution, 2021, 38, 4822-4831.	8.9	27
1393	Enhancers with tissue-specific activity are enriched in intronic regions. Genome Research, 2021, 31, 1325-1336.	5.5	21
1395	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	12.8	28
1396	Leveraging three-dimensional chromatin architecture for effective reconstruction of enhancer–target gene regulatory interactions. Nucleic Acids Research, 2021, 49, e97-e97.	14.5	6
1397	Large palindromes on the primate X Chromosome are preserved by natural selection. Genome Research, 2021, 31, 1337-1352.	5.5	10
1399	The effect of season of birth on brain epigenome-wide DNA methylation of older adults. Journal of Developmental Origins of Health and Disease, 2022, 13, 367-377.	1.4	2

#	ARTICLE	IF	CITATIONS
1400	Homeostatic functions of monocytes and interstitial lung macrophages are regulated via collagen domain-binding receptor LAIR1. <i>Immunity</i> , 2021, 54, 1511-1526.e8.	14.3	35
1401	Characterizing the Genetic Architecture of Parkinson's Disease in Latinos. <i>Annals of Neurology</i> , 2021, 90, 353-365.	5.3	48
1403	Genomic atlas of the proteome from brain, CSF and plasma prioritizes proteins implicated in neurological disorders. <i>Nature Neuroscience</i> , 2021, 24, 1302-1312.	14.8	105
1404	Genetic susceptibility to acute graft versus host disease in pediatric patients undergoing HSCT. <i>Bone Marrow Transplantation</i> , 2021, 56, 2697-2704.	2.4	2
1405	Identification of 22 susceptibility loci associated with testicular germ cell tumors. <i>Nature Communications</i> , 2021, 12, 4487.	12.8	27
1406	SLM2 Is A Novel Cardiac Splicing Factor Involved in Heart Failure due to Dilated Cardiomyopathy. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 129-146.	6.9	4
1407	Effect of sex chromosomes versus hormones in neonatal lung injury. <i>JCI Insight</i> , 2021, 6, .	5.0	18
1409	Transcriptional-regulatory convergence across functional MDD risk variants identified by massively parallel reporter assays. <i>Translational Psychiatry</i> , 2021, 11, 403.	4.8	11
1410	Genetic drivers of m6A methylation in human brain, lung, heart and muscle. <i>Nature Genetics</i> , 2021, 53, 1156-1165.	21.4	57
1411	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR-FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	21.4	36
1412	Identification of genetic variants for blood insulin level in sex-stratified Korean population and evaluation of the causal relationship between blood insulin level and polycystic ovary syndrome. <i>Genes and Genomics</i> , 2021, 43, 1105-1117.	1.4	3
1413	Revealing transcriptional and post-transcriptional regulatory mechanisms of β -glutamyl transferase and keratin isoforms as novel cooperative biomarkers in low-grade glioma and glioblastoma multiforme. <i>Genomics</i> , 2021, 113, 2623-2633.	2.9	3
1415	Search for genetic loci involved in the constitution and skin type of a Japanese women using a genome-wide association study. <i>Experimental Dermatology</i> , 2021, 30, 1787-1793.	2.9	6
1416	Mendelian randomization analysis identified genes pleiotropically associated with central corneal thickness. <i>BMC Genomics</i> , 2021, 22, 517.	2.8	9
1417	DNA methylation analyses identify an intronic ZDHHC6 locus associated with time to recurrent stroke in the Vitamin Intervention for Stroke Prevention (VISP) clinical trial. <i>PLoS ONE</i> , 2021, 16, e0254562.	2.5	5
1418	MegaLMM: Mega-scale linear mixed models for genomic predictions with thousands of traits. <i>Genome Biology</i> , 2021, 22, 213.	8.8	25
1419	A Panel of rSNPs Demonstrating Allelic Asymmetry in Both ChIP-seq and RNA-seq Data and the Search for Their Phenotypic Outcomes through Analysis of DEGs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7240.	4.1	6
1423	An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021, 7, .	10.3	47

#	ARTICLE	IF	CITATIONS
1424	Differences in the Platelet mRNA Landscape Portend Racial Disparities in Platelet Function and Suggest Novel Therapeutic Targets. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 110, 702-713.	4.7	5
1425	Untangling the genetic link between type 1 and type 2 diabetes using functional genomics. <i>Scientific Reports</i> , 2021, 11, 13871.	3.3	6
1427	The antiandrogen enzalutamide downregulates TMPRSS2 and reduces cellular entry of SARS-CoV-2 in human lung cells. <i>Nature Communications</i> , 2021, 12, 4068.	12.8	57
1428	Genetic Evidence for Repurposing of GLP1R (Glucagon-Like Peptide-1 Receptor) Agonists to Prevent Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, e020331.	3.7	13
1429	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021, 13, 114.	8.2	5
1430	Systematic evaluation of the association between hemoglobin levels and metabolic profile implicates beneficial effects of hypoxia. <i>Science Advances</i> , 2021, 7, .	10.3	19
1431	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. <i>Genes</i> , 2021, 12, 1049.	2.4	11
1432	Discovery and prioritization of variants and genes for kidney function in >1.2 million individuals. <i>Nature Communications</i> , 2021, 12, 4350.	12.8	125
1433	Profiling variable-number tandem repeat variation across populations using repeat-pangenome graphs. <i>Nature Communications</i> , 2021, 12, 4250.	12.8	27
1434	Prioritization of disease genes from GWAS using ensemble-based positive-unlabeled learning. <i>European Journal of Human Genetics</i> , 2021, 29, 1527-1535.	2.8	19
1435	Perspectives on Allele-Specific Expression. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 101-122.	6.5	20
1437	A global overview of genetically interpretable multimorbidities among common diseases in the UK Biobank. <i>Genome Medicine</i> , 2021, 13, 110.	8.2	31
1439	Genetic effects on liver chromatin accessibility identify disease regulatory variants. <i>American Journal of Human Genetics</i> , 2021, 108, 1169-1189.	6.2	22
1441	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms. <i>Nature Communications</i> , 2021, 12, 4571.	12.8	26
1442	Dopaminergic modulation of regional cerebral blood flow: An arterial spin labelling study of genetic and pharmacological manipulation of COMT activity. <i>NeuroImage</i> , 2021, 234, 117999.	4.2	5
1443	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. <i>Nature Neuroscience</i> , 2021, 24, 1313-1323.	14.8	44
1444	Integration of Multiple-Omics Data to Analyze the Population-Specific Differences for Coronary Artery Disease. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-11.	1.3	40
1448	Discovery of Novel Host Molecular Factors Underlying HBV/HCV Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690882.	3.7	0

#	ARTICLE	IF	CITATIONS
1449	IUSMMT: Survival mediation analysis of gene expression with multiple DNA methylation exposures and its application to cancers of TCGA. <i>PLoS Computational Biology</i> , 2021, 17, e1009250.	3.2	7
1451	Novel DNA methylation loci and genes showing pleiotropic association with Alzheimer's dementia: a network Mendelian randomization analysis. <i>Epigenetics</i> , 2022, 17, 746-758.	2.7	8
1452	Identification of novel drug targets for Alzheimer's disease by integrating genetics and proteomes from brain and blood. <i>Molecular Psychiatry</i> , 2021, 26, 6065-6073.	7.9	38
1453	The molecular basis, genetic control and pleiotropic effects of local gene co-expression. <i>Nature Communications</i> , 2021, 12, 4842.	12.8	18
1455	Scrutinizing the causal relationship between schizophrenia and vitamin supplementation. <i>Journal of Bio-X Research</i> , 2021, Publish Ahead of Print, .	0.2	0
1456	Assigning function to SNPs: Considerations when interpreting genetic variation. <i>Seminars in Cell and Developmental Biology</i> , 2022, 121, 135-142.	5.0	13
1458	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. <i>Nature Genetics</i> , 2021, 53, 1322-1333.	21.4	87
1459	Chromatin Looping Links Target Genes with Genetic Risk Loci for Dermatological Traits. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1975-1984.	0.7	19
1460	Size matters: Large copy number losses in Hirschsprung disease patients reveal genes involved in enteric nervous system development. <i>PLoS Genetics</i> , 2021, 17, e1009698.	3.5	14
1463	A primer on applying AI synergistically with domain expertise to oncology. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1876, 188548.	7.4	5
1464	Deleterious single nucleotide polymorphisms (SNPs) of human IFNAR2 gene facilitate COVID-19 severity in patients: a comprehensive <i>in silico</i> approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 11173-11189.	3.5	7
1466	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. <i>Genome Medicine</i> , 2021, 13, 123.	8.2	23
1467	Gene Polymorphisms of the Renin-Angiotensin System and Bleeding Complications of Warfarin: Genetic-Based Machine Learning Models. <i>Pharmaceuticals</i> , 2021, 14, 824.	3.8	1
1468	Integrative enrichment analysis of gene expression based on an artificial neuron. <i>BMC Medical Genomics</i> , 2021, 14, 173.	1.5	0
1469	Evaluating the impact of age on immune checkpoint therapy biomarkers. <i>Cell Reports</i> , 2021, 36, 109599.	6.4	27
1470	Genetic and Epigenetic Fine-Tuning of <i>TGFB1</i> Expression Within the Human Osteoarthritic Joint. <i>Arthritis and Rheumatology</i> , 2021, 73, 1866-1877.	5.6	22
1471	Seeing the forest through the trees: prioritising potentially functional interactions from Hi-C. <i>Epigenetics and Chromatin</i> , 2021, 14, 41.	3.9	3
1472	Haplotype-Specific Expression Analysis of MHC Class II Genes in Healthy Individuals and Rheumatoid Arthritis Patients. <i>Frontiers in Immunology</i> , 2021, 12, 707217.	4.8	10

#	ARTICLE	IF	CITATIONS
1473	Addiction-Associated Genetic Variants Implicate Brain Cell Type- and Region-Specific Cis-Regulatory Elements in Addiction Neurobiology. <i>Journal of Neuroscience</i> , 2021, 41, 9008-9030.	3.6	15
1474	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	8.2	16
1475	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. <i>Human Molecular Genetics</i> , 2021, 31, 289-299.	2.9	7
1476	APRIL limits atherosclerosis by binding to heparan sulfate proteoglycans. <i>Nature</i> , 2021, 597, 92-96.	27.8	38
1477	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. <i>Nature Medicine</i> , 2021, 27, 1564-1575.	30.7	40
1478	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. <i>BMC Bioinformatics</i> , 2021, 22, 403.	2.6	27
1479	Chromatin Alterations in Neurological Disorders and Strategies of (Epi)Genome Rescue. <i>Pharmaceuticals</i> , 2021, 14, 765.	3.8	3
1480	POSTAR3: an updated platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2022, 50, D287-D294.	14.5	65
1481	3aQTL-atlas: an atlas of 3'UTR alternative polyadenylation quantitative trait loci across human normal tissues. <i>Nucleic Acids Research</i> , 2022, 50, D39-D45.	14.5	13
1482	Genome-Wide Association Meta-Analysis Supports Genes Involved in Valve and Cardiac Development to Associate With Mitral Valve Prolapse. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003148.	3.6	7
1483	Next Generation Protein Structure Predictions and Genetic Variant Interpretation. <i>Journal of Molecular Biology</i> , 2021, 433, 167180.	4.2	21
1484	Expression and prognosis of CDC45 in cervical cancer based on the GEO database. <i>PeerJ</i> , 2021, 9, e12114.	2.0	10
1485	Relationship between DNA Methylation within the YJEFN3 Gene and Cognitive Deficit in Schizophrenia Spectrum Disorders. <i>Russian Journal of Genetics</i> , 2021, 57, 1092-1099.	0.6	0
1486	Association of CD2AP neuronal deposits with Braak neurofibrillary stage in Alzheimer's disease. <i>Brain Pathology</i> , 2022, 32, e13016.	4.1	13
1487	Identifying the lungs as a susceptible site for allele-specific regulatory changes associated with type 1 diabetes risk. <i>Communications Biology</i> , 2021, 4, 1072.	4.4	2
1488	A 584Åbp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. <i>American Journal of Human Genetics</i> , 2021, 108, 1852-1865.	6.2	15
1489	Impact on the Risk and Severity of Childhood Onset Schizophrenia of Schizophrenia Risk Genetic Variants at the DRD2 and ZNF804A Loci. <i>Child Psychiatry and Human Development</i> , 2023, 54, 241-247.	1.9	4
1490	Comprehensive characterization genetic regulation and chromatin landscape of enhancer-associated long non-coding RNAs and their implication in human cancer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	7

#	ARTICLE	IF	CITATIONS
1491	Identification of Estrogen Signaling in a Prioritization Study of Intraocular Pressure-Associated Genes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10288.	4.1	6
1492	Atypical genomic cortical patterning in autism with poor early language outcome. <i>Science Advances</i> , 2021, 7, eabh1663.	10.3	21
1493	Unraveling Risk Genes of COVID-19 by Multi-Omics Integrative Analyses. <i>Frontiers in Medicine</i> , 2021, 8, 738687.	2.6	22
1494	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. <i>Biological Psychiatry</i> , 2021, 90, 317-327.	1.3	49
1495	Kynurenine emerges from the shadows â€œ Current knowledge on its fate and function. , 2021, 225, 107845.		67
1496	G proteinâ€‘coupled receptor kinase 5 regulates thrombin signaling in platelets via PAR-1. <i>Blood Advances</i> , 2022, 6, 2319-2330.	5.2	8
1497	COPB2 loss of function causes a coatopathy with osteoporosis and developmental delay. <i>American Journal of Human Genetics</i> , 2021, 108, 1710-1724.	6.2	18
1498	Novel Insight Into Glycosaminoglycan Biosynthesis Based on Gene Expression Profiles. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 709018.	3.7	15
1499	MicroRNA Interactome Multiomics Characterization for Cancer Research and Personalized Medicine: An Expert Review. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 545-566.	2.0	5
1500	Differential transcript usage analysis of bulk and single-cell RNA-seq data with DTUrtle. <i>Bioinformatics</i> , 2021, 37, 3781-3787.	4.1	10
1501	Variation on a theme: mapping microglial heterogeneity. <i>Trends in Genetics</i> , 2021, 37, 1050-1052.	6.7	0
1502	Animal-eRNAdb: a comprehensive animal enhancer RNA database. <i>Nucleic Acids Research</i> , 2022, 50, D46-D53.	14.5	14
1503	GWAS meta-analysis followed by Mendelian randomization revealed potential control mechanisms for circulating IÎ±-Klotho levels. <i>Human Molecular Genetics</i> , 2022, 31, 792-802.	2.9	5
1504	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. <i>Genome Biology</i> , 2021, 22, 262.	8.8	56
1505	Genome-wide Association Study Identifies 2 New Loci Associated With Anti-NMDAR Encephalitis. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021, 8, .	6.0	11
1506	A transcriptome-wide association study of Alzheimerâ€™s disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. <i>Genome Medicine</i> , 2021, 13, 141.	8.2	25
1507	The Molecular Basis of Gender Variations in Mortality Rates Associated With the Novel Coronavirus (COVID-19) Outbreak. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 728409.	3.5	11
1509	Molecular Profiling of Spermatozoa Reveals Correlations between Morphology and Gene Expression: A Novel Biomarker Panel for Male Infertility. <i>BioMed Research International</i> , 2021, 2021, 1-14.	1.9	5

#	ARTICLE	IF	CITATIONS
1510	Genome-wide analysis reveals genetic overlap between alcohol use behaviours, schizophrenia and bipolar disorder and identifies novel shared risk loci. <i>Addiction</i> , 2022, 117, 600-610.	3.3	16
1511	Genome-wide functional screen of 3'UTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	28.9	62
1512	Characterization of the Testis-specific <i>LINC01016</i> Gene Reveals Isoform-specific Roles in Controlling Biological Processes. <i>Journal of the Endocrine Society</i> , 2021, 5, bvab153.	0.2	1
1513	FusionAI: Predicting Fusion Breakpoint from DNA Sequence with Deep Learning. <i>IScience</i> , 2021, 24, 103164.	4.1	5
1515	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	21.4	560
1516	Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis. <i>American Journal of Human Genetics</i> , 2021, 108, 1647-1668.	6.2	36
1517	Association of the functionally significant polymorphisms of the <i>MMP9</i> gene with <i>H. pylori</i> -positive gastric ulcer in the Caucasian population of Central Russia. <i>PLoS ONE</i> , 2021, 16, e0257060.	2.5	13
1518	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
1519	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
1520	Characteristics of p.Gln368Ter Myocilin Variant and Influence of Polygenic Risk on Glaucoma Penetrance in the UK Biobank. <i>Ophthalmology</i> , 2021, 128, 1300-1311.	5.2	27
1521	Predict long-range enhancer regulation based on protein-protein interactions between transcription factors. <i>Nucleic Acids Research</i> , 2021, 49, 10347-10368.	14.5	10
1522	Treatment Response and GWAS Risk Allele rs2514218 (C) of the Dopamine D2 Receptor Gene in Inpatients with Schizophrenia. <i>Neuropsychobiology</i> , 2022, 81, 149-155.	1.9	1
1523	Sex differences in genetic architecture in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 1283-1289.	21.4	69
1526	Evaluation of Genotype-Based Gene Expression Model Performance: A Cross-Framework and Cross-Dataset Study. <i>Genes</i> , 2021, 12, 1531.	2.4	2
1527	Single-Cell RNA-Seq Reveals Heterogeneous lncRNA Expression in Xenografted Triple-Negative Breast Cancer Cells. <i>Biology</i> , 2021, 10, 987.	2.8	6
1529	Stratification of risk of progression to colectomy in ulcerative colitis via measured and predicted gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 1765-1779.	6.2	6
1530	Disease-specific eQTL screening reveals an anti-fibrotic effect of <i>AGXT2</i> in non-alcoholic fatty liver disease. <i>Journal of Hepatology</i> , 2021, 75, 514-523.	3.7	16
1531	Convergent Usage of Amino Acids in Human Cancers as A Reversed Process of Tissue Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 147-162.	6.9	1

#	ARTICLE	IF	CITATIONS
1532	Common host variation drives malaria parasite fitness in healthy human red cells. <i>ELife</i> , 2021, 10, .	6.0	17
1533	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	1.3	114
1535	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	28.9	188
1537	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. <i>International Journal of Cancer</i> , 2022, 150, 80-90.	5.1	9
1538	From GWAS to Gene: Transcriptome-Wide Association Studies and Other Methods to Functionally Understand GWAS Discoveries. <i>Frontiers in Genetics</i> , 2021, 12, 713230.	2.3	55
1539	A genome-wide association study identifies a novel candidate locus at the <i>DLCAP1</i> gene with susceptibility to resistant hypertension in the Japanese population. <i>Scientific Reports</i> , 2021, 11, 19497.	3.3	12
1540	Responsiveness to perturbations is a hallmark of transcription factors that maintain cell identity in <i>Àvitro</i> . <i>Cell Systems</i> , 2021, 12, 885-899.e8.	6.2	17
1542	Transcriptome-Wide Association Study Provides Insights Into the Genetic Component of Gene Expression in Anxiety. <i>Frontiers in Genetics</i> , 2021, 12, 740134.	2.3	14
1543	VIP- <i>HL</i> : Semi-automated ACMG/AMP variant interpretation platform for genetic hearing loss. <i>Human Mutation</i> , 2021, 42, 1567-1575.	2.5	10
1544	A computational approach for identification of core modules from a co-expression network and GWAS data. <i>STAR Protocols</i> , 2021, 2, 100768.	1.2	0
1545	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
1547	Genetic risk model for in-stent restenosis of second-and third-generation drug-eluting stents. <i>IScience</i> , 2021, 24, 103082.	4.1	4
1548	Meta-GWAS of PCSK9 levels detects two novel loci at <i>APOB</i> and <i>TM6SF2</i> . <i>Human Molecular Genetics</i> , 2022, 31, 999-1011.	2.9	9
1551	XPF -673C>T variation is associated with the susceptibility to breast cancer. <i>Cancer Epidemiology</i> , 2021, 74, 102007.	1.9	0
1553	Analyses of nicotine metabolism biomarker genetics stratified by sex in African and European Americans. <i>Scientific Reports</i> , 2021, 11, 19572.	3.3	8
1554	Mesoscale T cell antigen discrimination emerges from intercellular feedback. <i>Trends in Immunology</i> , 2021, 42, 865-875.	6.8	4
1555	Genetic ablation of <i>Gpnmb</i> does not alter synuclein-related pathology. <i>Neurobiology of Disease</i> , 2021, 159, 105494.	4.4	7
1556	Host-specific asymmetric accumulation of mutation types reveals that the origin of SARS-CoV-2 is consistent with a natural process. <i>Innovation(China)</i> , 2021, 2, 100159.	9.1	15

#	ARTICLE	IF	CITATIONS
1557	Co-expression of the SARS-CoV-2 entry molecules ACE2 and TMPRSS2 in human ovaries: Identification of cell types and trends with age. <i>Genomics</i> , 2021, 113, 3449-3460.	2.9	17
1558	Machine learning for profile prediction in genomics. <i>Current Opinion in Chemical Biology</i> , 2021, 65, 35-41.	6.1	11
1559	Rare and de novo coding variants in chromodomain genes in Chiari I malformation. <i>American Journal of Human Genetics</i> , 2021, 108, 100-114.	6.2	17
1560	Integration of genome-wide association study and expression quantitative trait locus mapping for identification of endometriosis-associated genes. <i>Scientific Reports</i> , 2021, 11, 478.	3.3	8
1562	Different components of frailty in the aging subjectsâ€™The role of sarcopenia. , 2021, , 173-205.		0
1563	Advances and challenges in quantitative delineation of the genetic architecture of complex traits. <i>Quantitative Biology</i> , 2021, 9, 168-184.	0.5	0
1564	OUP accepted manuscript. <i>Brain</i> , 2021, , .	7.6	1
1565	Modulation of alternative cleavage and polyadenylation events by dCas9-mediated CRISPRpas. <i>Methods in Enzymology</i> , 2021, 655, 459-482.	1.0	2
1566	Prognostic and immunological role of Ras-related protein Rap1b in pan-cancer. <i>Bioengineered</i> , 2021, 12, 4828-4840.	3.2	17
1567	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. <i>Nature Genetics</i> , 2021, 53, 128-134.	21.4	155
1568	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	27.8	89
1569	Proteome-wide Systems Genetics to Identify Functional Regulators of Complex Traits. <i>Cell Systems</i> , 2021, 12, 5-22.	6.2	19
1571	Making Biological Sense of Genetic Studies of Age-Related Macular Degeneration. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1256, 201-219.	1.6	2
1572	Polygenic risk scores: effect estimation and model optimization. <i>Quantitative Biology</i> , 2021, 9, 133-140.	0.5	0
1573	Evolutionary genetics of skin pigmentation in African populations. <i>Human Molecular Genetics</i> , 2021, 30, R88-R97.	2.9	23
1574	Multi-omics analyses of cognitive traits and psychiatric disorders highlight brain-dependent mechanisms. <i>Human Molecular Genetics</i> , 2023, 32, 885-896.	2.9	11
1576	Genome-Wide Identification of Cis-acting Expression QTLs in Large Yellow Croaker. <i>Marine Biotechnology</i> , 2021, 23, 225-232.	2.4	3
1577	Long tracks of homozygosity predict the severity of alcohol use disorders in an American Indian population. <i>Molecular Psychiatry</i> , 2021, 26, 2200-2211.	7.9	2

#	ARTICLE	IF	CITATIONS
1578	Dosage-sensitive functions in embryonic development drove the survival of genes on sex-specific chromosomes in snakes, birds, and mammals. <i>Genome Research</i> , 2021, 31, 198-210.	5.5	28
1579	Genetic Variation in Sodium-glucose Cotransporter 2 and Heart Failure. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 110, 149-158.	4.7	11
1580	Multi-tissue transcriptome-wide association studies. <i>Genetic Epidemiology</i> , 2021, 45, 324-337.	1.3	8
1581	AutoPVS1: An automatic classification tool for PVS1 interpretation of null variants. <i>Human Mutation</i> , 2020, 41, 1488-1498.	2.5	34
1582	Introductory Methods for eQTL Analyses. <i>Methods in Molecular Biology</i> , 2020, 2082, 3-14.	0.9	4
1583	HLApers: HLA Typing and Quantification of Expression with Personalized Index. <i>Methods in Molecular Biology</i> , 2020, 2120, 101-112.	0.9	12
1584	Investigation of Schizophrenia with Human Induced Pluripotent Stem Cells. <i>Advances in Neurobiology</i> , 2020, 25, 155-206.	1.8	11
1585	Understanding human DNA variants affecting pre-mRNA splicing in the NGS era. <i>Advances in Genetics</i> , 2019, 103, 39-90.	1.8	24
1586	A High-Resolution Map of Human Enhancer RNA Loci Characterizes Super-enhancer Activities in Cancer. <i>Cancer Cell</i> , 2020, 38, 701-715.e5.	16.8	69
1587	The Shared Genetic Basis of Hyperuricemia, Gout, and Kidney Function. <i>Seminars in Nephrology</i> , 2020, 40, 586-599.	1.6	10
1588	Deregulated Regulators: Disease-Causing cis Variants in Transcription Factor Genes. <i>Trends in Genetics</i> , 2020, 36, 523-539.	6.7	26
1589	Gene-expression study raises thorny ethical issues. <i>Nature</i> , 2017, 550, 169-170.	27.8	4
1590	Human and mouse essentiality screens as a resource for disease gene discovery. <i>Nature Communications</i> , 2020, 11, 655.	12.8	64
1591	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 820.	12.8	30
1592	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. <i>Nature Communications</i> , 2020, 11, 4912.	12.8	89
1593	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	27.8	1,014
1594	Visualizing and interpreting cancer genomics data via the Xena platform. <i>Nature Biotechnology</i> , 2020, 38, 675-678.	17.5	2,069
1595	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. <i>Nature Neuroscience</i> , 2020, 23, 809-818.	14.8	242

#	ARTICLE	IF	CITATIONS
1596	DsbA-L deficiency exacerbates mitochondrial dysfunction of tubular cells in diabetic kidney disease. <i>Clinical Science</i> , 2020, 134, 677-694.	4.3	25
1597	svMIL: predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants through multiple instance learning. <i>Bioinformatics</i> , 2020, 36, i692-i699.	4.1	4
1598	Genetic variations in microRNA-binding sites of solute carrier transporter genes as predictors of clinical outcome in colorectal cancer. <i>Carcinogenesis</i> , 2021, 42, 378-394.	2.8	6
1599	Enhancer Locus in ch14q23.1 Modulates Brain Asymmetric Temporal Regions Involved in Language Processing. <i>Cerebral Cortex</i> , 2020, 30, 5322-5332.	2.9	12
1600	Genetic Determinants of Reduced Arsenic Metabolism Efficiency in the 10q24.32 Region Are Associated With Reduced <i>AS3MT</i> Expression in Multiple Human Tissue Types. <i>Toxicological Sciences</i> , 2020, 176, 382-395.	3.1	14
1601	Genome-Wide Association Study for Urinary and Fecal Incontinence in Women. <i>Journal of Urology</i> , 2020, 203, 978-983.	0.4	8
1602	ACE inhibition and cardiometabolic risk factors, lung <i>ACE2</i> and <i>TMPRSS2</i> gene expression, and plasma ACE2 levels: a Mendelian randomization study. <i>Royal Society Open Science</i> , 2020, 7, 200958.	2.4	12
1866	Determining the impact of uncharacterized inversions in the human genome by droplet digital PCR. <i>Genome Research</i> , 2020, 30, 724-735.	5.5	18
1867	Using single-cell entropy to describe the dynamics of reprogramming and differentiation of induced pluripotent stem cells. <i>International Journal of Modern Physics B</i> , 2020, 34, 2050288.	2.0	8
1868	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 564-575.	2.5	10
1869	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. <i>JCI Insight</i> , 2019, 4, .	5.0	15
1870	Targeting and silencing of rhodopsin by ectopic expression of the transcription factor KLF15. <i>JCI Insight</i> , 2017, 2, .	5.0	12
1871	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. <i>Journal of Clinical Investigation</i> , 2020, 130, 1948-1960.	8.2	61
1872	A conserved intratumoral regulatory T cell signature identifies 4-1BB as a pan-cancer target. <i>Journal of Clinical Investigation</i> , 2020, 130, 1405-1416.	8.2	64
1873	Integrative omics approaches provide biological and clinical insights: examples from mitochondrial diseases. <i>Journal of Clinical Investigation</i> , 2020, 130, 20-28.	8.2	39
1874	A curated benchmark of enhancer-gene interactions for evaluating enhancer-target gene prediction methods. <i>Genome Biology</i> , 2020, 21, 17.	8.8	83
1875	Comprehensive analysis of PM20D1 QTL in Alzheimer's disease. <i>Clinical Epigenetics</i> , 2020, 12, 20.	4.1	16
1876	Genomewide Association Study of Leisure-Time Exercise Behavior in Japanese Adults. <i>Medicine and Science in Sports and Exercise</i> , 2018, 50, 2433-2441.	0.4	36

#	ARTICLE	IF	CITATIONS
1877	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. F1000Research, 2018, 7, 121.	1.6	4
1878	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	63
1879	False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860.	1.6	51
1880	False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860.	1.6	45
1881	Stage 2 Registered Report: Variation in neurodevelopmental outcomes in children with sex chromosome trisomies: testing the double hit hypothesis. Wellcome Open Research, 2018, 3, 85.	1.8	10
1883	Transfer learning enables prediction of CYP2D6 haplotype function. PLoS Computational Biology, 2020, 16, e1008399.	3.2	32
1884	Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. PLoS Genetics, 2020, 16, e1008537.	3.5	35
1885	A powerful method for pleiotropic analysis under composite null hypothesis identifies novel shared loci between Type 2 Diabetes and Prostate Cancer. PLoS Genetics, 2020, 16, e1009218.	3.5	49
1886	Multi-ethnic transcriptome-wide association study of prostate cancer. PLoS ONE, 2020, 15, e0236209.	2.5	13
1887	Mining GWAS and eQTL data for CF lung disease modifiers by gene expression imputation. PLoS ONE, 2020, 15, e0239189.	2.5	9
1888	Whole-exome sequencing of 79 xenografts as a potential approach for the identification of genetic variants associated with sensitivity to cytotoxic anticancer drugs. PLoS ONE, 2020, 15, e0239614.	2.5	1
1889	Complex genetic dependencies among growth and neurological phenotypes in healthy children: Towards deciphering developmental mechanisms. PLoS ONE, 2020, 15, e0242684.	2.5	9
1890	A human population-based organotypic in vitro model for cardiotoxicity screening. ALTEX: Alternatives To Animal Experimentation, 2018, 35, 441-452.	1.5	47
1891	<scp>CEN</scp> â€tools: an integrative platform to identify the contexts of essential genes. Molecular Systems Biology, 2020, 16, e9698.	7.2	14
1892	The GENDULF algorithm: mining transcriptomics to uncover modifier genes for monogenic diseases. Molecular Systems Biology, 2020, 16, e9701.	7.2	2
1895	Prediction of competing endogenous RNA coexpression network as prognostic markers in AML. Aging, 2019, 11, 3333-3347.	3.1	43
1896	ASNEO: Identification of personalized alternative splicing based neoantigens with RNA-seq. Aging, 2020, 12, 14633-14648.	3.1	25
1899	The Landscape of Pervasive Horizontal Pleiotropy in Human Genetic Variation is Driven by Extreme Polygenicity of Human Traits and Diseases. SSRN Electronic Journal, 0, , .	0.4	3

#	ARTICLE	IF	CITATIONS
1900	Estimating Sample-Specific Regulatory Networks. SSRN Electronic Journal, 0, , .	0.4	3
1901	Identification of a functional 339 bp <i>Alu</i> insertion polymorphism in the schizophrenia-associated locus at 10q24.32. Zoological Research, 2020, 41, 84-89.	2.1	9
1902	Interaction modulation through arrays of clustered methyl-arginine protein modifications. Life Science Alliance, 2018, 1, e201800178.	2.8	11
1903	Use of the epigenetic toolbox to contextualize common variants associated with schizophrenia risk. Dialogues in Clinical Neuroscience, 2019, 21, 407-416.	3.7	3
1904	Disease Module Identification Based on Representation Learning of Complex Networks Integrated From GWAS, eQTL Summaries, and Human Interactome. Frontiers in Bioengineering and Biotechnology, 2020, 8, 418.	4.1	22
1905	Impact of Genetic Variability in ACE2 Expression on the Evolutionary Dynamics of SARS-CoV-2 Spike D614G Mutation. Genes, 2021, 12, 16.	2.4	19
1906	Downregulation of orosomucoid 2 acts as a prognostic factor associated with cancer-promoting pathways in liver cancer. World Journal of Gastroenterology, 2020, 26, 804-817.	3.3	24
1907	Battle of the sexes: contrasting roles of testis-specific protein Y-encoded (TSPY) and TSPX in human oncogenesis. Asian Journal of Andrology, 2019, 21, 260.	1.6	9
1908	Genetics of trans-regulatory variation in gene expression. ELife, 2018, 7, .	6.0	146
1909	Fine-mapping cis-regulatory variants in diverse human populations. ELife, 2019, 8, .	6.0	51
1910	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	6.0	170
1911	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. ELife, 2019, 8, .	6.0	53
1912	Nuclear genetic regulation of the human mitochondrial transcriptome. ELife, 2019, 8, .	6.0	56
1913	A generally conserved response to hypoxia in iPSC-derived cardiomyocytes from humans and chimpanzees. ELife, 2019, 8, .	6.0	35
1914	The long non-coding RNA Cerx1 is a post transcriptional regulator of mitochondrial complex I catalytic activity. ELife, 2019, 8, .	6.0	42
1915	Deep learning models predict regulatory variants in pancreatic islets and refine type 2 diabetes association signals. ELife, 2020, 9, .	6.0	28
1916	The single-cell eQTLGen consortium. ELife, 2020, 9, .	6.0	150
1917	Brain aging comprises many modes of structural and functional change with distinct genetic and biophysical associations. ELife, 2020, 9, .	6.0	122

#	ARTICLE	IF	CITATIONS
1918	Germline burden of rare damaging variants negatively affects human healthspan and lifespan. ELife, 2020, 9, .	6.0	12
1919	Genetic mapping of etiologic brain cell types for obesity. ELife, 2020, 9, .	6.0	79
1920	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	6.0	40
1921	Mutations primarily alter the inclusion of alternatively spliced exons. ELife, 2020, 9, .	6.0	24
1922	Simultaneous quantification of mRNA and protein in single cells reveals post-transcriptional effects of genetic variation. ELife, 2020, 9, .	6.0	33
1923	Systematic identification of cis-regulatory variants that cause gene expression differences in a yeast cross. ELife, 2020, 9, .	6.0	18
1924	Transcriptome association studies of neuropsychiatric traits in African Americans implicate <i>PRMT7</i> in schizophrenia. PeerJ, 2019, 7, e7778.	2.0	12
1925	Optimizing drug selection in psychopharmacology based on 40 significant CYP2C19- and CYP2D6-biased adverse drug reactions of selective serotonin reuptake inhibitors. PeerJ, 2019, 7, e7860.	2.0	17
1926	Xia-Gibbs Syndrome: A Review of Literature. Cureus, 2020, 12, e12352.	0.5	7
1927	De Novo Variants in Chinese Asd Trios Reveal Distinct Genetic Basis Underlying Autism with and Without Developmental Delay. SSRN Electronic Journal, 0, , .	0.4	0
1928	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. Nature Communications, 2021, 12, 5641.	12.8	46
1930	A sex-specific evolutionary interaction between ADCY9 and CETP. ELife, 2021, 10, .	6.0	8
1934	Gene4HL: An Integrated Genetic Database for Hearing Loss. Frontiers in Genetics, 2021, 12, 773009.	2.3	3
1935	Sex-specific genetic regulation of adipose mitochondria and metabolic syndrome by Ndufv2. Nature Metabolism, 2021, 3, 1552-1568.	11.9	32
1937	Modeling alpha-synuclein pathology in a human brain-chip to assess blood-brain barrier disruption. Nature Communications, 2021, 12, 5907.	12.8	97
1938	Integrative eQTL-weighted hierarchical Cox models for SNP-set based time-to-event association studies. Journal of Translational Medicine, 2021, 19, 418.	4.4	2
1940	Replication of LZTFL1 Gene Region as a Susceptibility Locus for COVID-19 in Latvian Population. Virologica Sinica, 2021, 36, 1241-1244.	3.0	6
1942	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. Science Immunology, 2021, 6, eabh3768.	11.9	19

#	ARTICLE	IF	CITATIONS
1943	<i>SCFD1</i> expression quantitative trait loci in amyotrophic lateral sclerosis are differentially expressed. Brain Communications, 2021, 3, fcab236.	3.3	14
1945	Joint-Tissue Integrative Analysis Identified Hundreds of Schizophrenia Risk Genes. Molecular Neurobiology, 2021, , 1.	4.0	4
1947	The Spatiotemporal Coupling: Regional Energy Failure and Aberrant Proteins in Neurodegenerative Diseases. International Journal of Molecular Sciences, 2021, 22, 11304.	4.1	8
1948	Mutations and variants of ONECUT1 in diabetes. Nature Medicine, 2021, 27, 1928-1940.	30.7	24
1949	A Computational Atlas of Tissue-specific Regulatory Networks. Frontiers in Systems Biology, 2021, 1, .	0.7	3
1952	Polygenic basis and biomedical consequences of telomere length variation. Nature Genetics, 2021, 53, 1425-1433.	21.4	145
1953	SNP-mediated binding of TBX1 to the enhancer element of IL-10 reduces the risk of Behçet's disease. Epigenomics, 2021, 13, 1523-1537.	2.1	1
1954	Mendelian Randomization Analysis Identified Potential Genes Pleiotropically Associated with Polycystic Ovary Syndrome. Reproductive Sciences, 2022, 29, 1028-1037.	2.5	6
1955	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	4.4	11
1956	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. Nature Communications, 2021, 12, 6031.	12.8	34
1957	Haplotype associated RNA expression (HARE) improves prediction of complex traits in maize. PLoS Genetics, 2021, 17, e1009568.	3.5	5
1958	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. Clinical Epigenetics, 2021, 13, 186.	4.1	32
1959	Multi-omics colocalization with genome-wide association studies reveals a context-specific genetic mechanism at a childhood onset asthma risk locus. Genome Medicine, 2021, 13, 157.	8.2	21
1960	A GWAS top hit for circulating leptin is associated with weight gain but not with leptin protein levels in lithium-augmented patients with major depression. European Neuropsychopharmacology, 2021, 53, 114-119.	0.7	3
1969	A Multiplexed Assay for Exon Recognition Reveals That an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Disruptions to Splicing. SSRN Electronic Journal, 0, , .	0.4	0
1971	Pan-Cancer Analysis of Heritable Genetic Variations Reveals Cancer-Specific Activation of Dormant Oncogenic Pathways. SSRN Electronic Journal, 0, , .	0.4	0
1975	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. F1000Research, 2018, 7, 121.	1.6	3
2020	Stage 2 Registered Report: Variation in neurodevelopmental outcomes in children with sex chromosome trisomies: testing the double hit hypothesis. Wellcome Open Research, 0, 3, 85.	1.8	4

#	ARTICLE	IF	CITATIONS
2025	SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. , 2018, , .		0
2026	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. , 2018, , .		3
2028	Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies. , 2018, , .		4
2042	Molecular Basis of Complex Heritability in Natural Genotype-to-Phenotype Relationships. SSRN Electronic Journal, 0, , .	0.4	0
2043	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. SSRN Electronic Journal, 0, , .	0.4	0
2044	Integrative Enrichment Analysis of Intra- and Inter- Tissuesâ€™ Differentially Expressed Genes Based on Perceptron. Lecture Notes in Computer Science, 2019, , 93-104.	1.3	0
2045	Genetic Basis of Alternative Polyadenylation is an Emerging Molecular Phenotype for Human Traits and Diseases. SSRN Electronic Journal, 0, , .	0.4	1
2056	Polymorphic locus rs652438 of the MMP12 gene is associated with the development of hypertension in women. Arterial Hypertension (Russian Federation), 2019, 25, 60-65.	0.4	4
2062	MORPHOLOGICAL AND FUNCTIONAL SYSTEM OF GRAFT-ARTERY JUNCTIONS. Complex Issues of Cardiovascular Diseases, 2019, 8, 112-122.	0.5	7
2125	SNPnotes: high-throughput tissue-specific functional annotation of single nucleotide variants. F1000Research, 0, 8, 1784.	1.6	0
2137	The role of obesity in the implementation of genetic predisposition to the development of essential hypertension in men. Obesity and Metabolism, 2019, 16, 66-72.	1.2	2
2138	Expression Quantitative Trait Loci Analysis in Multiple Tissues. Methods in Molecular Biology, 2020, 2082, 231-237.	0.9	1
2153	Sequence variation at 8q24.21 and risk of back pain. F1000Research, 0, 9, 424.	1.6	1
2170	Integrating genetic variation with DNA methylation at SKA2 rs7208505 in analyses of obsessive-compulsive disorder disease risk and symptom severity. Personalized Medicine in Psychiatry, 2020, 21-22, 100058.	0.1	1
2194	Sex-Specific Causal Relations between Steroid Hormones and Obesityâ€™A Mendelian Randomization Study. Metabolites, 2021, 11, 738.	2.9	7
2195	Integration of genetic, transcriptomic, and clinical data provides insight into 16p11.2 and 22q11.2 CNV genes. Genome Medicine, 2021, 13, 172.	8.2	16
2196	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	21.4	208
2197	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells. Nature, 2021, 599, 136-140.	27.8	89

#	ARTICLE	IF	CITATIONS
2198	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3
2201	The genetic basis of urate control and gout: Insights into molecular pathogenesis from follow-up study of genome-wide association study loci. Best Practice and Research in Clinical Rheumatology, 2021, 35, 101721.	3.3	8
2202	Glyoxalase 1 Confers Susceptibility to Schizophrenia: From Genetic Variants to Phenotypes of Neural Function. Frontiers in Molecular Neuroscience, 2021, 14, 739526.	2.9	9
2204	Genetics and Pharmacogenetics of COPD. Respiratory Medicine, 2020, , 39-55.	0.1	0
2209	Fine genetic mapping of the chromosome 11q23.3 region in a Han Chinese population: insights into the apolipoprotein genes underlying the blood lipid-lipoprotein variances. Journal of Genetics and Genomics, 2020, 47, 756-769.	3.9	0
2213	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 Seleksii, 2020, 24, 876-884.	1.1	7
2217	Dissecting intercellular and intracellular signaling networks with barcoded genetic tools. Current Opinion in Chemical Biology, 2022, 66, 102091.	6.1	3
2218	Overlapping common genetic architecture between major depressive disorders and anxiety and stress-related disorders. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2022, 113, 110450.	4.8	5
2219	DNA: The Greatest Text of All. , 2021, , 111-172.		0
2224	Phenotypic and Molecular Characterization of Risk Loci Associated With Asthma and Lung Function. Allergy, Asthma and Immunology Research, 2020, 12, 806.	2.9	1
2227	Commentary: lessons from molecular genetic studies on reporting false-positive results. Reproduction, Fertility and Development, 2020, 32, 1298.	0.4	1
2230	Precision Oncology. RSC Detection Science, 2020, , 345-362.	0.0	1
2231	Anti-CD3 Stimulated T Cell Transcriptome Reveals Novel ncRNAs and Correlates with a Suppressive Profile. Lecture Notes in Computer Science, 2020, , 180-191.	1.3	0
2250	A large Canadian cohort provides insights into the genetic architecture of human hair colour. Communications Biology, 2021, 4, 1253.	4.4	11
2251	Gene-level analysis of rare variants in 379,066 whole exome sequences identifies an association of GIGYF1 loss of function with type 2 diabetes. Scientific Reports, 2021, 11, 21565.	3.3	25
2252	Heritability Enrichment of Immunoglobulin G N-Glycosylation in Specific Tissues. Frontiers in Immunology, 2021, 12, 741705.	4.8	6
2253	CD36 maintains the gastric mucosa and associates with gastric disease. Communications Biology, 2021, 4, 1247.	4.4	8
2254	Characterisation of insomnia as an environmental risk factor for asthma via Mendelian randomization and gene environment interaction. Scientific Reports, 2021, 11, 21813.	3.3	5

#	ARTICLE	IF	CITATIONS
2255	Synonymous mutations reveal genome-wide levels of positive selection in healthy tissues. <i>Nature Genetics</i> , 2021, 53, 1597-1605.	21.4	33
2256	Transethnic analysis of psoriasis susceptibility in South Asians and Europeans enhances fine mapping in the MHC and genome wide. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100069.	1.7	8
2258	Genome-wide association studies identify the role of caspase-9 in kidney disease. <i>Science Advances</i> , 2021, 7, eabi8051.	10.3	14
2259	TIGAR-V2: Efficient TWAS tool with nonparametric Bayesian eQTL weights of 49 tissue types from GTEx V8. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100068.	1.7	12
2263	Integrative multiomics analysis highlights immune-cell regulatory mechanisms and shared genetic architecture for 14 immune-associated diseases and cancer outcomes. <i>American Journal of Human Genetics</i> , 2021, 108, 2259-2270.	6.2	7
2264	Mitochondrial-nuclear cross-talk in the human brain is modulated by cell type and perturbed in neurodegenerative disease. <i>Communications Biology</i> , 2021, 4, 1262.	4.4	8
2292	Maximizing the reusability of gene expression data by predicting missing metadata. <i>PLoS Computational Biology</i> , 2020, 16, e1007450.	3.2	4
2294	Germline variants are associated with increased primary melanoma tumor thickness at diagnosis. <i>Human Molecular Genetics</i> , 2021, 29, 3578-3587.	2.9	3
2296	Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 296-307.	0.7	3
2297	SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 184-195.	0.7	0
2298	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 308-319.	0.7	5
2299	Highly Variable Expression of Splice Variants in Human Liver: Implication in the Liver Gene Expression Regulation and Inter-Person Variability in Drug Metabolism and Liver Related Diseases. <i>Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research</i> , 2019, 13, .	0.1	3
2300	Incorporation of DNA methylation into eQTL mapping in African Americans. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2021, 26, 244-255.	0.7	0
2301	Genetic test for the personalization of sport training. <i>Acta Biomedica</i> , 2020, 91, e2020012.	0.3	6
2302	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. <i>Frontiers in Genetics</i> , 2021, 12, 609657.	2.3	1
2303	An efficient linear mixed model framework for meta-analytic association studies across multiple contexts. <i>Leibniz International Proceedings in Informatics, LIPIcs</i> , 2016, 2016, .	0.0	0
2304	Looking back at the first twenty years of genomics. <i>Quantitative Biology</i> , 2022, 10, 6-16.	0.5	0
2305	Trans-eQTLs of the CYP3A4 and CYP3A5 associated with tacrolimus trough blood concentration in Chinese renal transplant patients. <i>Biomedicine and Pharmacotherapy</i> , 2022, 145, 112407.	5.6	2

#	ARTICLE	IF	CITATIONS
2307	A genome-wide association study of childhood adiposity and blood lipids. Wellcome Open Research, 0, 6, 303.	1.8	1
2309	Defactinib inhibits PYK2 phosphorylation of IRF5 and reduces intestinal inflammation. Nature Communications, 2021, 12, 6702.	12.8	13
2312	Challenges and opportunities in network-based solutions for biological questions. Briefings in Bioinformatics, 2022, 23, .	6.5	10
2313	Systems Approach to Integrating Preclinical Apolipoprotein E-Knockout Investigations Reveals Novel Etiologic Pathways and Master Atherosclerosis Network in Humans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 35-48.	2.4	4
2314	Discovering metabolite quantitative trait loci in asthma using an isolated population. Journal of Allergy and Clinical Immunology, 2022, 149, 1807-1811.e16.	2.9	8
2315	Peanut oral immunotherapy differentially suppresses clonally distinct subsets of T helper cells. Journal of Clinical Investigation, 2022, 132, .	8.2	54
2316	Impact of fetal expression quantitative trait loci on transcriptome-wide association study of childhood leukemia. Human Molecular Genetics, 2021, , .	2.9	0
2317	The genetic architecture of DNA replication timing in human pluripotent stem cells. Nature Communications, 2021, 12, 6746.	12.8	26
2319	Posttranscriptional Regulation of the Human LDL Receptor by the U2-Spliceosome. Circulation Research, 2022, 130, 80-95.	4.5	9
2320	Cell population-based framework of genetic epidemiology in the single-cell omics era. BioEssays, 2022, 44, e2100118.	2.5	5
2321	Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. PLoS Computational Biology, 2021, 17, e1009563.	3.2	3
2322	Genetic ancestry effects on the response to viral infection are pervasive but cell type specific. Science, 2021, 374, 1127-1133.	12.6	68
2323	The splicing effect of variants at branchpoint elements in cancer genes. Genetics in Medicine, 2022, 24, 398-409.	2.4	9
2325	Structure-Based Design of Potent, Selective, and Orally Bioavailable VPS34 Kinase Inhibitors. Journal of Medicinal Chemistry, 2022, 65, 11500-11512.	6.4	12
2326	A five-lncRNA model predicting overall survival in gastric cancer compared with normal tissues. Aging, 2021, 13, 24349-24359.	3.1	3
2327	Comprehensive Characterization of the Coding and Non-Coding Single Nucleotide Polymorphisms in the Tumor Protein p63 (TP63) Gene Using In Silico Tools. Biomolecules, 2021, 11, 1733.	4.0	2
2328	Integrative metabolomics-genomics approach reveals key metabolic pathways and regulators of Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1260-1278.	0.8	57
2330	Cis-regulatory architecture of human ESC-derived hypothalamic neuron differentiation aids in variant-to-gene mapping of relevant complex traits. Nature Communications, 2021, 12, 6749.	12.8	11

#	ARTICLE	IF	CITATIONS
2332	scPower accelerates and optimizes the design of multi-sample single cell transcriptomic studies. Nature Communications, 2021, 12, 6625.	12.8	38
2333	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. JAMA Network Open, 2021, 4, e2136560.	5.9	16
2334	Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics. American Journal of Human Genetics, 2021, 108, 2336-2353.	6.2	12
2335	Genomics and transcriptomics landscapes associated to changes in insulin sensitivity in response to endurance exercise training. Scientific Reports, 2021, 11, 23314.	3.3	3
2336	Integrative epigenomics in Sjögren's syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. Scientific Reports, 2021, 11, 23292.	3.3	16
2337	Computational Methods and Approaches in Pharmacogenomic Research. , 2022, , 53-83.		1
2338	Quantitative Genetics of Human Protein N-Glycosylation. Advances in Experimental Medicine and Biology, 2021, 1325, 151-171.	1.6	1
2339	Stem Cell-Derived \hat{I}^2 Cells: A Versatile Research Platform to Interrogate the Genetic Basis of \hat{I}^2 Cell Dysfunction. International Journal of Molecular Sciences, 2022, 23, 501.	4.1	4
2341	Thirteen Independent Genetic Loci Associated with Preserved Processing Speed in a Study of Cognitive Resilience in 330,097 Individuals in the UK Biobank. Genes, 2022, 13, 122.	2.4	3
2342	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
2343	Machine Learning Identifies Six Genetic Variants and Alterations in the Heart Atrial Appendage as Key Contributors to PD Risk Predictivity. Frontiers in Genetics, 2021, 12, 785436.	2.3	4
2344	<i>BIN1</i> rs744373 located in enhancers of brain tissues upregulates <i>BIN1</i> mRNA expression, thereby leading to Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1587-1588.	0.8	8
2345	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	12.8	17
2346	Genetic Regulation of Transcription in the Endometrium in Health and Disease. Frontiers in Reproductive Health, 2022, 3, .	1.9	8
2347	Circulating inflammatory cytokines and risk of five cancers: a Mendelian randomization analysis. BMC Medicine, 2022, 20, 3.	5.5	41
2349	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.	4.1	4
2352	Whole Blood Transcriptome Analysis in Children with Sickle Cell Anemia. Frontiers in Genetics, 2021, 12, 737741.	2.3	4
2353	Variant interpretation: UCSC Genome Browser Recommended Track Sets. Human Mutation, 2022, , .	2.5	2

#	ARTICLE	IF	CITATIONS
2354	Bacon: a comprehensive computational benchmarking framework for evaluating targeted chromatin conformation capture-specific methodologies. <i>Genome Biology</i> , 2022, 23, 30.	8.8	7
2355	Transcription factor regulation of eQTL activity across individuals and tissues. <i>PLoS Genetics</i> , 2022, 18, e1009719.	3.5	14
2356	Genome-wide annotation of protein-coding genes in pig. <i>BMC Biology</i> , 2022, 20, 25.	3.8	14
2357	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. <i>Nature Genetics</i> , 2022, 54, 161-169.	21.4	49
2358	Fine mapping with epigenetic information and 3D structure. <i>Seminars in Immunopathology</i> , 2022, 44, 115-125.	6.1	8
2360	Genome-wide association studies of 27 accelerometry-derived physical activity measurements identified novel loci and genetic mechanisms. <i>Genetic Epidemiology</i> , 2022, 46, 122-138.	1.3	7
2361	Meta-imputation of transcriptome from genotypes across multiple datasets by leveraging publicly available summary-level data. <i>PLoS Genetics</i> , 2022, 18, e1009571.	3.5	3
2363	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. <i>Neuron</i> , 2022, 110, 992-1008.e11.	8.1	51
2365	FILER: a framework for harmonizing and querying large-scale functional genomics knowledge. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab123.	3.2	7
2368	Genetic Factors of Renin-Angiotensin System Associated with Major Bleeding for Patients Treated with Direct Oral Anticoagulants. <i>Pharmaceutics</i> , 2022, 14, 231.	4.5	2
2369	Network biology and artificial intelligence drive the understanding of the multidrug resistance phenotype in cancer. <i>Drug Resistance Updates</i> , 2022, 60, 100811.	14.4	13
2370	Limb development genes underlie variation in human fingerprint patterns. <i>Cell</i> , 2022, 185, 95-112.e18.	28.9	30
2372	Genome-wide meta-analysis of phytosterols reveals five novel loci and a detrimental effect on coronary atherosclerosis. <i>Nature Communications</i> , 2022, 13, 143.	12.8	17
2374	Genome-wide analysis of genetic predisposition to common polygenic cancers. <i>Journal of Applied Genetics</i> , 2022, 63, 315.	1.9	2
2375	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	6.5	29
2377	Genome-Wide Association Study Identifies Two Common Loci Associated with Pigment Dispersion Syndrome/Pigmentary Glaucoma and Implicates Myopia in its Development. <i>Ophthalmology</i> , 2022, 129, 626-636.	5.2	10
2379	Genome-wide analysis identified abundant genetic modulators of contributions of the apolipoprotein E alleles to Alzheimer's disease risk. <i>Alzheimer's and Dementia</i> , 2022, , .	0.8	4
2380	Association of Essential Tremor With Novel Risk Loci. <i>JAMA Neurology</i> , 2022, 79, 185.	9.0	17

#	ARTICLE	IF	CITATIONS
2381	Redefining tissue specificity of genetic regulation of gene expression in the presence of allelic heterogeneity. <i>American Journal of Human Genetics</i> , 2022, 109, 223-239.	6.2	26
2382	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. <i>Endocrine Reviews</i> , 2022, 43, 927-965.	20.1	75
2383	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. <i>Genome Medicine</i> , 2022, 14, 7.	8.2	12
2384	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. <i>Communications Biology</i> , 2022, 5, 80.	4.4	12
2386	Harnessing tissue-specific genetic variation to dissect putative causal pathways between body mass index and cardiometabolic phenotypes. <i>American Journal of Human Genetics</i> , 2022, 109, 240-252.	6.2	15
2387	Inter-tissue convergence of gene expression during ageing suggests age-related loss of tissue and cellular identity. <i>ELife</i> , 2022, 11, .	6.0	26
2388	Leveraging gene co-regulation to identify gene sets enriched for disease heritability. <i>American Journal of Human Genetics</i> , 2022, 109, 393-404.	6.2	10
2389	Identification of potential functional variants and genes at 18q21.1 associated with the carcinogenesis of colorectal cancer. <i>PLoS Genetics</i> , 2022, 18, e1010050.	3.5	3
2391	The Human Eye Transcriptome Atlas: A searchable comparative transcriptome database for healthy and diseased human eye tissue. <i>Genomics</i> , 2022, 114, 110286.	2.9	25
2392	The genetic architecture of language functional connectivity. <i>NeuroImage</i> , 2022, 249, 118795.	4.2	14
2393	A common TMPRSS2 variant has a protective effect against severe COVID-19. <i>Current Research in Translational Medicine</i> , 2022, 70, 103333.	1.8	30
2394	rs9390123 and rs9399451 influence the DNA repair capacity of lung cancer by regulating <i>PEX3</i> and <i>PHACTR2</i> expression instead of <i>PHACTR2</i> . <i>Oncology Reports</i> , 2022, 47, .	2.6	4
2395	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac002.	3.2	1
2396	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes. <i>Human Molecular Genetics</i> , 2022, 31, 3191-3205.	2.9	4
2397	Interpretable network-guided epistasis detection. <i>GigaScience</i> , 2022, 11, .	6.4	5
2398	Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. <i>ELife</i> , 2022, 11, .	6.0	7
2399	The Carbon Footprint of Bioinformatics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	29
2400	Network-Based Approach to Repurpose Approved Drugs for COVID-19 by Integrating GWAS and Text Mining Data. <i>Processes</i> , 2022, 10, 326.	2.8	1

#	ARTICLE	IF	CITATIONS
2403	Evolutionary history of type II transmembrane serine proteases involved in viral priming. Human Genetics, 2022, 141, 1705-1722.	3.8	6
2404	An effector index to predict target genes at GWAS loci. Human Genetics, 2022, 141, 1431-1447.	3.8	28
2406	Comprehensive analysis of N6-methyladenosine regulators with the tumor immune landscape and correlation between the insulin-like growth factor 2 mRNA-binding protein 3 and programmed death ligand 1 in bladder cancer. Cancer Cell International, 2022, 22, 72.	4.1	8
2407	Cell types of origin of the cell-free transcriptome. Nature Biotechnology, 2022, 40, 855-861.	17.5	41
2410	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. Nature Communications, 2022, 13, 826.	12.8	31
2415	Comparison Between Expression Microarrays and RNA-Sequencing Using UKBEC Dataset Identified a -eQTL Associated with Gene in Substantia Nigra. , 2020, 1, 100001.		0
2416	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. Frontiers in Genetics, 2021, 12, 609657.	2.3	8
2417	Network Approaches for Precision Oncology. Advances in Experimental Medicine and Biology, 2022, 1361, 199-213.	1.6	1
2418	Bioinformatics pipeline to guide late-onset Alzheimer's disease (LOAD) post-GWAS studies: Prioritizing transcription regulatory variants within LOAD-associated regions. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2022, 8, e12244.	3.7	5
2420	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.	3.3	9
2421	A guide for the diagnosis of rare and undiagnosed disease: beyond the exome. Genome Medicine, 2022, 14, 23.	8.2	101
2422	Allele-specific gene expression can underlie altered transcript abundance in zebrafish mutants. ELife, 2022, 11, .	6.0	9
2423	EVIHVR: A platform for analysis of expression, variation and identification of human virus receptors. , 2022, , .		0
2425	Genome-wide association study of brain arteriolosclerosis. Journal of Cerebral Blood Flow and Metabolism, 2022, 42, 1437-1450.	4.3	2
2426	Genetic associations with carotid intima-media thickness link to atherosclerosis with sex-specific effects in sub-Saharan Africans. Nature Communications, 2022, 13, 855.	12.8	10
2427	STAT3-mediated allelic imbalance of novel genetic variant Rs1047643 and B-cell-specific super-enhancer in association with systemic lupus erythematosus. ELife, 2022, 11, .	6.0	5
2428	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.	1.6	3
2429	A statistical framework for recovering pseudo-dynamic networks from static data. Bioinformatics, 2022, , .	4.1	2

#	ARTICLE	IF	CITATIONS
2431	Genome-wide association analyses identify new Brugada syndrome risk loci and highlight a new mechanism of sodium channel regulation in disease susceptibility. <i>Nature Genetics</i> , 2022, 54, 232-239.	21.4	55
2432	PSRC1 May Affect Coronary Artery Disease Risk by Altering CELSR2, PSRC1, and SORT1 Gene Expression and Circulating Granulin and Apolipoprotein B Protein Levels. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 763015.	2.4	3
2433	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. <i>Basic Research in Cardiology</i> , 2022, 117, 6.	5.9	22
2434	Fine-mapping of intracranial aneurysm susceptibility based on a genome-wide association study. <i>Scientific Reports</i> , 2022, 12, 2717.	3.3	6
2437	Integrating single-cell sequencing data with GWAS summary statistics reveals CD16+monocytes and memory CD8+T cells involved in severe COVID-19. <i>Genome Medicine</i> , 2022, 14, 16.	8.2	25
2439	Leveraging a Surrogate Outcome to Improve Inference on a Partially Missing Target Outcome. <i>Biometrics</i> , 2023, 79, 1472-1484.	1.4	1
2440	Computational and Experimental Analysis of Genetic Variants. , 2022, 12, 3303-3336.		5
2441	UACA locus is associated with breast cancer chemoresistance and survival. <i>Npj Breast Cancer</i> , 2022, 8, 39.	5.2	7
2443	Colocalization analysis of pancreas eQTLs with risk loci from alcoholic and novel non-alcoholic chronic pancreatitis GWAS suggests potential disease causing mechanisms. <i>Pancreatology</i> , 2022, 22, 449-456.	1.1	3
2444	Guidelines for bioinformatics of single-cell sequencing data analysis in Alzheimer's disease: review, recommendation, implementation and application. <i>Molecular Neurodegeneration</i> , 2022, 17, 17.	10.8	40
2446	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. <i>PLoS Genetics</i> , 2022, 18, e1010076.	3.5	13
2447	DNA methylation signatures in human neonatal blood following maternal antenatal corticosteroid treatment. <i>Translational Psychiatry</i> , 2022, 12, 132.	4.8	3
2449	Allele-specific expression reveals genes with recurrent cis-regulatory alterations in high-risk neuroblastoma. <i>Genome Biology</i> , 2022, 23, 71.	8.8	2
2450	StemSC: a cross-dataset human stemness index for single-cell samples. <i>Stem Cell Research and Therapy</i> , 2022, 13, 115.	5.5	4
2451	Andersen-Tawil syndrome: deep phenotyping reveals significant cardiac and neuromuscular morbidity. <i>Brain</i> , 2022, 145, 2108-2120.	7.6	9
2452	Incorporating regulatory interactions into gene-set analyses for GWAS data: A controlled analysis with the MAGMA tool. <i>PLoS Computational Biology</i> , 2022, 18, e1009908.	3.2	3
2453	High-throughput characterization of the role of non-B DNA motifs on promoter function. <i>Cell Genomics</i> , 2022, 2, 100111.	6.5	17
2454	Positive selection acts on regulatory genetic variants in populations of European ancestry that affect ALDH2 gene expression. <i>Scientific Reports</i> , 2022, 12, 4563.	3.3	4

#	ARTICLE	IF	CITATIONS
2455	Revisiting the embryogenesis of lip and palate development. <i>Oral Diseases</i> , 2022, 28, 1306-1326.	3.0	27
2457	Identification of Genetic Risk Factors of Severe COVID-19 Using Extensive Phenotypic Data: A Proof-of-Concept Study in a Cohort of Russian Patients. <i>Genes</i> , 2022, 13, 534.	2.4	2
2458	Comprehensive evaluation of deconvolution methods for human brain gene expression. <i>Nature Communications</i> , 2022, 13, 1358.	12.8	32
2459	LncRNA RP5-998N21.4 promotes immune defense through upregulation of IFIT2 and IFIT3 in schizophrenia. <i>NPJ Schizophrenia</i> , 2022, 8, 11.	3.6	6
2460	Exploring common genetic contributors to neuroprotection from amyloid pathology. <i>Brain Communications</i> , 2022, 4, fcac066.	3.3	10
2461	Loss of EMP2 Inhibits Melanogenesis of MNT1 Melanoma Cells via Regulation of TRP-2. <i>Biomolecules and Therapeutics</i> , 2022, 30, 203-211.	2.4	2
2462	The druggable schizophrenia genome: from repurposing opportunities to unexplored drug targets. <i>Npj Genomic Medicine</i> , 2022, 7, 25.	3.8	8
2463	Transcriptome-wide association study reveals increased neuronal FLT3 expression is associated with Tourette's syndrome. <i>Communications Biology</i> , 2022, 5, 289.	4.4	4
2464	GREEN-DB: a framework for the annotation and prioritization of non-coding regulatory variants from whole-genome sequencing data. <i>Nucleic Acids Research</i> , 2022, 50, 2522-2535.	14.5	13
2467	Oxytocin receptor expression patterns in the human brain across development. <i>Neuropsychopharmacology</i> , 2022, 47, 1550-1560.	5.4	23
2469	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. <i>Nature Communications</i> , 2022, 13, 1632.	12.8	24
2470	Genetic variants associated mRNA stability in lung. <i>BMC Genomics</i> , 2022, 23, 196.	2.8	2
2472	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. <i>Nature Neuroscience</i> , 2022, 25, 381-389.	14.8	27
2474	Evolutionary insights into primate skeletal gene regulation using a comparative cell culture model. <i>PLoS Genetics</i> , 2022, 18, e1010073.	3.5	10
2475	The Power of Single-Cell RNA Sequencing in eQTL Discovery. <i>Genes</i> , 2022, 13, 502.	2.4	6
2477	Fibrillar Collagen Variants in Spontaneous Coronary Artery Dissection. <i>JAMA Cardiology</i> , 2022, 7, 396.	6.1	19
2478	Addressing the mean-correlation relationship in co-expression analysis. <i>PLoS Computational Biology</i> , 2022, 18, e1009954.	3.2	11
2479	Understanding signatures of positive natural selection in human zinc transporter genes. <i>Scientific Reports</i> , 2022, 12, 4320.	3.3	2

#	ARTICLE	IF	CITATIONS
2481	New Insights for Biosensing: Lessons from Microbial Defense Systems. Chemical Reviews, 2022, 122, 8126-8180.	47.7	15
2482	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	21.4	23
2485	Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 2022, 185, 794-814.e30.	28.9	39
2486	Signatures of genetic variation in human microRNAs point to processes of positive selection and population-specific disease risks. Human Genetics, 2022, 141, 1673-1693.	3.8	3
2487	The Ca ²⁺ -gated channel TMEM16A amplifies capillary pericyte contraction and reduces cerebral blood flow after ischemia. Journal of Clinical Investigation, 2022, 132, .	8.2	46
2488	Identifying causal genes for depression via integration of the proteome and transcriptome from brain and blood. Molecular Psychiatry, 2022, 27, 2849-2857.	7.9	27
2489	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	6.5	26
2491	Clinical Implications of KrÄ½apple-like Transcription Factor KLF-14 and Certain Micro-RNA (miR-27a,) Tj ETQq1 1 0.784314 rgBT /Overl Personalized Medicine, 2022, 12, 586.	2.5	3
2492	A year of COVID-19 GWAS results from the GRASP portal reveals potential genetic risk factors. Human Genetics and Genomics Advances, 2022, 3, 100095.	1.7	21
2493	Single-cell eQTL mapping identifies cell typeâ€“specific genetic control of autoimmune disease. Science, 2022, 376, eabf3041.	12.6	171
2495	Characterization of differential gene expression of broiler chicken to thermal stress in discrete developmental stages. Animal Cells and Systems, 2022, 26, 62-69.	2.2	2
2496	Powerful eQTL mapping through low-coverage RNA sequencing. Human Genetics and Genomics Advances, 2022, 3, 100103.	1.7	2
2497	A Genotypeâ€“Phenotype Analysis of Glutathione Peroxidase 4 in Human Atrial Myocardium and Its Association with Postoperative Atrial Fibrillation. Antioxidants, 2022, 11, 721.	5.1	1
2498	Clinical implementation of RNA sequencing for Mendelian disease diagnostics. Genome Medicine, 2022, 14, 38.	8.2	85
2499	Dietary<i>Lactobacillus</i>-Derived Exopolysaccharide Enhances Immune-Checkpoint Blockade Therapy. Cancer Discovery, 2022, 12, 1336-1355.	9.4	56
2500	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
2501	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
2502	A whole genome sequencing study of moderate to severe asthma identifies a lung function locus associated with asthma risk. Scientific Reports, 2022, 12, 5574.	3.3	9

#	ARTICLE	IF	CITATIONS
2503	Twenty-Five Novel Loci for Carotid Intima-Media Thickness: A Genome-Wide Association Study in >45,000 Individuals and Meta-Analysis of >100,000 Individuals. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 484-501.	2.4	17
2507	The Impact of Donor and Recipient Genetic Variation on Outcomes After Solid Organ Transplantation: A Scoping Review and Future Perspectives. Transplantation, 2022, 106, 1548-1557.	1.0	2
2508	Overlapping Genetic Architecture Between Schizophrenia and Neurodegenerative Disorders. Frontiers in Cell and Developmental Biology, 2021, 9, 797072.	3.7	8
2509	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. Translational Psychiatry, 2021, 11, 618.	4.8	17
2510	Restricted maximum-likelihood method for learning latent variance components in gene expression data with known and unknown confounders. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	3
2511	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. Cell Genomics, 2021, 1, 100069.	6.5	15
2513	Environmental and genome-wide association study on children anxiety and depression. , 2021, , .		1
2514	Prioritising positively selected variants in whole-genome sequencing data using FineMAV. BMC Bioinformatics, 2021, 22, 604.	2.6	0
2515	Transcript-Specific Loss-of-Function Variants in <i>VPS16</i> Are Enriched in Patients With Dystonia. Neurology: Genetics, 2022, 8, e644.	1.9	9
2518	Combination of Genomic and Transcriptomic Approaches Highlights Vascular and Circadian Clock Components in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 310.	4.1	9
2519	Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. Genome Research, 2022, 32, 389-402.	5.5	8
2520	The Cancer Surfaceome Atlas integrates genomic, functional and drug response data to identify actionable targets. Nature Cancer, 2021, 2, 1406-1422.	13.2	33
2521	Genome-wide association and functional interrogation identified a variant at 3p26.1 modulating ovarian cancer survival among Chinese women. Cell Discovery, 2021, 7, 121.	6.7	5
2522	RegVar: Tissue-Specific Prioritization of Non-Coding Regulatory Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 385-395.	6.9	2
2524	Genetic Contributors of Incident Stroke in 10,700 African Americans With Hypertension: A Meta-Analysis From the Genetics of Hypertension Associated Treatments and Reasons for Geographic and Racial Differences in Stroke Studies. Frontiers in Genetics, 2021, 12, 781451.	2.3	7
2525	Multi-Omic Approaches to Identify Genetic Factors in Metabolic Syndrome. , 2021, 12, 3045-3084.		4
2526	Alternative Splicing in Myeloid Malignancies. Biomedicines, 2021, 9, 1844.	3.2	5
2527	Bi-allelic variants in OGDHL cause a neurodevelopmental spectrum disease featuring epilepsy, hearing loss, visual impairment, and ataxia. American Journal of Human Genetics, 2021, 108, 2368-2384.	6.2	12

#	ARTICLE	IF	CITATIONS
2529	Long-read isoform sequencing reveals tissue-specific isoform expression between active and hibernating brown bears (<i>Ursus arctos</i>). G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
2530	Identification of a Risk Locus at 7p22.3 for Schizophrenia and Bipolar Disorder in East Asian Populations. Frontiers in Genetics, 2021, 12, 789512.	2.3	0
2531	The neurobiological basis of divergent thinking: Insight from gene co-expression network-based analysis. NeuroImage, 2021, 245, 118762.	4.2	1
2532	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	6.5	0
2534	Gene expression changes following chronic antipsychotic exposure in single cells from mouse striatum. Molecular Psychiatry, 2022, 27, 2803-2812.	7.9	10
2538	Genome-Wide Association Study of Campylobacter Positive Diarrhea Identifies Genes Involved in Toxin Processing and Inflammatory Response. MBio, 2022, 13, e0055622.	4.1	5
2539	Polygenic and Network-based studies in risk identification and demystification of cancer. Expert Review of Molecular Diagnostics, 2022, 22, 427-438.	3.1	7
2540	Genetic variation of putative myokine signaling is dominated by biological sex and sex hormones. ELife, 2022, 11, .	6.0	13
2541	Horizontal transmission of disseminated neoplasia in the widespread clam <i>Macoma balthica</i> from the Southern Baltic Sea. Molecular Ecology, 2022, 31, 3128-3136.	3.9	11
2543	Somatic genomic changes in single Alzheimer's disease neurons. Nature, 2022, 604, 714-722.	27.8	92
2663	Genetic Regulation of DNA Methylation Yields Novel Discoveries in GWAS of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1068-1076.	2.5	1
2664	Genetic variation in ALDH4A1 is associated with muscle health over the lifespan and across species. ELife, 2022, 11, .	6.0	7
2665	WebCSEA: web-based cell-type-specific enrichment analysis of genes. Nucleic Acids Research, 2022, 50, W782-W790.	14.5	29
2666	Association of Predicted Expression and Multimodel Association Analysis of Substance Abuse Traits. Complex Psychiatry, 2022, 8, 35-46.	0.9	0
2667	GWAS of Hematuria. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 672-683.	4.5	7
2669	The dynamic effect of genetic variation on the in vivo ER stress transcriptional response in different tissues. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	3
2670	Genetic insight into Birt-Hogg-Dubé syndrome in Indian patients reveals novel mutations at FLCN. Orphanet Journal of Rare Diseases, 2022, 17, 176.	2.7	1
2671	NeoSplice: a bioinformatics method for prediction of splice variant neoantigens. Bioinformatics Advances, 2022, 2, .	2.4	13

#	ARTICLE	IF	CITATIONS
2672	Comprehensive and integrative analyses identify TYW5 as a schizophrenia risk gene. BMC Medicine, 2022, 20, 169.	5.5	5
2673	Genome-Wide Association Study Suggests the Variant rs7551288*A within the DHCR24 Gene Is Associated with Poor Overall Survival in Melanoma Patients. Cancers, 2022, 14, 2410.	3.7	2
2674	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
2675	Genome-wide association and Mendelian randomization study of blood copper levels and 213 deep phenotypes in humans. Communications Biology, 2022, 5, 405.	4.4	7
2677	Germline and somatic genetic variability of oxysterol-related genes in breast cancer patients with early disease of the luminal subtype. Biochimie, 2022, 199, 158-169.	2.6	3
2678	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. Science, 2022, 376, eabl4290.	12.6	180
2679	Transcriptome-wide association study identifies <i>PSMB9</i> as a susceptibility gene for coal workers' pneumoconiosis. Environmental Toxicology, 2022, , .	4.0	1
2680	Multi-omics single-cell data integration and regulatory inference with graph-linked embedding. Nature Biotechnology, 2022, 40, 1458-1466.	17.5	153
2681	Use of viral motif mimicry improves the proteome-wide discovery of human linear motifs. Cell Reports, 2022, 39, 110764.	6.4	10
2682	Profiling the Genome-Wide Landscape of Short Tandem Repeats by Long-Read Sequencing. Frontiers in Genetics, 2022, 13, .	2.3	4
2683	Shared genetic loci between depression and cardiometabolic traits. PLoS Genetics, 2022, 18, e1010161.	3.5	18
2684	Brain region-specific effects of nearly fixed sapiens-derived alleles. BMC Genomic Data, 2022, 23, 36.	1.7	1
2685	Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. Nature Genetics, 2022, 54, 593-602.	21.4	98
2686	Analysis of MRI-derived spleen iron in the UK Biobank identifies genetic variation linked to iron homeostasis and hemolysis. American Journal of Human Genetics, 2022, 109, 1092-1104.	6.2	7
2687	An optimal variant to gene distance window derived from an empirical definition of cis and trans protein QTLs. BMC Bioinformatics, 2022, 23, 169.	2.6	22
2688	Recombination affects allele-specific expression of deleterious variants in human populations. Science Advances, 2022, 8, eabl3819.	10.3	3
2689	3' untranslated regions of tumor suppressor genes evolved specific features to favor cancer resistance. Oncogene, 2022, , .	5.9	0
2690	Prioritization of risk genes in multiple sclerosis by a refined Bayesian framework followed by tissue-specificity and cell type feature assessment. BMC Genomics, 2022, 23, 362.	2.8	4

#	ARTICLE	IF	CITATIONS
2691	GWAS of thyroid dysgenesis identifies a risk locus at 2q33.3 linked to regulation of Wnt signaling. Human Molecular Genetics, 2022, 31, 3967-3974.	2.9	2
2692	Functional Characterization of Genetic Variant Effects on Expression. Annual Review of Biomedical Data Science, 2022, 5, 119-139.	6.5	7
2693	Impact of natural selection on global patterns of genetic variation and association with clinical phenotypes at genes involved in SARS-CoV-2 infection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123000119.	7.1	7
2694	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. American Journal of Human Genetics, 2022, 109, 1077-1091.	6.2	27
2695	Annotating functional effects of non-coding variants in neuropsychiatric cell types by deep transfer learning. PLoS Computational Biology, 2022, 18, e1010011.	3.2	7
2696	Molecular Quantitative Trait Locus Mapping in Human Complex Diseases. Current Protocols, 2022, 2, e426.	2.9	3
2697	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type composition—implications for COVID-19. International Journal of Obesity, 2022, 46, 1478-1486.	3.4	18
2702	Neuronal Cells Display Distinct Stability Controls of Alternative Polyadenylation mRNA Isoforms, Long Non-Coding RNAs, and Mitochondrial RNAs. Frontiers in Genetics, 2022, 13, .	2.3	3
2705	Genetically regulated gene expression and proteins revealed discordant effects. PLoS ONE, 2022, 17, e0268815.	2.5	1
2708	ezQTL: A Web Platform for Interactive Visualization and Colocalization of QTLs and GWAS Loci. Genomics, Proteomics and Bioinformatics, 2022, 20, 541-548.	6.9	17
2709	Genotype–phenotype correlation of T-cell subtypes reveals senescent and cytotoxic genes in Alzheimer’s disease. Human Molecular Genetics, 2022, 31, 3355-3366.	2.9	2
2710	Identification of gene signatures for COAD using feature selection and Bayesian network approaches. Scientific Reports, 2022, 12, .	3.3	4
2712	Construction of an inter-organ transomic network for whole-body metabolism. Current Opinion in Endocrine and Metabolic Research, 2022, , 100361.	1.4	0
2715	Diverse molecular causes of unsolved autosomal dominant tubulointerstitial kidney diseases. Kidney International, 2022, 102, 405-420.	5.2	10
2717	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. Genome Medicine, 2022, 14, .	8.2	2
2718	Genetic overlap between idiopathic pulmonary fibrosis and COVID-19. European Respiratory Journal, 2022, 60, 2103132.	6.7	22
2719	Investigating the genetic architecture of eye colour in a Canadian cohort. IScience, 2022, 25, 104485.	4.1	2
2722	Polymorphisms of the matrix metalloproteinase 9 gene are associated with duodenal ulcer in a Caucasian population of Central Russia. Journal of King Saud University - Science, 2022, 34, 102142.	3.5	3

#	ARTICLE	IF	CITATIONS
2723	Epigenome-wide DNA methylation in obsessive-compulsive disorder. <i>Translational Psychiatry</i> , 2022, 12, .	4.8	10
2725	Associations of genetic risk, BMI trajectories, and the risk of non-small cell lung cancer: a population-based cohort study. <i>BMC Medicine</i> , 2022, 20, .	5.5	10
2726	Genome-wide association analysis and replication in 810,625 individuals with varicose veins. <i>Nature Communications</i> , 2022, 13, .	12.8	8
2727	Population-scale analysis of common and rare genetic variation associated with hearing loss in adults. <i>Communications Biology</i> , 2022, 5, .	4.4	12
2730	Mechanisms and pathophysiology of Barrett oesophagus. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2022, 19, 605-620.	17.8	11
2731	Contribution and clinical relevance of germline variation to the cancer transcriptome. <i>BMC Cancer</i> , 2022, 22, .	2.6	0
2732	Predicting which genes will respond to transcription factor perturbations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	1
2734	Discovering Innate Driver Variants for Risk Assessment of Early Colorectal Cancer Metastasis. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	0
2735	The Involvement of ALPK3 in Hypertrophic Cardiomyopathy in East Asia. <i>Frontiers in Medicine</i> , 0, 9, .	2.6	2
2736	The risk variant rs11836367 contributes to breast cancer onset and metastasis by attenuating Wnt signaling via regulating <i>NTN4</i> expression. <i>Science Advances</i> , 2022, 8, .	10.3	1
2737	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1286-1297.	6.2	30
2738	Microbiome-associated human genetic variants impact phenome-wide disease risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
2739	A Novel Locus on 6p21.2 for Cancer Treatmentâ€‘Induced Cardiac Dysfunction Among Childhood Cancer Survivors. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1109-1116.	6.3	4
2741	Genomic architecture and functional effects of potential human inversion supergenes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	13
2742	The impact of species-wide gene expression variation on <i>Caenorhabditis elegans</i> complex traits. <i>Nature Communications</i> , 2022, 13, .	12.8	23
2744	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 0, , .	2.5	1
2746	Epigenomic analysis reveals a dynamic and context-specific macrophage enhancer landscape associated with innate immune activation and tolerance. <i>Genome Biology</i> , 2022, 23, .	8.8	9
2748	Knockout of Sorbin And SH3 Domain Containing 2 (<i>Sorbs2</i>) in Cardiomyocytes Leads to Dilated Cardiomyopathy in Mice. <i>Journal of the American Heart Association</i> , 2022, 11, .	3.7	5

#	ARTICLE	IF	CITATIONS
2749	Allelic imbalance of chromatin accessibility in cancer identifies candidate causal risk variants and their mechanisms. <i>Nature Genetics</i> , 2022, 54, 837-849.	21.4	11
2750	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	17
2751	TCF7L2 plays a complex role in human adipose progenitor biology, which might contribute to genetic susceptibility to type 2 diabetes. <i>Metabolism: Clinical and Experimental</i> , 2022, 133, 155240.	3.4	6
2752	dbBIP: a comprehensive bipolar disorder database for genetic research. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
2753	Exploring the Effects of Mitonuclear Interactions on Mitochondrial DNA Gene Expression in Humans. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
2754	Genome-wide association and multi-omics studies identify <i>MGMT</i> as a novel risk gene for Alzheimer's disease among women. <i>Alzheimer's and Dementia</i> , 2023, 19, 896-908.	0.8	19
2755	3DFAACTS-SNP: using regulatory T cell-specific epigenomics data to uncover candidate mechanisms of type 1 diabetes (T1D) risk. <i>Epigenetics and Chromatin</i> , 2022, 15, .	3.9	2
2756	Epigenetic regulation in cardiovascular disease: mechanisms and advances in clinical trials. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	17.1	76
2757	A Computational Framework to Characterize the Cancer Drug Induced Effect on Aging Using Transcriptomic Data. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	0
2758	Harnessing the Full Potential of Multi-Omic Analyses to Advance the Study and Treatment of Chronic Kidney Disease. , 0, 2, .		1
2759	Genes and Diseases: Insights from Transcriptomics Studies. <i>Genes</i> , 2022, 13, 1168.	2.4	5
2760	Genetic variant rs9848497 up-regulates <i>MST1R</i> expression, thereby influencing leadership phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	4
2761	Inter- and intra-chromosomal modulators of the APOE ϵ 2 and ϵ 4 effects on the Alzheimer's disease risk. <i>GeroScience</i> , 0, , .	4.6	2
2762	Association between Ancestry-Specific 6q25 Variants and Breast Cancer Subtypes in Peruvian Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 0, , OF1-OF8.	2.5	2
2763	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. <i>Nature Cancer</i> , 2022, 3, 994-1011.	13.2	20
2764	Context-specific regulation and function of mRNA alternative polyadenylation. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 779-796.	37.0	89
2766	Large-Scale Multi-Omics Studies Provide New Insights into Blood Pressure Regulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7557.	4.1	10
2770	Translational impact of omics studies in alopecia areata: recent advances and future perspectives. <i>Expert Review of Clinical Immunology</i> , 2022, 18, 845-857.	3.0	2

#	ARTICLE	IF	CITATIONS
2771	A high-resolution map of human RNA translation. <i>Molecular Cell</i> , 2022, 82, 2885-2899.e8.	9.7	37
2772	ILRUN Promotes Atherosclerosis Through Lipid-Dependent and Lipid-Independent Factors. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 0, , .	2.4	2
2773	Endocrine and behavioural features of Lowe syndrome and their potential molecular mechanisms. <i>Journal of Medical Genetics</i> , 2022, 59, 1171-1178.	3.2	1
2774	Characterizing the extracellular matrix transcriptome of cervical, endometrial, and uterine cancers. <i>Matrix Biology Plus</i> , 2022, 15, 100117.	3.5	6
2775	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. <i>Cell Genomics</i> , 2022, 2, 100145.	6.5	19
2777	DeCAF: a novel method to identify cell-type specific regulatory variants and their role in cancer risk. <i>Genome Biology</i> , 2022, 23, .	8.8	1
2779	Random Field Modeling of Multi-trait Multi-locus Association for Detecting Methylation Quantitative Trait Loci. <i>Bioinformatics</i> , 0, , .	4.1	0
2780	Parkinsonâ€™s Disease rs117896735 Variant Regulates INPP5F Expression in Brain Tissues and Increases Risk of Alzheimerâ€™s Disease. <i>Journal of Alzheimer's Disease</i> , 2022, 89, 67-77.	2.6	3
2781	Patterns of Convergence and Divergence Between Bipolar Disorder Type I and Type II: Evidence From Integrative Genomic Analyses. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	3.7	6
2782	Colocalization of Gene Expression and DNA Methylation with Genetic Risk Variants Supports Functional Roles of <i>MUC5B</i> and <i>DSP</i> in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1259-1270.	5.6	12
2783	Impact of FOXP3 gene polymorphisms and gene-environment interactions in asthma and atopy in a Brazilian population. <i>Gene</i> , 2022, 838, 146706.	2.2	1
2786	Aggregative trans-eQTL analysis detects trait-specific target gene sets in whole blood. <i>Nature Communications</i> , 2022, 13, .	12.8	7
2787	High-dimension to high-dimension screening for detecting genome-wide epigenetic and noncoding RNA regulators of gene expression. <i>Bioinformatics</i> , 2022, 38, 4078-4087.	4.1	1
2788	Singleâ€cell expression Quantitative Trait Loci: Tâ€cell immunology teams up with statistical genetics. <i>Immunology and Cell Biology</i> , 2022, 100, 588-590.	2.3	1
2789	Variation in TAF1 Expression in Female Carrier-Induced Pluripotent Stem Cells and Human Brain Ontogeny Has Implications for Adult Neostriatum Vulnerability in X-Linked Dystonia Parkinsonism. <i>ENeuro</i> , 2022, 9, ENEURO.0129-22.2022.	1.9	0
2790	Identification of RNA modification-associated single-nucleotide polymorphisms in genomic loci for low-density lipoprotein cholesterol concentrations. <i>Pharmacogenomics</i> , 2022, 23, 655-665.	1.3	0
2791	Shared genetic susceptibility between trigger finger and carpal tunnel syndrome: a genome-wide association study. <i>Lancet Rheumatology</i> , The, 2022, 4, e556-e565.	3.9	5
2792	Contrastive latent variable modeling with application to case-control sequencing experiments. <i>Annals of Applied Statistics</i> , 2022, 16, .	1.1	3

#	ARTICLE	IF	CITATIONS
2793	Rare loss of function variants in the hepatokine gene INHBE protect from abdominal obesity. <i>Nature Communications</i> , 2022, 13, .	12.8	15
2794	RNA modification-related variants in genomic loci associated with body mass index. <i>Human Genomics</i> , 2022, 16, .	2.9	3
2795	Sex-dependent transcription of cardiac electrophysiology and links to acetylation modifiers based on the GTEx database. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	2.4	12
2798	GWAS meta-analysis of 16 790 patients with Barrett's oesophagus and oesophageal adenocarcinoma identifies 16 novel genetic risk loci and provides insights into disease aetiology beyond the single marker level. <i>Gut</i> , 2023, 72, 612-623.	12.1	6
2799	Incomplete Penetrance and Variable Expressivity: From Clinical Studies to Population Cohorts. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	67
2800	Strategies to identify causal common genetic variants and corresponding effector genes for paediatric obesity. <i>Pediatric Obesity</i> , 2022, 17, .	2.8	1
2801	Predicting genes associated with RNA methylation pathways using machine learning. <i>Communications Biology</i> , 2022, 5, .	4.4	1
2802	Genetic identification of tissues and cell types underlying attention-deficit/hyperactivity disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	2.6	1
2803	Common Variants Near <i>ZIC1</i> and <i>ZIC4</i> in Autopsy-Confirmed Multiple System Atrophy. <i>Movement Disorders</i> , 2022, 37, 2110-2121.	3.9	6
2804	Multi-ancestry fine-mapping improves precision to identify causal genes in transcriptome-wide association studies. <i>American Journal of Human Genetics</i> , 2022, 109, 1388-1404.	6.2	18
2805	Transcriptomic Responses of Human Retinal Vascular Endothelial Cells to Inflammatory Cytokines. <i>Translational Vision Science and Technology</i> , 2022, 11, 27.	2.2	7
2806	Comprehensive in Silico Analyses of Single Nucleotide Variants of the Human Orthologues of 171 Murine Loci to Seek Novel Insights into the Genetics of Human Pigmentation. <i>Proceedings of the Zoological Society</i> , 0, , .	1.0	0
2807	Differences in set-based tests for sparse alternatives when testing sets of outcomes compared to sets of explanatory factors in genetic association studies. <i>Biostatistics</i> , 2023, 25, 171-187.	1.5	0
2809	Genetic association-based functional analysis detects HOGA1 as a potential gene involved in fat accumulation. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1
2810	Genomic-Analysis-Oriented Drug Repurposing in the Search for Novel Antidepressants. <i>Biomedicines</i> , 2022, 10, 1947.	3.2	6
2811	Genome-wide meta-analyses reveal novel loci for verbal short-term memory and learning. <i>Molecular Psychiatry</i> , 2022, 27, 4419-4431.	7.9	6
2812	Cell non-autonomous effect of hepatic growth differentiation factor 15 on the thyroid gland. <i>Frontiers in Endocrinology</i> , 0, 13, .	3.5	1
2815	A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids. <i>American Journal of Human Genetics</i> , 2022, 109, 1366-1387.	6.2	24

#	ARTICLE	IF	CITATIONS
2820	A cross-disorder dosage sensitivity map of the human genome. <i>Cell</i> , 2022, 185, 3041-3055.e25.	28.9	117
2821	Replication Study for the Association of Five SNPs Identified by GWAS and Trastuzumab-Induced Cardiotoxicity in Japanese and Singaporean Cohorts. <i>Biological and Pharmaceutical Bulletin</i> , 2022, 45, 1198-1202.	1.4	2
2822	Scalable approaches for functional analyses of whole-genome sequencing non-coding variants. <i>Human Molecular Genetics</i> , 2022, 31, R62-R72.	2.9	2
2824	Genetic variant rs11136000 upregulates clusterin expression and reduces Alzheimer's disease risk. <i>Frontiers in Neuroscience</i> , 0, 16, .	2.8	3
2825	Telescoping bimodal latent Dirichlet allocation to identify expression QTLs across tissues. <i>Life Science Alliance</i> , 2022, 5, e202101297.	2.8	3
2826	Exploring Lead loci shared between schizophrenia and Cardiometabolic traits. <i>BMC Genomics</i> , 2022, 23, .	2.8	1
2827	Cellular Genome-wide Association Study Identifies Common Genetic Variation Influencing Lithium-Induced Neural Progenitor Proliferation. <i>Biological Psychiatry</i> , 2023, 93, 8-17.	1.3	6
2828	Longitudinal lung function and gas transfer in individuals with idiopathic pulmonary fibrosis: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , the, 2023, 11, 65-73.	10.7	20
2830	Circulating Proteins Influencing Psychiatric Disease: A Mendelian Randomization Study. <i>Biological Psychiatry</i> , 2023, 93, 82-91.	1.3	10
2833	Fc Fragment of <i>IG</i> Receptor Ig (<i>FCER1G</i>) acts as a key gene involved in cancer immune infiltration and tumour microenvironment. <i>Immunology</i> , 2023, 168, 302-319.	4.4	7
2834	GPNMB confers risk for Parkinson's disease through interaction with α -synuclein. <i>Science</i> , 2022, 377, .	12.6	65
2835	Transcriptome-wide association study of HIV-1 acquisition identifies <i>HERC1</i> as a susceptibility gene. <i>IScience</i> , 2022, 25, 104854.	4.1	2
2836	Shared genetics and causality underlying epilepsy and attention-deficit hyperactivity disorder. <i>Psychiatry Research</i> , 2022, 316, 114794.	3.3	10
2837	The oxytocin signalling gene pathway contributes to the association between loneliness and cardiometabolic health. <i>Psychoneuroendocrinology</i> , 2022, 144, 105875.	2.7	2
2838	Post-traumatic stress disorder in the Canadian Longitudinal Study on Aging: A genome-wide association study. <i>Journal of Psychiatric Research</i> , 2022, 154, 209-218.	3.1	0
2839	Genetic determinants of chromatin reveal prostate cancer risk mediated by context-dependent gene regulation. <i>Nature Genetics</i> , 2022, 54, 1364-1375.	21.4	19
2840	Variants in the <i>GPR146</i> Gene Are Associated With a Favorable Cardiometabolic Risk Profile. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 1262-1271.	2.4	3
2841	Genetic polymorphism of cytokines IL-1 β , IL-4 and TNF- α as a factor modifying the impact of childhood adversity on schizophrenia symptoms. <i>Zhurnal Nevrologii I Psikiatrii Imeni S S Korsakova</i> , 2022, 122, 110.	0.7	1

#	ARTICLE	IF	CITATIONS
2842	The genetic basis of Gilles de la Tourette syndrome. <i>International Review of Movement Disorders</i> , 2022, , 3-38.	0.1	0
2843	Identification of circadian clock genes as regulators of immune infiltration in Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2022, 13, 3199-3208.	2.5	4
2844	ipaQTL-atlas: an atlas of intronic polyadenylation quantitative trait loci across human tissues. <i>Nucleic Acids Research</i> , 2023, 51, D1046-D1052.	14.5	4
2847	Cross-ancestry meta-analysis of opioid use disorder uncovers novel loci with predominant effects in brain regions associated with addiction. <i>Nature Neuroscience</i> , 2022, 25, 1279-1287.	14.8	26
2848	Web-based gene expression analysis“paving the way to decode healthy and diseased ocular tissue. , 2023, 120, 59-65.		2
2849	TVAR: assessing tissue-specific functional effects of non-coding variants with deep learning. <i>Bioinformatics</i> , 2022, 38, 4697-4704.	4.1	4
2850	Nucleophosmin 1 is a prognostic marker of gastrointestinal cancer and is associated with m6A and cuproptosis. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	5
2851	Long Noncoding RNA TPRG1-AS1 Suppresses Migration of Vascular Smooth Muscle Cells and Attenuates Atherogenesis via Interacting With MYH9 Protein. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 1378-1397.	2.4	10
2852	A <scp>pyroptosis“related</scp> signature predicts prognosis and indicates immune microenvironment infiltration in glioma. <i>Cancer Medicine</i> , 0, , .	2.8	3
2853	Nonparametric single-cell multiomic characterization of trio relationships between transcription factors, target genes, and cis-regulatory regions. <i>Cell Systems</i> , 2022, 13, 737-751.e4.	6.2	16
2855	Sex- and age-dependent genetics of longevity in a heterogeneous mouse population. <i>Science</i> , 2022, 377, .	12.6	29
2856	Rethinking cancer targeting strategies in the era of smart cell therapeutics. <i>Nature Reviews Cancer</i> , 2022, 22, 693-702.	28.4	21
2857	DNA methylation landscapes from pig“limbic structures underline regulatory mechanisms relevant for brain plasticity. <i>Scientific Reports</i> , 2022, 12, .	3.3	0
2858	Pathway-Specific Polygenic Risk Scores Identify Obstructive Sleep Apnea“Related Pathways Differentially Moderating Genetic Susceptibility to Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	3.6	10
2859	A quantile integral linear model to quantify genetic effects on phenotypic variability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	7
2860	Exploring the association of interleukin polymorphisms with aggression and internalizing behaviors in children and adolescents. <i>Brain and Behavior</i> , 2022, 12, .	2.2	3
2861	Genome-wide association analyses of physical activity and sedentary behavior provide insights into underlying mechanisms and roles in disease prevention. <i>Nature Genetics</i> , 2022, 54, 1332-1344.	21.4	64
2862	Stroke genetics informs drug discovery and risk prediction across ancestries. <i>Nature</i> , 2022, 611, 115-123.	27.8	143

#	ARTICLE	IF	CITATIONS
2863	Genetic analyses of the electrocardiographic QT interval and its components identify additional loci and pathways. <i>Nature Communications</i> , 2022, 13, .	12.8	15
2865	Variants influencing age at diagnosis of HNF1A-MODY. <i>Molecular Medicine</i> , 2022, 28, .	4.4	1
2866	Multi-context genetic modeling of transcriptional regulation resolves novel disease loci. <i>Nature Communications</i> , 2022, 13, .	12.8	6
2867	Interpretation of the role of germline and somatic non-coding mutations in cancer: expression and chromatin conformation informed analysis. <i>Clinical Epigenetics</i> , 2022, 14, .	4.1	3
2868	Characterization of the functional effects of ferredoxin 1 as a cuproptosis biomarker in cancer. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	6
2869	A transcriptome-wide association study of uterine fibroids to identify potential genetic markers and toxic chemicals. <i>PLoS ONE</i> , 2022, 17, e0274879.	2.5	3
2870	Identifying enhancer properties associated with genetic risk for complex traits using regulome-wide association studies. <i>PLoS Computational Biology</i> , 2022, 18, e1010430.	3.2	4
2871	Novel insight into the aetiology of rheumatoid arthritis gained by a cross-tissue transcriptome-wide association study. <i>RMD Open</i> , 2022, 8, e002529.	3.8	2
2872	GATA4 and GATA6 loss-of-expression is associated with extinction of the classical programme and poor outcome in pancreatic ductal adenocarcinoma. <i>Gut</i> , 2023, 72, 535-548.	12.1	10
2874	A resource for integrated genomic analysis of the human liver. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
2875	Multitissue Integrative Analysis Identifies Susceptibility Genes for Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2023, 143, 602-611.e14.	0.7	0
2876	A comprehensive genomic and transcriptomic dataset of triple-negative breast cancers. <i>Scientific Data</i> , 2022, 9, .	5.3	6
2877	Coronary artery disease risk factors affected by RNA modification-related genetic variants. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	2.4	5
2880	Comprehensive analysis of 124 transcriptomes from 31 tissues in developing, juvenile, and adult Japanese Black Cattle. <i>DNA Research</i> , 0, , .	3.4	2
2881	Neandertal introgression partitions the genetic landscape of neuropsychiatric disorders and associated behavioral phenotypes. <i>Translational Psychiatry</i> , 2022, 12, .	4.8	7
2882	Immune system disruptions implicated in whole blood epigenome-wide association study of depression among Parkinson's disease patients. <i>Brain, Behavior, & Immunity - Health</i> , 2022, , 100530.	2.5	2
2883	Integrating transcriptomics, metabolomics, and GWAS helps reveal molecular mechanisms for metabolite levels and disease risk. <i>American Journal of Human Genetics</i> , 2022, 109, 1727-1741.	6.2	16
2884	Prevalence and mechanisms of somatic deletions in single human neurons during normal aging and in DNA repair disorders. <i>Nature Communications</i> , 2022, 13, .	12.8	10

#	ARTICLE	IF	CITATIONS
2886	Tissue-specific impacts of aging and genetics on gene expression patterns in humans. Nature Communications, 2022, 13, .	12.8	23
2887	Transcriptome-wide summary data-based Mendelian randomization analysis reveals 38 novel genes associated with severe COVID-19. Journal of Medical Virology, 2023, 95, .	5.0	15
2891	Identifying pleiotropic genes for major psychiatric disorders with GWAS summary statistics using multivariate adaptive association tests. Journal of Psychiatric Research, 2022, 155, 471-482.	3.1	1
2892	Breast cancer-associated SNP rs72755295 is a cis-regulatory variation for human EXO1. Genetics and Molecular Biology, 2022, 45, .	1.3	2
2893	Genetisch-molekulare Grundlagen von Gesundheit und Krankheit. The Springer Reference Pflege, Gesundheit, 2022, , 51-61.	0.3	0
2894	Anti-Epileptic Drug Target Perturbation and Intracranial Aneurysm Risk: Mendelian Randomization and Colocalization Study. Stroke, 2023, 54, 208-216.	2.0	9
2895	Trans-ancestry, Bayesian meta-analysis discovers 20 novel risk loci for inflammatory bowel disease in an African American, East Asian and European cohort. Human Molecular Genetics, 2023, 32, 873-882.	2.9	8
2896	Animal-SNPAtlas: a comprehensive SNP database for multiple animals. Nucleic Acids Research, 2023, 51, D816-D826.	14.5	8
2897	PCA outperforms popular hidden variable inference methods for molecular QTL mapping. Genome Biology, 2022, 23, .	8.8	18
2898	Discovering Breast Cancer Biomarkers Candidates through mRNA Expression Analysis Based on The Cancer Genome Atlas Database. Journal of Personalized Medicine, 2022, 12, 1753.	2.5	4
2899	A Role of DNA Methylation within the CYP17A1 Gene in the Association of Genetic and Environmental Risk Factors with Stress-Related Manifestations of Schizophrenia. International Journal of Molecular Sciences, 2022, 23, 12629.	4.1	0
2900	Evolution and antiviral activity of a human protein of retroviral origin. Science, 2022, 378, 422-428.	12.6	37
2901	DRESIS: the first comprehensive landscape of drug resistance information. Nucleic Acids Research, 2023, 51, D1263-D1275.	14.5	28
2903	Systematic analysis of the effects of genetic variants on chromatin accessibility to decipher functional variants in non-coding regions. Frontiers in Oncology, 0, 12, .	2.8	2
2904	Function and constraint in enhancer sequences with multiple evolutionary origins. Genome Biology and Evolution, 0, , .	2.5	5
2905	Repurposing Antihypertensive Drugs for the Prevention of Glaucoma: A Mendelian Randomization Study. Translational Vision Science and Technology, 2022, 11, 32.	2.2	3
2906	A synthetic transcription platform for programmable gene expression in mammalian cells. Nature Communications, 2022, 13, .	12.8	7
2907	Stem Cell Models for Context-Specific Modeling in Psychiatric Disorders. Biological Psychiatry, 2023, 93, 642-650.	1.3	9

#	ARTICLE	IF	CITATIONS
2908	Whole genome sequence analysis of blood lipid levels in >66,000 individuals. Nature Communications, 2022, 13, .	12.8	26
2909	COX7A2L genetic variants determine cardiorespiratory fitness in mice and human. Nature Metabolism, 2022, 4, 1336-1351.	11.9	10
2910	The regulatory landscape of multiple brain regions in outbred heterogeneous stock rats. Nucleic Acids Research, 2022, 50, 10882-10895.	14.5	20
2911	RNA Modification-Related Genetic Variants in Genomic Loci Associated with Bone Mineral Density and Fracture. Genes, 2022, 13, 1892.	2.4	4
2912	Association between genetic variants and the risk of nivolumab-induced immune-related adverse events. Pharmacogenomics, 2022, 23, 887-901.	1.3	5
2916	Diverse environmental perturbations reveal the evolution and context-dependency of genetic effects on gene expression levels. Genome Research, 0, , .	5.5	6
2917	Epigenetics of neural differentiation: Spotlight on enhancers. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	5
2918	Using human genetics to improve safety assessment of therapeutics. Nature Reviews Drug Discovery, 2023, 22, 145-162.	46.4	20
2920	Multimomics study of nonalcoholic fatty liver disease. Nature Genetics, 2022, 54, 1652-1663.	21.4	53
2922	SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification. Nature Communications, 2022, 13, .	12.8	6
2923	A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis. Cell Genomics, 2022, 2, 100190.	6.5	13
2924	Genome-Wide Association Study for eGFR in a Taiwanese Population. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 1598-1608.	4.5	1
2925	HiChIPdb: a comprehensive database of HiChIP regulatory interactions. Nucleic Acids Research, 2023, 51, D159-D166.	14.5	7
2926	Common and rare variants of EGF increase the genetic risk of Alzheimer's disease as revealed by targeted sequencing of growth factors in Han Chinese. Neurobiology of Aging, 2022, , .	3.1	1
2927	Phenome-wide analysis of Taiwan Biobank reveals novel glycemia-related loci and genetic risks for diabetes. Communications Biology, 2022, 5, .	4.4	9
2928	The landscape of hervRNAs transcribed from human endogenous retroviruses across human body sites. Genome Biology, 2022, 23, .	8.8	9
2929	Rational drug repositioning for coronavirus-associated diseases using directional mapping and side-effect inference. IScience, 2022, 25, 105348.	4.1	3
2931	GenomicKB: a knowledge graph for the human genome. Nucleic Acids Research, 2023, 51, D950-D956.	14.5	8

#	ARTICLE	IF	CITATIONS
2932	Leaf physiology variations are modulated by natural variations that underlie stomatal morphology in <i>Populus</i> . Plant, Cell and Environment, 2023, 46, 150-170.	5.7	6
2933	Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. Nature Neuroscience, 2022, 25, 1559-1568.	14.8	19
2934	Genetic and epigenetic links to asthma. , 2023, , 173-194.		0
2935	Integrating Multimorbidity into a Whole-Body Understanding of Disease Using Spatial Genomics. Results and Problems in Cell Differentiation, 2022, , 157-187.	0.7	0
2936	Collective genomic segments with differential pleiotropic patterns between cognitive dimensions and psychopathology. Nature Communications, 2022, 13, .	12.8	3
2937	Combining genetic constraint with predictions of alternative splicing to prioritize deleterious splicing in rare disease studies. BMC Bioinformatics, 2022, 23, .	2.6	7
2939	Discerning asthma endotypes through comorbidity mapping. Nature Communications, 2022, 13, .	12.8	8
2940	Network reconstruction for trans acting genetic loci using multi-omics data and prior information. Genome Medicine, 2022, 14, .	8.2	1
2941	Retrotransposon insertions associated with risk of neurologic and psychiatric diseases. EMBO Reports, 2023, 24, .	4.5	3
2944	Promoter sequence and architecture determine expression variability and confer robustness to genetic variants. ELife, 0, 11, .	6.0	12
2945	Genetic Mimicry Analysis Reveals the Specific Lipases Targeted by the ANGPTL3-ANGPTL8 Complex and ANGPTL4. Journal of Lipid Research, 2023, 64, 100313.	4.2	6
2946	Multi-ancestry genome-wide association analyses identify novel genetic mechanisms in rheumatoid arthritis. Nature Genetics, 2022, 54, 1640-1651.	21.4	68
2947	Prioritization of Drug Targets for Neurodegenerative Diseases by Integrating Genetic and Proteomic Data From Brain and Blood. Biological Psychiatry, 2023, 93, 770-779.	1.3	9
2948	The engineering challenges and opportunities when designing potent ionizable materials for the delivery of ribonucleic acids. Expert Opinion on Drug Delivery, 2022, 19, 1650-1663.	5.0	2
2949	Comparative immune-relevant transcriptome reveals the evolutionary basis of complex traits. IScience, 2022, 25, 105572.	4.1	0
2953	Genome-wide analyses of early-onset acute myocardial infarction identify 29 novel loci by whole genome sequencing. Human Genetics, 2023, 142, 231-243.	3.8	1
2954	DNA replication initiation shapes the mutational landscape and expression of the human genome. Science Advances, 2022, 8, .	10.3	4
2955	Identification of genetic loci that overlap between schizophrenia and metabolic syndrome. Psychiatry Research, 2022, 318, 114947.	3.3	1

#	ARTICLE	IF	CITATIONS
2956	The RNA editing landscape in acute myeloid leukemia reveals associations with disease mutations and clinical outcome. IScience, 2022, 25, 105622.	4.1	1
2957	Vitamin D Deficiency and COVID-19: A Biological Database Study on Pathways and Gene-Disease Associations. International Journal of Molecular Sciences, 2022, 23, 14256.	4.1	2
2959	Whole-exome sequence analysis of anthropometric traits illustrates challenges in identifying effects of rare genetic variants. Human Genetics and Genomics Advances, 2023, 4, 100163.	1.7	2
2960	Amplitudes of resting-state functional networks – investigation into their correlates and biophysical properties. NeuroImage, 2023, 265, 119779.	4.2	0
2961	Genetic influences on human blood metabolites in the Japanese population. IScience, 2023, 26, 105738.	4.1	1
2962	CRISPR/Cas9 genome editing demonstrates functionality of the autoimmunity-associated SNP rs12946510. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2023, 1869, 166599.	3.8	3
2963	Genome-wide association studies for thyroid physiology and diseases. Endocrine Journal, 2023, 70, 9-17.	1.6	3
2966	Investigating the shared genetic architecture and causal relationship between pain and neuropsychiatric disorders. Human Genetics, 2023, 142, 431-443.	3.8	6
2967	Bidirectional genetic overlap between bipolar disorder and intelligence. BMC Medicine, 2022, 20, .	5.5	2
2968	Evaluation of commercially available glucagon receptor antibodies and glucagon receptor expression. Communications Biology, 2022, 5, .	4.4	7
2969	Whole genome DNA and RNA sequencing of whole blood elucidates the genetic architecture of gene expression underlying a wide range of diseases. Scientific Reports, 2022, 12, .	3.3	3
2970	Transcriptome-wide association study and eQTL colocalization identify potentially causal genes responsible for human bone mineral density GWAS associations. ELife, 0, 11, .	6.0	13
2971	HGFAC is a ChREBP-regulated hepatokine that enhances glucose and lipid homeostasis. JCI Insight, 2023, 8, .	5.0	6
2972	Illuminating links between cis-regulators and trans-acting variants in the human prefrontal cortex. Genome Medicine, 2022, 14, .	8.2	5
2974	CHD6 promotes broad nucleosome eviction for transcriptional activation in prostate cancer cells. Nucleic Acids Research, 2022, 50, 12186-12201.	14.5	4
2976	Prediction of the cell-type-specific transcription of non-coding RNAs from genome sequences via machine learning. Nature Biomedical Engineering, 2023, 7, 830-844.	22.5	8
2977	Integration of genome-scale data identifies candidate sleep regulators. Sleep, 2023, 46, .	1.1	4
2978	The missing link between genetic association and regulatory function. ELife, 0, 11, .	6.0	46

#	ARTICLE	IF	CITATIONS
2980	Identification of Novel Metabolic Subtypes Using Multi-Trait Limited Mixed Regression in the Chinese Population. <i>Biomedicines</i> , 2022, 10, 3093.	3.2	0
2981	Multi-Omics Studies in Historically Excluded Populations: The Road to Equity. <i>Clinical Pharmacology and Therapeutics</i> , 2023, 113, 541-556.	4.7	6
2983	Expression Profile of Housekeeping Genes and Tissue-Specific Genes in Multiple Tissues of Pigs. <i>Animals</i> , 2022, 12, 3539.	2.3	2
2985	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants. <i>Nature Genetics</i> , 2022, 54, 1803-1815.	21.4	150
2986	Quantifying the role of transcript levels in mediating DNA methylation effects on complex traits and diseases. <i>Nature Communications</i> , 2022, 13, .	12.8	15
2987	Going broad and deep: sequencing-driven insights into plant physiology, evolution, and crop domestication. <i>Plant Journal</i> , 2023, 113, 446-459.	5.7	5
2988	Bayesian Genetic Colocalization Test of Two Traits Using <i>coloc</i> . <i>Current Protocols</i> , 2022, 2, .	2.9	3
2989	A Poisson reduced-rank regression model for association mapping in sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	2
2990	Comparative epigenomics reveals the impact of ruminant-specific regulatory elements on complex traits. <i>BMC Biology</i> , 2022, 20, .	3.8	2
2991	A comparison of the genes and genesets identified by GWAS and EWAS of fifteen complex traits. <i>Nature Communications</i> , 2022, 13, .	12.8	6
2992	DNA methylation QTL mapping across diverse human tissues provides molecular links between genetic variation and complex traits. <i>Nature Genetics</i> , 2023, 55, 112-122.	21.4	45
2993	Altered and allele-specific open chromatin landscape reveals epigenetic and genetic regulators of innate immunity in COVID-19. <i>Cell Genomics</i> , 2023, 3, 100232.	6.5	9
2994	XCVATR: detection and characterization of variant impact on the Embeddings of single -cell and bulk RNA-sequencing samples. <i>BMC Genomics</i> , 2022, 23, .	2.8	1
2997	De novo mutation hotspots in homologous protein domains identify function-altering mutations in neurodevelopmental disorders. <i>American Journal of Human Genetics</i> , 2023, 110, 92-104.	6.2	3
2998	New Research Perspectives on the Interplay Between Genes and Environment on Executive Function Development. <i>Biological Psychiatry</i> , 2023, 94, 131-141.	1.3	7
2999	A DNA methylation atlas of normal human cell types. <i>Nature</i> , 2023, 613, 355-364.	27.8	130
3000	Genome-Wide Feature Selection of Robust mRNA Biomarkers for Body Fluid Identification. <i>Communications in Computer and Information Science</i> , 2022, , 29-42.	0.5	0
3004	The Genetic Landscape of Familial Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2023, 207, 1345-1357.	5.6	7

#	ARTICLE	IF	CITATIONS
3006	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. <i>ELife</i> , 0, 12, .	6.0	2
3008	MicroRNA-mRNA networks are dysregulated in opioid use disorder postmortem brain: Further evidence for opioid-induced neurovascular alterations. <i>Frontiers in Psychiatry</i> , 0, 13, .	2.6	4
3009	Identifying key multifunctional components shared by critical cancer and normal liver pathways via SparseGMM. <i>Cell Reports Methods</i> , 2023, 3, 100392.	2.9	1
3010	Genome-wide association study of brain biochemical phenotypes reveals distinct genetic architecture of Alzheimer's disease related proteins. <i>Molecular Neurodegeneration</i> , 2023, 18, .	10.8	5
3011	Insights into familial adult myoclonus epilepsy pathogenesis: How the same repeat expansion in six unrelated genes may lead to cortical excitability. <i>Epilepsia</i> , 2023, 64, .	5.1	6
3012	Systemic interindividual epigenetic variation in humans is associated with transposable elements and under strong genetic control. <i>Genome Biology</i> , 2023, 24, .	8.8	11
3013	Random allelic expression in the adult human body. <i>Cell Reports</i> , 2023, 42, 111945.	6.4	10
3014	Biochemical association between the prevalence of genetic polymorphism and myocardial infarction. <i>Biocell</i> , 2023, 47, 473-484.	0.7	4
3015	Association between comorbid asthma and depression and depression-related gene SNPs. <i>Journal of Radiation Research and Applied Sciences</i> , 2023, 16, 100496.	1.2	0
3016	DNA methylation in human gastric epithelial cells defines regional identity without restricting lineage plasticity. <i>Clinical Epigenetics</i> , 2022, 14, .	4.1	1
3017	Genetic overlap between Parkinson's disease and inflammatory bowel disease. <i>Brain Communications</i> , 2022, 5, .	3.3	3
3018	Antisense-oligonucleotide-mediated perturbation of long non-coding RNA reveals functional features in stem cells and across cell types. <i>Cell Reports</i> , 2022, 41, 111893.	6.4	9
3020	Discovering eQTL Regulatory Patterns Through eQTLMotif. , 2022, , .		0
3021	Investigating the potential impact of PCSK9-inhibitors on mood disorders using eQTL-based Mendelian randomization. <i>PLoS ONE</i> , 2022, 17, e0279381.	2.5	3
3022	Identification of the expression, prognostic value and cancer immunity of Gasdermin E based on multi-omics data, machine learning and gene ontology. , 2022, , .		0
3023	Genome- and Transcriptome-Wide Association Studies Identify Susceptibility Genes and Pathways for Periodontitis. <i>Cells</i> , 2023, 12, 70.	4.1	2
3024	Genetic correlation and gene-based pleiotropy analysis for four major neurodegenerative diseases with summary statistics. <i>Neurobiology of Aging</i> , 2023, 124, 117-128.	3.1	4
3025	The ETS transcription factor ETV6 constrains the transcriptional activity of EWS-FLI1 to promote Ewing sarcoma. <i>Nature Cell Biology</i> , 0, , .	10.3	6

#	ARTICLE	IF	CITATIONS
3026	Cross-ancestry genome-wide analysis of atrial fibrillation unveils disease biology and enables cardioembolic risk prediction. <i>Nature Genetics</i> , 2023, 55, 187-197.	21.4	19
3030	A five-gene expression signature of centromeric proteins with prognostic value in lung adenocarcinoma. <i>Translational Cancer Research</i> , 2023, .	1.0	0
3031	Sequencing-based fine-mapping and in silico functional characterization of the 10q24.32 arsenic metabolism efficiency locus across multiple arsenic-exposed populations. <i>PLoS Genetics</i> , 2023, 19, e1010588.	3.5	1
3032	Multiallelic Copy Number Variation in ORM1 is Associated with Plasma Cell-Free DNA Levels as an Intermediate Phenotype for Venous Thromboembolism. <i>Thrombosis and Haemostasis</i> , 0, , .	3.4	0
3033	A <scp>Genomeâ€Wide</scp> Association Study <scp>Metaâ€Analysis</scp> of Alpha Angle Suggests <scp>Camâ€Type</scp> Morphology May Be a Specific Feature of Hip Osteoarthritis in Older Adults. <i>Arthritis and Rheumatology</i> , 2023, 75, 900-909.	5.6	6
3036	A Comprehensive Landscape of Imaging Feature-Associated RNA Expression Profiles in Human Breast Tissue. <i>Sensors</i> , 2023, 23, 1432.	3.8	2
3037	Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. <i>Nature Communications</i> , 2023, 14, .	12.8	11
3039	A genome-wide association study for allergen component sensitizations identifies allergen componentâ€specific and allergen protein groupâ€specific associations. , 2023, 2, 100086.		0
3040	Nutrigenomics in the context of evolution. <i>Redox Biology</i> , 2023, 62, 102656.	9.0	3
3041	Polygenic influences on the behavioral effects of alcohol withdrawal in a mixed-ancestry population from the collaborative study on the genetics of alcoholism (COGA). <i>Molecular and Cellular Neurosciences</i> , 2023, 125, 103851.	2.2	1
3043	Genetic associations between bipolar disorder and brain structural phenotypes. <i>Cerebral Cortex</i> , 2023, 33, 6990-7000.	2.9	1
3044	Decoding transcriptional regulation via a human gene expression predictor. <i>Journal of Genetics and Genomics</i> , 2023, , .	3.9	1
3045	Host variation in type I interferon signaling genes (MX1), Câ€C chemokine receptor type 5 gene, and major histocompatibility complex class I alleles in treated HIV+ noncontrollers predict viral reservoir size. <i>Aids</i> , 2023, 37, 477-488.	2.2	4
3046	Molecular quantitative trait loci. <i>Nature Reviews Methods Primers</i> , 2023, 3, .	21.2	13
3047	Aggregation tests identify new gene associations with breast cancer in populations with diverse ancestry. <i>Genome Medicine</i> , 2023, 15, .	8.2	4
3048	Liver-Specific Polygenic Risk Score Is Associated with Alzheimerâ€™s Disease Diagnosis. <i>Journal of Alzheimer's Disease</i> , 2023, 92, 395-409.	2.6	4
3049	Functional genomics identify causal variant underlying the protective CTSH locus for Alzheimerâ€™s disease. <i>Neuropsychopharmacology</i> , 2023, 48, 1555-1566.	5.4	4
3052	Functional link between sarcoidosis-associated gene variants and quantitative levels of bronchoalveolar lavage fluid cell types. <i>Frontiers in Medicine</i> , 0, 10, .	2.6	1

#	ARTICLE	IF	CITATIONS
3055	The human inactive X chromosome modulates expression of the active X chromosome. <i>Cell Genomics</i> , 2023, 3, 100259.	6.5	20
3056	Human pancreatic islet microRNAs implicated in diabetes and related traits by large-scale genetic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	9
3057	HuCoPIA: An Atlas of Human vs. SARS-CoV-2 Interactome and the Comparative Analysis with Other Coronaviridae Family Viruses. <i>Viruses</i> , 2023, 15, 492.	3.3	1
3059	Genetic polymorphism (rs6587666) in FLG protects from eczema in admixed Brazilian children population with high African ancestry. <i>Heliyon</i> , 2023, 9, e13659.	3.2	0
3063	Neurodegeneration cell per cell. <i>Neuron</i> , 2023, 111, 767-786.	8.1	8
3065	Genetic correlates of vitamin D-binding protein and 25-hydroxyvitamin D in neonatal dried blood spots. <i>Nature Communications</i> , 2023, 14, .	12.8	5
3067	Natural variation in gene expression and viral susceptibility revealed by neural progenitor cell villages. <i>Cell Stem Cell</i> , 2023, 30, 312-332.e13.	11.1	20
3069	An integrated strategy to identify COVID-19 causal genes and characteristics represented by LRRC37A2. <i>Journal of Medical Virology</i> , 2023, 95, .	5.0	2
3070	Analysis of genetically determined gene expression suggests role of inflammatory processes in exfoliation syndrome. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
3071	Multiomic prioritisation of risk genes for anorexia nervosa. <i>Psychological Medicine</i> , 2023, 53, 6754-6762.	4.5	2
3072	Escape from X-inactivation in twins exhibits intra- and inter-individual variability across tissues and is heritable. <i>PLoS Genetics</i> , 2023, 19, e1010556.	3.5	8
3073	Brain expression quantitative trait locus and network analyses reveal downstream effects and putative drivers for brain-related diseases. <i>Nature Genetics</i> , 2023, 55, 377-388.	21.4	54
3074	Protective effect of antihypertensive drugs on the risk of Parkinson's disease lacks causal evidence from mendelian randomization. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	0
3075	Pitfalls and opportunities for applying latent variables in single-cell eQTL analyses. <i>Genome Biology</i> , 2023, 24, .	8.8	2
3076	Genetic overlap between cortical brain morphometry and frontotemporal dementia risk. <i>Cerebral Cortex</i> , 0, , .	2.9	0
3077	Mendelian randomization and clinical trial evidence supports TYK2 inhibition as a therapeutic target for autoimmune diseases. <i>EBioMedicine</i> , 2023, 89, 104488.	6.1	19
3079	Single-cell sequencing of entorhinal cortex reveals widespread disruption of neuropeptide networks in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2023, 19, 3575-3592.	0.8	1
3081	Fine mapping spatiotemporal mechanisms of genetic variants underlying cardiac traits and disease. <i>Nature Communications</i> , 2023, 14, .	12.8	3

#	ARTICLE	IF	CITATIONS
3082	An autoimmune pleiotropic SNP modulates IRF5 alternative promoter usage through ZBTB3-mediated chromatin looping. <i>Nature Communications</i> , 2023, 14, .	12.8	6
3087	The molecular consequences of androgen activity in the human breast. <i>Cell Genomics</i> , 2023, 3, 100272.	6.5	4
3089	Identification of significant gene expression changes in multiple perturbation experiments using knockoffs. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	1
3090	Convergent coexpression of autism-associated genes suggests some novel risk genes may not be detectable in large-scale genetic studies. <i>Cell Genomics</i> , 2023, 3, 100277.	6.5	2
3092	A de novo low-frequency mosaic variant of KIF1A causes hereditary spastic paraplegia: A literature review. <i>Annals of Human Genetics</i> , 0, , .	0.8	0
3093	Identifying polymorphic cis-regulatory variants as risk markers for lung carcinogenesis and chemotherapy responses in tobacco smokers from eastern India. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3094	Shared genetic architecture between attention-deficit/hyperactivity disorder and lifespan. <i>Neuropsychopharmacology</i> , 2023, 48, 981-990.	5.4	1
3096	The genetic basis of endometriosis and comorbidity with other pain and inflammatory conditions. <i>Nature Genetics</i> , 2023, 55, 423-436.	21.4	50
3097	Genetic architecture of spatial electrical biomarkers for cardiac arrhythmia and relationship with cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	12.8	1
3098	RNA Pol II preferentially regulates ribosomal protein expression by trapping disassociated subunits. <i>Molecular Cell</i> , 2023, 83, 1280-1297.e11.	9.7	3
3099	Pharmacogenomics: Driving Personalized Medicine. <i>Pharmacological Reviews</i> , 2023, 75, 789-814.	16.0	15
3100	Association of CTNND2 gene polymorphism with schizophrenia: Two-sample case-control study in Chinese Han population. <i>International Journal of Psychiatry in Medicine</i> , 0, , 009121742311646.	1.8	0
3102	Maternal and fetal origins of offspring blood pressure: statistical analysis using genetic correlation and genetic risk score-based Mendelian randomization. <i>International Journal of Epidemiology</i> , 2023, 52, 1360-1376.	1.9	3
3103	Multi-omics analysis identifies drivers of protein phosphorylation. <i>Genome Biology</i> , 2023, 24, .	8.8	5
3104	Clinical and genetic associations of deep learning-derived cardiac magnetic resonance-based left ventricular mass. <i>Nature Communications</i> , 2023, 14, .	12.8	8
3106	Expression profiles of east-west highly differentiated genes in Uyghur genomes. <i>National Science Review</i> , 2023, 10, .	9.5	3
3107	<i>IL16</i> and factor V gene variations are associated with asparaginase-related thrombosis in childhood acute lymphoblastic leukemia patients. <i>Pharmacogenomics</i> , 2023, 24, 199-206.	1.3	0
3108	A genome-wide association study of childhood adiposity and blood lipids. <i>Wellcome Open Research</i> , 0, 6, 303.	1.8	1

#	ARTICLE	IF	CITATIONS
3109	Multiscale network analysis identifies potential receptors for SARS-CoV-2 and reveals their tissue-specific and age-dependent expression. FEBS Letters, 2023, 597, 1384-1402.	2.8	0
3110	PR-DUB safeguards Polycomb repression through H2AK119ub1 restriction. Cell Proliferation, 0, , .	5.3	2
3111	Loss of TTC17 promotes breast cancer metastasis through RAP1/CDC42 signaling and sensitizes it to rapamycin and paclitaxel. Cell and Bioscience, 2023, 13, .	4.8	2
3112	Decrease in naturally occurring antibodies against epitopes of Alzheimer's disease (AD) risk gene products is associated with cognitive decline in AD. Journal of Neuroinflammation, 2023, 20, .	7.2	1
3113	Genome-Wide Association Studies of Diarrhea Frequency and Duration in the First Year of Life in Bangladeshi Infants. Journal of Infectious Diseases, 0, , .	4.0	2
3114	Genome-wide identification of RNA modification-related single nucleotide polymorphisms associated with rheumatoid arthritis. BMC Genomics, 2023, 24, .	2.8	7
3115	Functional characterization of human genomic variation linked to polygenic diseases. Trends in Genetics, 2023, 39, 462-490.	6.7	5
3116	Genetic variation in cis-regulatory domains suggests cell type-specific regulatory mechanisms in immunity. Communications Biology, 2023, 6, .	4.4	3
3117	Multi-omics cannot replace sample size in genome-wide association studies. Genes, Brain and Behavior, 2023, 22, .	2.2	0
3118	The EN-TEx resource of multi-tissue personal epigenomes & variant-impact models. Cell, 2023, 186, 1493-1511.e40.	28.9	13
3119	Interplay Between Polymorphic Short Tandem Repeats and Gene Expression Variation in <i>Caenorhabditis elegans</i> . Molecular Biology and Evolution, 2023, 40, .	8.9	2
3120	The mitochondrial protease OMA1 acts as a metabolic safeguard upon nuclear DNA damage. Cell Reports, 2023, 42, 112332.	6.4	1
3122	OTTERS: a powerful TWAS framework leveraging summary-level reference data. Nature Communications, 2023, 14, .	12.8	7
3123	Esearch3D: propagating gene expression in chromatin networks to illuminate active enhancers. Nucleic Acids Research, 0, , .	14.5	1
3124	A gene-level test for directional selection on gene expression. Genetics, 2023, 224, .	2.9	2
3125	FOXI3 pathogenic variants cause one form of craniofacial microsomia. Nature Communications, 2023, 14, .	12.8	5
3126	Interactions between genetic variants and environmental risk factors are associated with the severity of pelvic organ prolapse. Menopause, 2023, 30, 621-628.	2.0	1
3127	Casein Kinase 1 as a Novel Factor Affects Thyrotropin Synthesis via PKC/ERK/CREB Signaling. International Journal of Molecular Sciences, 2023, 24, 7034.	4.1	0

#	ARTICLE	IF	CITATIONS
3128	Integrative Post-Genome-Wide Association Study Analyses Relevant to Psychiatric Disorders: Imputing Transcriptome and Proteome Signals. <i>Complex Psychiatry</i> , 2023, 9, 130-144.	0.9	0
3129	Scalable generation of sensory neurons from human pluripotent stem cells. <i>Stem Cell Reports</i> , 2023, 18, 1030-1047.	4.8	8
3131	The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles. <i>Genome Biology</i> , 2023, 24, .	8.8	6
3132	Genome-wide mRNA profiling in urinary extracellular vesicles reveals stress gene signature for diabetic kidney disease. <i>IScience</i> , 2023, 26, 106686.	4.1	4
3133	PCB126 exposure during pregnancy alters maternal and fetal gene expression. <i>Reproductive Toxicology</i> , 2023, 119, 108385.	2.9	1
3134	Mapping genomic regulation of kidney disease and traits through high-resolution and interpretable eQTLs. <i>Nature Communications</i> , 2023, 14, .	12.8	7
3135	Integrating genetics and transcriptomics to study major depressive disorder: a conceptual framework, bioinformatic approaches, and recent findings. <i>Translational Psychiatry</i> , 2023, 13, .	4.8	3
3136	Genetics of myocardial interstitial fibrosis in the human heart and association with disease. <i>Nature Genetics</i> , 2023, 55, 777-786.	21.4	13
3137	Single-cell genomics meets human genetics. <i>Nature Reviews Genetics</i> , 2023, 24, 535-549.	16.3	18
3138	Association of asthma genetic variants with asthma-associated traits reveals molecular pathways of eosinophilic asthma. <i>Clinical and Translational Allergy</i> , 2023, 13, .	3.2	7
3139	Genetics and genomics of endometriosis. <i>PLoS Genetics</i> , 2023, , 599-631.		0
3140	The X-factor in ART: does the use of assisted reproductive technologies influence DNA methylation on the X chromosome?. <i>Human Genomics</i> , 2023, 17, .	2.9	0
3141	CD8 ⁺ T cell infiltration is associated with improved survival and negatively correlates with hypoxia in clear cell ovarian cancer. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
3142	Topologically associating domain underlies tissue specific expression of long intergenic non-coding RNAs. <i>IScience</i> , 2023, 26, 106640.	4.1	1
3144	A functional genomics approach reveals suggestive quantitative trait loci associated with combined TLR4 and BCP crystal-induced inflammation and osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2023, 31, 1022-1034.	1.3	2
3145	Potential Protective Link Between Type I Diabetes and Parkinson's Disease Risk and Progression. <i>Movement Disorders</i> , 2023, 38, 1350-1355.	3.9	4
3146	Genetic correlation, causal relationship, and shared loci between vitamin D and COVID-19: A genome-wide cross-trait analysis. <i>Journal of Medical Virology</i> , 2023, 95, .	5.0	6
3147	IRIS: Discovery of cancer immunotherapy targets arising from pre-mRNA alternative splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	6

#	ARTICLE	IF	CITATIONS
3148	Aneuploidy effects on human gene expression across three cell types. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	8
3149	Discovery of target genes and pathways at GWAS loci by pooled single-cell CRISPR screens. Science, 2023, 380, .	12.6	36
3150	Twelve Years of Genome-Wide Association Studies of Human Protein N-Glycosylation. Engineering, 2023, 26, 17-31.	6.7	2
3151	Evolution and phylogenetic distribution of <i>endo</i> - α -mannosidase. Glycobiology, 2023, 33, 687-699.	2.5	1
3152	Genome-wide association study of chronic sputum production implicates loci involved in mucus production and infection. European Respiratory Journal, 2023, 61, 2201667.	6.7	2
3153	Transforming RNA-Seq gene expression to track cancer progression in the multi-stage early to advanced-stage cancer development. PLoS ONE, 2023, 18, e0284458.	2.5	2
3154	Brain transcriptome-wide association study implicates novel risk genes underlying schizophrenia risk. Psychological Medicine, 2023, 53, 6867-6877.	4.5	0
3156	The landscape of somatic mutations in lymphoblastoid cell lines. Cell Genomics, 2023, 3, 100305.	6.5	2
3157	From function to translation: Decoding genetic susceptibility to human diseases via artificial intelligence. Cell Genomics, 2023, 3, 100320.	6.5	4
3161	Genome-wide Association Studies Categorized by Class of Antihypertensive Drugs Reveal Complex Pathogenesis of Hypertension with Drug Resistance. Clinical Pharmacology and Therapeutics, 2023, 114, 393-403.	4.7	1
3162	Genetics implicates overactive osteogenesis in the development of diffuse idiopathic skeletal hyperostosis. Nature Communications, 2023, 14, .	12.8	6
3163	Single-Cell Multiomics. Annual Review of Biomedical Data Science, 2023, 6, 313-337.	6.5	5
3164	Sequencing of 19,219 exomes identifies a low-frequency variant in FKBP5 promoter predisposing to high myopia in a Han Chinese population. Cell Reports, 2023, 42, 112510.	6.4	4
3166	Refined expression quantitative trait locus analysis on adenocarcinoma at the gastroesophageal junction reveals susceptibility and prognostic markers. Frontiers in Genetics, 0, 14, .	2.3	1
3167	Proteins: Neglected active ingredients in edible bird's nest. Chinese Herbal Medicines, 2023, 15, 383-390.	3.0	2
3168	Disentangling the genetic overlap and causal relationships between primary open-angle glaucoma, brain morphology and four major neurodegenerative disorders. EBioMedicine, 2023, 92, 104615.	6.1	3
3171	Investigating the shared genetic architecture of post-traumatic stress disorder and gastrointestinal tract disorders: a genome-wide cross-trait analysis. Psychological Medicine, 2023, 53, 7627-7635.	4.5	1
3172	Gene expression in African Americans, Puerto Ricans and Mexican Americans reveals ancestry-specific patterns of genetic architecture. Nature Genetics, 2023, 55, 952-963.	21.4	9

#	ARTICLE	IF	CITATIONS
3174	Polygenic prediction of preeclampsia and gestational hypertension. <i>Nature Medicine</i> , 2023, 29, 1540-1549.	30.7	16
3175	The RNA helicase DDX39B activates FOXP3 RNA splicing to control T regulatory cell fate. <i>ELife</i> , 0, 12, .	6.0	5
3176	Epromoters are new players in the regulatory landscape with potential pleiotropic roles. <i>BioEssays</i> , 0, , .	2.5	1
3177	Human gain-of-function variants in HNF1A confer protection from diabetes but independently increase hepatic secretion of atherogenic lipoproteins. <i>Cell Genomics</i> , 2023, 3, 100339.	6.5	2
3178	Rare penetrant mutations confer severe risk of common diseases. <i>Science</i> , 2023, 380, .	12.6	13
3179	Genetic architecture of heart mitochondrial proteome influencing cardiac hypertrophy. <i>ELife</i> , 0, 12, .	6.0	0
3180	150 risk variants for diverticular disease of intestine prioritize cell types and enable polygenic prediction of disease susceptibility. <i>Cell Genomics</i> , 2023, 3, 100326.	6.5	2
3181	Genetic studies of paired metabolomes reveal enzymatic and transport processes at the interface of plasma and urine. <i>Nature Genetics</i> , 2023, 55, 995-1008.	21.4	7
3183	3D genome organization and epigenetic regulation in autoimmune diseases. <i>Frontiers in Immunology</i> , 0, 14, .	4.8	2
3184	Coexistence of Multiple Functional Variants and Genes Underlies Genetic Risk Locus 11p11.2 of Alzheimer's Disease. <i>Biological Psychiatry</i> , 2023, 94, 743-759.	1.3	4
3185	Mapping genetic effects on cell type-specific chromatin accessibility and annotating complex immune trait variants using single nucleus ATAC-seq in peripheral blood. <i>PLoS Genetics</i> , 2023, 19, e1010759.	3.5	3
3186	Minor intron splicing is critical for survival of lethal prostate cancer. <i>Molecular Cell</i> , 2023, 83, 1983-2002.e11.	9.7	3
3187	Dissecting shared genetic architecture between obesity and multiple sclerosis. <i>EBioMedicine</i> , 2023, 93, 104647.	6.1	1
3188	A village in a dish model system for population-scale hiPSC studies. <i>Nature Communications</i> , 2023, 14, .	12.8	9
3189	MTM: a multi-task learning framework to predict individualized tissue gene expression profiles. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
3191	Mapping interindividual dynamics of innate immune response at single-cell resolution. <i>Nature Genetics</i> , 2023, 55, 1066-1075.	21.4	4
3193	Circulating cell-free methylated DNA reveals tissue-specific, cellular damage from radiation treatment. <i>JCI Insight</i> , 2023, 8, .	5.0	3
3194	Phenotypic variance partitioning by transcriptomic gene expression levels and environmental variables for anthropometric traits using GTEx data. <i>Genetic Epidemiology</i> , 2023, 47, 465-474.	1.3	1

#	ARTICLE	IF	CITATIONS
3195	A shared genetic contribution to osteoarthritis and COVID-19 outcomes: a large-scale genome-wide cross-trait analysis. <i>Frontiers in Immunology</i> , 0, 14, .	4.8	1
3196	Loss of cytochrome P450 (CYP)1B1 mitigates hyperoxia response in adult mouse lung by reprogramming metabolism and translation. <i>Redox Biology</i> , 2023, 64, 102790.	9.0	0
3197	Predicting mechanisms of action at genetic loci associated with discordant effects on type 2 diabetes and abdominal fat accumulation. <i>ELife</i> , 0, 12, .	6.0	1
3198	Applications of genomic research in pediatric endocrine diseases. <i>Clinical and Experimental Pediatrics</i> , 0, , .	2.2	0
3199	Comorbidity genetic risk and pathways impact SARS-CoV-2 infection outcomes. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
3200	Cross-ancestry genome-wide association meta-analyses of hippocampal and subfield volumes. <i>Nature Genetics</i> , 2023, 55, 1126-1137.	21.4	1
3201	Identification of highly reliable risk genes for Alzheimer's disease through joint-tissue integrative analysis. <i>Frontiers in Aging Neuroscience</i> , 0, 15, .	3.4	0
3203	Identification of transcriptional regulatory variants in pig duodenum, liver, and muscle tissues. <i>GigaScience</i> , 2022, 12, .	6.4	3
3206	Considerations for reproducible omics in aging research. <i>Nature Aging</i> , 2023, 3, 921-930.	11.6	2
3207	COVID-19 severity: does the genetic landscape of rare variants matter?. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	2
3208	Multi-Omics Profiling for Health. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100561.	3.8	26
3209	Multi-scale systems genomics analysis predicts pathways, cell types, and drug targets involved in normative variation in peri-adolescent human cognition. <i>Cerebral Cortex</i> , 2023, 33, 8581-8593.	2.9	0
3210	Mendelian Randomization and Transcriptome-Wide Association Analysis Identified Genes That Were Pleiotropically Associated with Intraocular Pressure. <i>Genes</i> , 2023, 14, 1027.	2.4	1
3211	Genetic association study identifies genetic variants for non-alcoholic fatty liver without comorbidities in the Korean population. <i>Genes and Genomics</i> , 2023, 45, 847-854.	1.4	0
3212	Mapping splice QTLs reveals distinct transcriptional and post-transcriptional regulatory variation of gene expression and identifies putative alternative splicing variation mediating complex trait variation in pigs. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3213	meQTL mapping in the GENOA study reveals genetic determinants of DNA methylation in African Americans. <i>Nature Communications</i> , 2023, 14, .	12.8	4
3214	The eQTL colocalization and transcriptome-wide association study identify potentially causal genes responsible for economic traits in Simmental beef cattle. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	5.3	4
3215	The genetics of autism spectrum disorder in an East African familial cohort. <i>Cell Genomics</i> , 2023, 3, 100322.	6.5	2

#	ARTICLE	IF	CITATIONS
3216	Evaluating the Contribution of Cell Type-Specific Alternative Splicing to Variation in Lipid Levels. Circulation Genomic and Precision Medicine, 2023, 16, 248-257.	3.6	0
3218	Dissecting the genetic heterogeneity of gastric cancer. EBioMedicine, 2023, 92, 104616.	6.1	1
3219	Systematic analyses of GWAS summary statistics from UK Biobank identified novel susceptibility loci and genes for upper gastrointestinal diseases. Journal of Human Genetics, 0, , .	2.3	0
3220	Investigating the shared genetic architecture between schizophrenia and body mass index. Molecular Psychiatry, 2023, 28, 2312-2319.	7.9	2
3221	Juvenile idiopathic arthritis-associated genetic loci exhibit spatially constrained gene regulatory effects across multiple tissues and immune cell types. Journal of Autoimmunity, 2023, 138, 103046.	6.5	2
3222	Foreign RNA spike-ins enable accurate allele-specific expression analysis at scale. Bioinformatics, 2023, 39, i431-i439.	4.1	1
3223	Testing associations between human anxiety and genes previously implicated by mouse anxiety models. Genes, Brain and Behavior, 2023, 22, .	2.2	1
3225	Genome-wide association study of thoracic aortic aneurysm and dissection in the Million Veteran Program. Nature Genetics, 2023, 55, 1106-1115.	21.4	7
3226	APOE Locus-Associated Mitochondrial Function and Its Implication in Alzheimer's Disease and Aging. International Journal of Molecular Sciences, 2023, 24, 10440.	4.1	4
3227	Gene regulatory network inference in the era of single-cell multi-omics. Nature Reviews Genetics, 2023, 24, 739-754.	16.3	40
3228	Multivariate genetic analysis of personality and cognitive traits reveals abundant pleiotropy. Nature Human Behaviour, 2023, 7, 1584-1600.	12.0	7
3231	Multivariate adaptive shrinkage improves cross-population transcriptome prediction and association studies in underrepresented populations. Human Genetics and Genomics Advances, 2023, 4, 100216.	1.7	0
3233	The role of tandem repeat expansions in brain disorders. Emerging Topics in Life Sciences, 0, , .	2.6	3
3235	Impact of the acquired subgenome on the transcriptional landscape in <i>Brettanomyces bruxellensis</i> allopolyploids. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	0
3237	Characterizing the landscape of gene expression variance in humans. PLoS Genetics, 2023, 19, e1010833.	3.5	1
3238	<i>Cis</i> -regulatory Landscape Size, Constraint, and Tissue Specificity Associate with Gene Function and Expression. Genome Biology and Evolution, 2023, 15, .	2.5	0
3240	Comprehensive Analysis for Anti-Cancer Target-Indication Prioritization of Placental Growth Factor Inhibitor (PGF) by Use of Omics and Patient Survival Data. Biology, 2023, 12, 970.	2.8	1
3241	Mapping genetic variants for nonsense-mediated mRNA decay regulation across human tissues. Genome Biology, 2023, 24, .	8.8	6

#	ARTICLE	IF	CITATIONS
3243	Leveraging polygenic enrichments of gene features to predict genes underlying complex traits and diseases. <i>Nature Genetics</i> , 2023, 55, 1267-1276.	21.4	27
3244	Sex-specific estimation of <i>cis</i> and <i>trans</i> regulation of gene expression in heads and gonads of <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
3246	Genetic Polymorphism of Cytokines IL-1 β , IL-4, and TNF- α as a Factor Modifying the Influence of Adverse Childhood Experiences on the Symptoms of Schizophrenia. <i>Neuroscience and Behavioral Physiology</i> , 0, , .	0.4	0
3247	Forkhead transcription factor FKH-8 cooperates with RFX in the direct regulation of sensory cilia in <i>Caenorhabditis elegans</i> . <i>ELife</i> , 0, 12, .	6.0	1
3248	A murine model of hnRNPH2-related neurodevelopmental disorder reveals a mechanism for genetic compensation by Hnrnp1. <i>Journal of Clinical Investigation</i> , 2023, 133, .	8.2	2
3249	TGF- β 1 dominates stromal fibroblast-mediated EMT via the FAP/VCAN axis in bladder cancer cells. <i>Journal of Translational Medicine</i> , 2023, 21, .	4.4	6
3250	Depression pathophysiology, risk prediction of recurrence and comorbid psychiatric disorders using genome-wide analyses. <i>Nature Medicine</i> , 2023, 29, 1832-1844.	30.7	31
3251	PINNED: identifying characteristics of druggable human proteins using an interpretable neural network. <i>Journal of Cheminformatics</i> , 2023, 15, .	6.1	1
3252	Synthetic whole-slide image tile generation with gene expression profile-infused deep generative models. <i>Cell Reports Methods</i> , 2023, 3, 100534.	2.9	3
3253	Candidate pathway analysis of surfactant proteins identifies <i>CTSH</i> and <i>SFTA2</i> that influences lung cancer risk. <i>Human Molecular Genetics</i> , 0, , .	2.9	0
3254	Molecular bases of comorbidities: present and future perspectives. <i>Trends in Genetics</i> , 2023, , .	6.7	1
3258	Integrating Omics Data in Genome-Scale Metabolic Modeling: A Methodological Perspective for Precision Medicine. <i>Metabolites</i> , 2023, 13, 855.	2.9	2
3259	The non-specific lethal complex regulates genes and pathways genetically linked to Parkinson's disease. <i>Brain</i> , 0, , .	7.6	0
3260	Biallelic <i>MED27</i> variants lead to variable ponto-cerebello-lental degeneration with movement disorders. <i>Brain</i> , 0, , .	7.6	0
3261	Reply to Ren et al.: The role of a liver-specific mitochondrial carrier SLC25A47 in glucose homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	0
3263	5. Collaborative Study on the Genetics of Alcoholism: Functional genomics. <i>Genes, Brain and Behavior</i> , 2023, 22, .	2.2	2
3264	Loss of microRNA-30a and sex-specific effects on the neonatal hyperoxic lung injury. <i>Biology of Sex Differences</i> , 2023, 14, .	4.1	0
3266	Colocalization of corneal resistance factor GWAS loci with GTEx e/sQTLs highlights plausible candidate causal genes for keratoconus postnatal corneal stroma weakening. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0

#	ARTICLE	IF	CITATIONS
3267	Analysis of reproducibility and robustness of a renal proximal tubule microphysiological system OrganoPlate 3-lane 40 for <i>in vitro</i> studies of drug transport and toxicity. Toxicological Sciences, 2023, 196, 52-70.	3.1	2
3268	Integrative omics approaches to advance rare disease diagnostics. Journal of Inherited Metabolic Disease, 2023, 46, 824-838.	3.6	2
3269	Cell-type-specific cis-regulatory divergence in gene expression and chromatin accessibility revealed by human-chimpanzee hybrid cells. ELife, 0, 12, .	6.0	0
3270	The identification of distinct protective and susceptibility mechanisms for hip osteoarthritis: findings from a genome-wide association study meta-analysis of minimum joint space width and Mendelian randomisation cluster analyses. EBioMedicine, 2023, 95, 104759.	6.1	4
3271	Structural Variations Contribute to the Genetic Etiology of Autism Spectrum Disorder and Language Impairments. International Journal of Molecular Sciences, 2023, 24, 13248.	4.1	0
3272	Multiple genes in a single GWAS risk locus synergistically mediate aberrant synaptic development and function in human neurons. Cell Genomics, 2023, , 100399.	6.5	3
3273	A Bayesian method for estimating gene-level polygenicity under the framework of transcriptome-wide association study. Statistics in Medicine, 2023, 42, 4867-4885.	1.6	0
3274	Finding the Common Single-Nucleotide Polymorphisms in Three Autoimmune Diseases and Exploring Their Bio-Function by Using a Reporter Assay. Biomedicines, 2023, 11, 2426.	3.2	0
3276	GWAS meta-analysis of over 29,000 people with epilepsy identifies 26 risk loci and subtype-specific genetic architecture. Nature Genetics, 2023, 55, 1471-1482.	21.4	14
3278	Linkage analysis using whole exome sequencing data implicates SLC17A1, SLC17A3, TATDN2 and TMEM131L in type 1 diabetes in Kuwaiti families. Scientific Reports, 2023, 13, .	3.3	3
3279	Modeling of horizontal pleiotropy identifies possible causal gene expression in systemic lupus erythematosus. , 0, 1, .		1
3280	Bidirectional genetic overlap between autism spectrum disorder and cognitive traits. Translational Psychiatry, 2023, 13, .	4.8	0
3281	Integration of eQTL and machine learning to dissect causal genes with pleiotropic effects in genetic regulation networks of seed cotton yield. Cell Reports, 2023, 42, 113111.	6.4	0
3282	Structural variation of the coding and non-coding human pharmacogenome. Npj Genomic Medicine, 2023, 8, .	3.8	3
3283	Integrative analysis of transcriptome dynamics during human craniofacial development identifies candidate disease genes. Nature Communications, 2023, 14, .	12.8	5
3284	Dissecting the high-resolution genetic architecture of complex phenotypes by accurately estimating gene-based conditional heritability. American Journal of Human Genetics, 2023, 110, 1534-1548.	6.2	1
3285	Multitissue H3K27ac profiling of GTEx samples links epigenomic variation to disease. Nature Genetics, 2023, 55, 1665-1676.	21.4	1
3286	Differential gene expression analysis based on linear mixed model corrects false positive inflation for studying quantitative traits. Scientific Reports, 2023, 13, .	3.3	2

#	ARTICLE	IF	CITATIONS
3287	Multidimensional computational study to understand non-coding RNA interactions in breast cancer metastasis. Scientific Reports, 2023, 13, .	3.3	2
3288	Genetic analysis of blood molecular phenotypes reveals common properties in the regulatory networks affecting complex traits. Nature Communications, 2023, 14, .	12.8	2
3289	KidneyGPS: a user-friendly web application to help prioritize kidney function genes and variants based on evidence from genome-wide association studies. BMC Bioinformatics, 2023, 24, .	2.6	0
3290	Identification of candidate genes and chemicals associated with osteoarthritis by transcriptome-wide association study and chemical-gene interaction analysis. Arthritis Research and Therapy, 2023, 25, .	3.5	0
3291	Functional Enrichment Analysis Identifying Regulatory Information Associated with Human Fracture. Calcified Tissue International, 2023, 113, 286-294.	3.1	0
3292	Identifying novel regulatory effects for clinically relevant genes through the study of the Greek population. BMC Genomics, 2023, 24, .	2.8	2
3293	The human glucose and lipid homeostasis-associated genetic polymorphisms do not regulate <i>SLC25A47</i> gene expression in the liver. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	2
3294	Single-cell allele-specific expression analysis reveals dynamic and cell-type-specific regulatory effects. Nature Communications, 2023, 14, .	12.8	2
3295	The genetic architecture and evolution of the human skeletal form. Science, 2023, 381, .	12.6	7
3296	Mapping the epigenomic landscape of human monocytes following innate immune activation reveals context-specific mechanisms driving endotoxin tolerance. BMC Genomics, 2023, 24, .	2.8	1
3297	Genetic insights into resting heart rate and its role in cardiovascular disease. Nature Communications, 2023, 14, .	12.8	1
3298	Polymorphism of the rs1815739 Locus of the ACTN3 Gene and rs11227639 cis-eQTL Affecting Its Expression in Populations of Siberia. Russian Journal of Genetics, 2023, 59, 408-413.	0.6	0
3299	Systematic differences in discovery of genetic effects on gene expression and complex traits. Nature Genetics, 2023, 55, 1866-1875.	21.4	19
3300	Multifaceted analysis of cross-tissue transcriptomes reveals phenotype-endotype associations in atopic dermatitis. Nature Communications, 2023, 14, .	12.8	3
3301	Identifying genetic loci that are associated with changes in gene expression in PTSD in a South African cohort. Journal of Neurochemistry, 2023, 166, 705-719.	3.9	1
3302	Mapping microRNA expression quantitative trait loci in the prenatal human brain implicates miR-1908-5p expression in bipolar disorder and other brain-related traits. Human Molecular Genetics, 2023, 32, 2941-2949.	2.9	0
3305	Machine learning reveals genetic modifiers of the immune microenvironment of cancer. IScience, 2023, 26, 107576.	4.1	0
3307	Leveraging osteoclast genetic regulatory data to identify genes with a role in osteoarthritis. Genetics, 2023, 225, .	2.9	0

#	ARTICLE	IF	CITATIONS
3308	Polygenic regression uncovers trait-relevant cellular contexts through pathway activation transformation of single-cell RNA sequencing data. <i>Cell Genomics</i> , 2023, 3, 100383.	6.5	6
3309	Cross-trait genome-wide association analysis of C-reactive protein level and psychiatric disorders. <i>Psychoneuroendocrinology</i> , 2023, 157, 106368.	2.7	0
3311	Gene expression and RNA splicing explain large proportions of the heritability for complex traits in cattle. <i>Cell Genomics</i> , 2023, 3, 100385.	6.5	8
3316	Pleiotropy with sex-specific traits reveals genetic aspects of sex differences in Parkinson's disease. <i>Brain</i> , 2024, 147, 858-870.	7.6	0
3318	Cardiac muscle's restricted partial loss of <i>Nos1ap</i> expression has limited but significant impact on electrocardiographic features. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
3319	Allele-specific RNA N ⁶ -methyladenosine modifications reveal functional genetic variants in human tissues. <i>Genome Research</i> , 2023, 33, 1369-1380.	5.5	1
3322	Genetic features and genomic targets of human KRAB-zinc finger proteins. <i>Genome Research</i> , 2023, 33, 1409-1423.	5.5	5
3323	rs56405341 Variant Associates with Expression of C4orf33 and C4orf33 Was Downregulated in Alzheimer's Disease and Progressive Supranuclear Palsy. <i>Journal of Alzheimer's Disease</i> , 2023, 96, 57-64.	2.6	0
3324	Genome-Wide Copy Number Variation and Structural Variation: A Novel Tool for Improved Livestock Genomic Selection. <i>Livestock Diseases and Management</i> , 2023, , 75-88.	0.5	0
3329	Unraveling the role of non-coding rare variants in epilepsy. <i>PLoS ONE</i> , 2023, 18, e0291935.	2.5	0
3330	Splicing transcriptome-wide association study to identify splicing events for pancreatic cancer risk. <i>Carcinogenesis</i> , 0, , .	2.8	0
3331	CWAS Meta-Analysis of Suicide Attempt: Identification of 12 Genome-Wide Significant Loci and Implication of Genetic Risks for Specific Health Factors. <i>American Journal of Psychiatry</i> , 2023, 180, 723-738.	7.2	15
3333	Characterizing genetic variation in the regulation of the ER stress response through computational and cis-eQTL analyses. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	1.8	0
3334	Testing for Allele-specific Expression from Human Brain Samples. <i>Bio-protocol</i> , 2023, 13, .	0.4	0
3335	Effects of oxytocin pathway gene polymorphisms and adverse childhood experiences on emotion recognition in schizophrenia spectrum disorders. <i>Zhurnal Nevrologii I Psikhiiatrii Imeni S S Korsakova</i> , 2023, 123, 90.	0.7	0
3337	Predicting Age from Human Lung Tissue Through Multi-modal Data Integration. <i>Lecture Notes in Computer Science</i> , 2023, , 644-658.	1.3	0
3338	An Predictive Deep Learning Model is used to Identify Human Tissue-Specific Regulatory Variations For Diabetes. , 2023, , .		0
3340	Integration of multiple-omics data to reveal the shared genetic architecture of educational attainment, intelligence, cognitive performance, and Alzheimer's disease. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	1

#	ARTICLE	IF	CITATIONS
3341	Interindividual variation in human cortical cell type abundance and expression. <i>Science</i> , 2023, 382, .	12.6	7
3342	Robustness of quantifying mediating effects of genetically regulated expression on complex traits with mediated expression score regression. <i>Biology Methods and Protocols</i> , 2023, 8, .	2.2	0
3344	Massively parallel functional dissection of schizophrenia-associated noncoding genetic variants. <i>Cell</i> , 2023, 186, 5165-5182.e33.	28.9	2
3347	Potential roles of lncRNA MALAT1-miRNA interactions in ocular diseases. <i>Journal of Cell Communication and Signaling</i> , 2023, 17, 1203-1217.	3.4	0
3349	Identification of asthma-related genes using asthmatic blood eQTLs of Korean patients. <i>BMC Medical Genomics</i> , 2023, 16, .	1.5	0
3351	ONECUT1 variants beyond type 1 and type 2 diabetes: exploring clinical diversity and epigenetic associations in Arab cohorts. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
3353	A pan-tissue survey of mosaic chromosomal alterations in 948 individuals. <i>Nature Genetics</i> , 2023, 55, 1901-1911.	21.4	0
3354	DeepGAMI: deep biologically guided auxiliary learning for multimodal integration and imputation to improve genotypeâ€“phenotype prediction. <i>Genome Medicine</i> , 2023, 15, .	8.2	1
3355	A Mendelian randomization study for drug repurposing reveals bezafibrate and fenofibric acid as potential osteoporosis treatments. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	0
3356	Allele-dependent expression and functionality of lipid enzyme phospholipid:diacylglycerol acyltransferase affect diatom carbon storage and growth. <i>Plant Physiology</i> , 0, , .	4.8	0
3357	Speos: an ensemble graph representation learning framework to predict core gene candidates for complex diseases. <i>Nature Communications</i> , 2023, 14, .	12.8	0
3358	eQTL mapping in fetal-like pancreatic progenitor cells reveals early developmental insights into diabetes risk. <i>Nature Communications</i> , 2023, 14, .	12.8	1
3359	Comprehensive analyses of 435 goat transcriptomes provides insight into male reproduction. <i>International Journal of Biological Macromolecules</i> , 2024, 255, 127942.	7.5	0
3360	Estimating gene-level false discovery probability improves eQTL statistical fine-mapping precision. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	3.2	0
3361	Evaluation of input data modality choices on functional gene embeddings. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	3.2	0
3362	Phenotype integration improves power and preserves specificity in biobank-based genetic studies of major depressive disorder. <i>Nature Genetics</i> , 2023, 55, 2082-2093.	21.4	2
3363	Genome-wide meta-analysis, functional genomics and integrative analyses implicate new risk genes and therapeutic targets for anxiety disorders. <i>Nature Human Behaviour</i> , 2024, 8, 361-379.	12.0	2
3364	Integrative genome-wide analyses identify novel loci associated with kidney stones and provide insights into its genetic architecture. <i>Nature Communications</i> , 2023, 14, .	12.8	1

#	ARTICLE	IF	CITATIONS
3365	hipFG: high-throughput harmonization and integration pipeline for functional genomics data. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
3366	Cross-ancestry analyses identify new genetic loci associated with 25-hydroxyvitamin D. <i>PLoS Genetics</i> , 2023, 19, e1011033.	3.5	0
3367	A mutation rate model at the basepair resolution identifies the mutagenic effect of polymerase III transcription. <i>Nature Genetics</i> , 2023, 55, 2235-2242.	21.4	2
3368	Benchmarking of deep neural networks for predicting personal gene expression from DNA sequence highlights shortcomings. <i>Nature Genetics</i> , 2023, 55, 2060-2064.	21.4	3
3369	Epigenomic mapping reveals distinct B cell acute lymphoblastic leukemia chromatin architectures and regulators. <i>Cell Genomics</i> , 2023, 3, 100442.	6.5	0
3370	Human-genome single nucleotide polymorphisms affecting transcription factor binding and their role in pathogenesis. <i>Vavilovskii Zhurnal Genetiki i Selekcii</i> , 2023, 27, 662-675.	1.1	0
3371	An evolutionary perspective on complex neuropsychiatric disease. <i>Neuron</i> , 2024, 112, 7-24.	8.1	1
3372	Evaluating 17 methods incorporating biological function with GWAS summary statistics to accelerate discovery demonstrates a tradeoff between high sensitivity and high positive predictive value. <i>Communications Biology</i> , 2023, 6, .	4.4	0
3373	Systems genetics approaches for understanding complex traits with relevance for human disease. <i>ELife</i> , 0, 12, .	6.0	3
3375	Genome-Wide Association Study of Pericardial Fat Area in 28â€‰%161 UK Biobank Participants. <i>Journal of the American Heart Association</i> , 2023, 12, .	3.7	1
3382	Dominant negative variants in KIF5B cause osteogenesis imperfecta via down regulation of mTOR signaling. <i>PLoS Genetics</i> , 2023, 19, e1011005.	3.5	0
3383	Integrative single-cell meta-analysis reveals disease-relevant vascular cell states and markers in human atherosclerosis. <i>Cell Reports</i> , 2023, 42, 113380.	6.4	4
3385	MAJQlopedia: an encyclopedia of RNA splicing variations in human tissues and cancer. <i>Nucleic Acids Research</i> , 0, , .	14.5	0
3388	Construction of a risk scoring system using clinical factors and RYR2 polymorphisms for bleeding complications in patients on direct oral anticoagulants. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	0
3389	Expression quantitative trait loci analysis in rheumatoid arthritis identifies tissue specific variants associated with severity and outcome. <i>Annals of the Rheumatic Diseases</i> , 2024, 83, 288-299.	0.9	0
3390	Genome-wide association study of susceptibility to hospitalised respiratory infections. <i>Wellcome Open Research</i> , 0, 6, 290.	1.8	0
3391	Longitudinal change in memory performance as a strong endophenotype for Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2024, 20, 1268-1283.	0.8	0
3392	Patterns of Gene Expression, Splicing, and Allele-Specific Expression Vary among Macular Tissues and Clinical Stages of Age-Related Macular Degeneration. <i>Cells</i> , 2023, 12, 2668.	4.1	1

#	ARTICLE	IF	CITATIONS
3394	Improved detection of aberrant splicing with FRASER 2.0 and the intron Jaccard index. American Journal of Human Genetics, 2023, 110, 2056-2067.	6.2	0
3395	Genome-wide meta-analysis and fine-mapping prioritize potential causal variants and genes related to leprosy. MedComm, 2023, 4, .	7.2	0
3397	Comprehensive gene profiling of the metabolic landscape of humanized livers in mice. Journal of Hepatology, 2023, , .	3.7	1
3398	Non-additive genetic components contribute significantly to population-wide gene expression variation. Cell Genomics, 2024, 4, 100459.	6.5	2
3400	Genome-wide association study meta-analysis of dizygotic twinning illuminates genetic regulation of female fecundity. Human Reproduction, 0, , .	0.9	5
3401	A mitochondrial inside-out iron-calcium signal reveals drug targets for Parkinson's disease. Cell Reports, 2023, 42, 113544.	6.4	1
3402	FROM PATHOPHYSIOLOGY TO POTENTIAL INTERVENTIONS: INVESTIGATING THE INTRICATE DYNAMICS OF POLYCYSTIC OVARY SYNDROME, AGING, AND FERTILITY. , 2023, 2, 132-142.		0
3404	Nicotinic acetylcholine receptor signaling maintains epithelial barrier integrity. ELife, 0, 12, .	6.0	3
3407	Genome-wide analysis study of gestational diabetes mellitus and related pathogenic factors in a Chinese Han population. BMC Pregnancy and Childbirth, 2023, 23, .	2.4	0
3408	Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. Cell Genomics, 2024, 4, 100465.	6.5	1
3409	Role of Genetic Variation in Transcriptional Regulatory Elements in Heart Rhythm. Cells, 2024, 13, 4.	4.1	0
3410	A Bayesian noisy logic model for inference of transcription factor activity from single cell and bulk transcriptomic data. NAR Genomics and Bioinformatics, 2023, 5, .	3.2	1
3411	A novel and innovative cancer classification framework through a consecutive utilization of hybrid feature selection. BMC Bioinformatics, 2023, 24, .	2.6	2
3412	Age-dependent genetic regulation of osteoarthritis: independent effects of immune system genes. Arthritis Research and Therapy, 2023, 25, .	3.5	0
3413	SUMMIT-FA: a new resource for improved transcriptome imputation using functional annotations. Human Molecular Genetics, 0, , .	2.9	0
3414	The correlates of neonatal complement component 3 and 4 protein concentrations with a focus on psychiatric and autoimmune disorders. Cell Genomics, 2023, 3, 100457.	6.5	1
3416	Immune-response 3'UTR alternative polyadenylation quantitative trait loci contribute to variation in human complex traits and diseases. Nature Communications, 2023, 14, .	12.8	0
3420	Systematic analysis of Mendelian disease-associated gene variants reveals new classes of cancer-predisposing genes. Genome Medicine, 2023, 15, .	8.2	0

#	ARTICLE	IF	CITATIONS
3421	Multiple genomic solutions for local adaptation in two closely related species (sheep and goats) facing the same climatic constraints. <i>Molecular Ecology</i> , 0, , .	3.9	0
3424	Haplotype-aware modeling of cis-regulatory effects highlights the gaps remaining in eQTL data. <i>Nature Communications</i> , 2024, 15, .	12.8	0
3425	Integrating genetic regulation and single-cell expression with GWAS prioritizes causal genes and cell types for glaucoma. <i>Nature Communications</i> , 2024, 15, .	12.8	0
3426	Molecular quantitative trait loci in reproductive tissues impact male fertility in cattle. <i>Nature Communications</i> , 2024, 15, .	12.8	2
3427	SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. <i>International Journal of Molecular Sciences</i> , 2024, 25, 1183.	4.1	0
3428	Letter to the editor on: Hornerin deposits in neuronal intranuclear inclusion disease: direct identification of proteins with compositionally biased regions in inclusions by Park et al. (2022). <i>Acta Neuropathologica Communications</i> , 2024, 12, .	5.2	0
3429	The ALT pathway generates telomere fusions that can be detected in the blood of cancer patients. <i>Nature Communications</i> , 2024, 15, .	12.8	0
3430	Protocol for detecting rare and common genetic associations in whole-exome sequencing studies using MAGICpipeline. <i>STAR Protocols</i> , 2024, 5, 102806.	1.2	0
3431	Immune infiltration is associated with pan-cancer prognostic biomarker <sc>RING</sc> finger protein 187. <i>Journal of Molecular Recognition</i> , 2024, 37, .	2.1	0
3432	Genetic determinants of IgG antibody response to COVID-19 vaccination. <i>American Journal of Human Genetics</i> , 2024, 111, 181-199.	6.2	0
3433	Systematic identification of genotype-dependent enhancer variants in eosinophilic esophagitis. <i>American Journal of Human Genetics</i> , 2024, 111, 280-294.	6.2	0
3434	High-dimensional phenotyping to define the genetic basis of cellular morphology. <i>Nature Communications</i> , 2024, 15, .	12.8	2
3436	Identification of the shared genetic architecture underlying seven autoimmune diseases with GWAS summary statistics. <i>Frontiers in Immunology</i> , 0, 14, .	4.8	0
3437	Expression Pattern and Prognostic Significance of the Long Non-Coding RNA Metastasis-Associated Lung Adenocarcinoma Transcript 1 in Chronic Lymphocytic Leukemia. <i>International Journal of Molecular Sciences</i> , 2024, 25, 922.	4.1	0
3438	Transcription readthrough is prevalent in healthy human tissues and associated with inherent genomic features. <i>Communications Biology</i> , 2024, 7, .	4.4	0
3439	Leveraging inter-individual transcriptional correlation structure to infer discrete signaling mechanisms across metabolic tissues. <i>ELife</i> , 0, 12, .	6.0	0
3440	Regulatory features aid interpretation of 3'UTR variants. <i>American Journal of Human Genetics</i> , 2024, 111, 350-363.	6.2	1
3441	Pyroptosis-Related Gene Signature Predicts Prognosis and Response to Immunotherapy and Medication in Pediatric and Young Adult Osteosarcoma Patients. <i>Journal of Inflammation Research</i> , 0, Volume 17, 417-445.	3.5	0

#	ARTICLE	IF	CITATIONS
3442	Shared Proteins and Pathways of Cardiovascular and Cognitive Diseases: Relation to Vascular Cognitive Impairment. <i>Journal of Proteome Research</i> , 2024, 23, 560-573.	3.7	0
3444	PICALO: principal interaction component analysis for the identification of discrete technical, cell-type, and environmental factors that mediate eQTLs. <i>Genome Biology</i> , 2024, 25, .	8.8	0
3445	Epigenetic reprogramming as a key to reverse ageing and increase longevity. <i>Ageing Research Reviews</i> , 2024, 95, 102204.	10.9	0
3446	Gene expression variation underlying tissue-specific responses to copper stress in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
3447	MMCT-Loop: a mix model-based pipeline for calling targeted 3D chromatin loops. <i>Nucleic Acids Research</i> , 2024, 52, e25-e25.	14.5	0
3448	Genome-wide analysis reveals extensive genetic overlap between childhood phenotypes and later-life type 2 diabetes. <i>Computers in Biology and Medicine</i> , 2024, 171, 108065.	7.0	0
3449	Genetically proxied low-density lipoprotein cholesterol lowering via PCSK9-inhibitor drug targets and risk of congenital malformations. <i>European Journal of Preventive Cardiology</i> , 0, , .	1.8	0
3451	Circadian clock-related genome-wide mendelian randomization identifies putatively genes for ulcerative colitis and its comorbidity. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
3453	Cell-type deconvolution of bulk-blood RNA-seq reveals biological insights into neuropsychiatric disorders. <i>American Journal of Human Genetics</i> , 2024, 111, 323-337.	6.2	0
3454	Multi-organ single-cell <i>scRNA</i> sequencing in mice reveals early hyperglycemia responses that converge on fibroblast dysregulation. <i>FASEB Journal</i> , 2024, 38, .	0.5	0
3455	The role of oxytocin receptor gene variants in appetitive aggression: A study in a South African male sample. <i>Aggressive Behavior</i> , 2024, 50, .	2.4	0
3456	Links between melanoma germline risk loci, driver genes and comorbidities: insight from a tissue-specific multi-omic analysis. <i>Molecular Oncology</i> , 2024, 18, 1031-1048.	4.6	0
3457	Placental expression quantitative trait loci in an East Asian population. <i>Human Genetics and Genomics Advances</i> , 2024, 5, 100276.	1.7	0
3458	Transcriptome-wide association study of the plasma proteome reveals cis and trans regulatory mechanisms underlying complex traits. <i>American Journal of Human Genetics</i> , 2024, 111, 445-455.	6.2	0
3460	The effect of sevoflurane exposure on cell-type-specific changes in the prefrontal cortex in young mice. <i>Journal of Neurochemistry</i> , 0, , .	3.9	0
3461	Accelerated Computing A Biomedical Engineering and Medical Science Perspective. , 2023, 12, 138-164.		0
3462	Transcriptome-Wide Association Studies (TWAS): Methodologies, Applications, and Challenges. <i>Current Protocols</i> , 2024, 4, .	2.9	0
3464	Large-scale integrative analysis of juvenile idiopathic arthritis for new insight into its pathogenesis. <i>Arthritis Research and Therapy</i> , 2024, 26, .	3.5	0

#	ARTICLE	IF	CITATIONS
3465	The dynamic genetic determinants of increased transcriptional divergence in spermatids. <i>Nature Communications</i> , 2024, 15, .	12.8	0
3468	Diallel panel reveals a significant impact of low-frequency genetic variants on gene expression variation in yeast. <i>Molecular Systems Biology</i> , 2024, 20, 362-373.	7.2	0
3469	Cell-type-specific cis-regulatory divergence in gene expression and chromatin accessibility revealed by human-chimpanzee hybrid cells. <i>ELife</i> , 0, 12, .	6.0	0
3470	Association of statin use with osteoporosis risk: a drug-targeted Mendelian randomization study. <i>Inflammopharmacology</i> , 2024, 32, 1253-1261.	3.9	0
3471	Functional enrichment analysis reveals the involvement of DARS2 in multiple biological pathways and its potential as a therapeutic target in esophageal carcinoma. <i>Aging</i> , 2024, 16, 3934-3954.	3.1	0
3472	Identification of regulons modulating the transcriptional response to SARS-CoV-2 infection in humans. , 0, 2, .		0
3473	Transcriptome-wide association studies associated with Crohn's disease: challenges and perspectives. <i>Cell and Bioscience</i> , 2024, 14, .	4.8	0
3476	Epigenetic variation impacts individual differences in the transcriptional response to influenza infection. <i>Nature Genetics</i> , 2024, 56, 408-419.	21.4	0
3477	Genetic and molecular architecture of complex traits. <i>Cell</i> , 2024, 187, 1059-1075.	28.9	0
3478	Targeting postsynaptic glutamate receptor scaffolding proteins PSD-95 and PICK1 for obesity treatment. <i>Science Advances</i> , 2024, 10, .	10.3	0
3479	Osteoarthritis as an Enhanceropathy: Gene Regulation in Complex Musculoskeletal Disease. <i>Current Rheumatology Reports</i> , 0, , .	4.7	0
3480	Effects of gene dosage and development on subcortical nuclei volumes in individuals with 22q11.2 copy number variations. <i>Neuropsychopharmacology</i> , 2024, 49, 1024-1032.	5.4	0
3481	Mendelian randomization study on causal association of FAM210B with drug-induced lupus. <i>Clinical Rheumatology</i> , 2024, 43, 1513-1520.	2.2	0
3482	Critical evaluation of artificial intelligence as a digital twin of pathologists for prostate cancer pathology. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
3483	Sex-specific genetic architecture of blood pressure. <i>Nature Medicine</i> , 2024, 30, 818-828.	30.7	0
3484	Isoform alterations in the ubiquitination machinery impacting gastrointestinal malignancies. <i>Cell Death and Disease</i> , 2024, 15, .	6.3	0
3485	The association of cigarette smoking with DNA methylation and gene expression in human tissue samples. <i>American Journal of Human Genetics</i> , 2024, 111, 636-653.	6.2	0
3486	Targeting MicroRNAs with Small Molecules. <i>Non-coding RNA</i> , 2024, 10, 17.	2.6	0

#	ARTICLE	IF	CITATIONS
3487	Genetic Markers in Predicting Three Common Vascular Diseases. , 2024, , 357-369.		0
3488	Challenges in the discovery of tumor-specific alternative splicing-derived cell-surface antigens in glioma. Scientific Reports, 2024, 14, .	3.3	0
3489	Integrative cross-omics and cross-context analysis elucidates molecular links underlying genetic effects on complex traits. Nature Communications, 2024, 15, .	12.8	0
3491	Epigenetic landscape of 5-hydroxymethylcytosine and associations with gene expression in placenta. Epigenetics, 2024, 19, .	2.7	0
3492	Joint-tissue integrative analysis identifies high-risk genes for Parkinsonâ€™s disease. Frontiers in Neuroscience, 0, 18, .	2.8	0
3493	Polygenic risk associated with Alzheimerâ€™s disease and other traits influences genes involved in T cell signaling and activation. Frontiers in Immunology, 0, 15, .	4.8	0
3494	The Potential of Genomics and Electronic Health Records to Invigorate Drug Development. Biological Psychiatry, 2024, 95, 715-717.	1.3	0
3495	Genetic associations with dementiaâ€™related proteinopathy: Application of item response theory. Alzheimer's and Dementia, 2024, 20, 2906-2921.	0.8	0
3496	Integrating multi-omics data to reveal the effect of genetic variant rs6430538 on Alzheimer's disease risk. Frontiers in Neuroscience, 0, 18, .	2.8	0
3498	Genome-wide analyses in Lyme borreliosis: identification of a genetic variant associated with disease susceptibility and its immunological implications. BMC Infectious Diseases, 2024, 24, .	2.9	0
3500	The impact of genetically controlled splicing on exon inclusion and protein structure. PLoS ONE, 2024, 19, e0291960.	2.5	0