An Expanded View of Complex Traits: From Polygenic t

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Citation Report

#	Article	IF	Citations
1	Genetic insights into the neurodevelopmental origins of schizophrenia. Nature Reviews Neuroscience, 2017, 18, 727-740.	4.9	377
2	Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. American Journal of Human Genetics, 2017, 101, 686-699.	2.6	102
3	Understanding Tissue-Specific Gene Regulation. Cell Reports, 2017, 21, 1077-1088.	2.9	314
4	Rethinking ovarian cancer genomics: where genome-wide association studies stand?. Pharmacogenomics, 2017, 18, 1611-1625.	0.6	8
5	Bagging Nearest-Neighbor Prediction independence Test: an efficient method for nonlinear dependence of two continuous variables. Scientific Reports, 2017, 7, 12736.	1.6	5
6	Gene Regulatory Network Inference from Single-Cell Data Using Multivariate Information Measures. Cell Systems, 2017, 5, 251-267.e3.	2.9	414
7	Genome-wide association studies of cancer: current insights and future perspectives. Nature Reviews Cancer, 2017, 17, 692-704.	12.8	285
8	Blood Pressure Genome-Wide Association Studies, Missing Heritability, and Omnigenics. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	4
9	The Com-PLEC-sity of Atrial FibrillationÂGenetics. Journal of the American College of Cardiology, 2017, 70, 2169-2170.	1.2	3
10	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. Cell Systems, 2017, 5, 386-398.e4.	2.9	102
11	Genomic Studies of Local Adaptation in Natural Plant Populations. Journal of Heredity, 2017, 109, 3-15.	1.0	83
12	Modes of Rapid Polygenic Adaptation. Molecular Biology and Evolution, 2017, 34, 3169-3175.	3.5	65
13	Accumulation of minor alleles and risk prediction in schizophrenia. Scientific Reports, 2017, 7, 11661.	1.6	16
14	Knowledgeâ€driven computational modeling in Alzheimer's disease research: Current state and future trends. Alzheimer's and Dementia, 2017, 13, 1292-1302.	0.4	11
15	The neurodevelopmental origins of schizophrenia in the penumbra of genomic medicine. World Psychiatry, 2017, 16, 225-226.	4.8	30
16	Role of mitochondria and energy metabolism in schizophrenia and psychotic disorders. Schizophrenia Research, 2017, 187, 1-2.	1.1	28
17	The infinitesimal model: Definition, derivation, and implications. Theoretical Population Biology, 2017, 118, 50-73.	0.5	250
18	Endocrinology Meets Metabolomics: Achievements, Pitfalls, and Challenges. Trends in Endocrinology and Metabolism, 2017, 28, 705-721.	3.1	29

#	ARTICLE	IF	CITATIONS
19	Classification of common human diseases derived from shared genetic and environmental determinants. Nature Genetics, 2017, 49, 1319-1325.	9.4	181
20	Segmental allotetraploidy generates extensive homoeologous expression rewiring and phenotypic diversity at the population level in rice. Molecular Ecology, 2017, 26, 5451-5466.	2.0	35
21	Height associated variants demonstrate assortative mating in human populations. Scientific Reports, 2017, 7, 15689.	1.6	15
22	Genomics of Human Pulmonary Tuberculosis: from Genes to Pathways. Current Genetic Medicine Reports, 2017, 5, 149-166.	1.9	30
23	Epigenetic switch turns on genetic behavioral variations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12365-12367.	3.3	3
24	What have humans done for evolutionary biology? Contributions from genes to populations. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20171164.	1.2	10
25	The role of human host genetics in tuberculosis resistance. Expert Review of Respiratory Medicine, 2017, 11, 721-737.	1.0	16
26	Vasopressin and the Neurogenetics of Parental Care. Neuron, 2017, 95, 9-11.	3.8	10
27	Developmental plasticity. Evolution, Medicine and Public Health, 2017, 2017, 162-175.	1.1	78
28	Dosage-sensitive genes in evolution and disease. BMC Biology, 2017, 15, 78.	1.7	79
30	The Genetic Architecture of Type 1 Diabetes. Genes, 2017, 8, 209.	1.0	49
31	The Necessity of Diploid Genome Sequencing to Unravel the Genetic Component of Complex Phenotypes. Frontiers in Genetics, 2017, 8, 148.	1.1	7
32	Physical Interactions and Expression Quantitative Traits Loci Identify Regulatory Connections for Obesity and Type 2 Diabetes Associated SNPs. Frontiers in Genetics, 2017, 8, 150.	1.1	84
33	Cynefin as Reference Framework to Facilitate Insight and Decision-Making in Complex Contexts of Biomedical Research. Frontiers in Neuroscience, 2017, 11, 634.	1.4	17
34	How the Genome Folds, Divides, Lives, and Dies. Cold Spring Harbor Symposia on Quantitative Biology, 2017, 82, 349-360.	2.0	1
35	Genome-wide association study identifies a locus associated with rotator cuff injury. PLoS ONE, 2017, 12, e0189317.	1.1	25
36	A comprehensive data mining study shows that most nuclear receptors act as newly proposed homeostasis-associated molecular pattern receptors. Journal of Hematology and Oncology, 2017, 10, 168.	6.9	23
37	Neuroimaging genomics in psychiatryâ€"a translational approach. Genome Medicine, 2017, 9, 102.	3.6	48

#	ARTICLE	IF	CITATIONS
38	Recurrent de novo mutations in neurodevelopmental disorders: properties and clinical implications. Genome Medicine, 2017, 9, 101.	3.6	112
40	Was the Watchmaker Blind? Or Was She One-Eyed?. Biology, 2017, 6, 47.	1.3	35
41	Harnessing Diversity In The Face Of Environmental Variability: Robustness, Canalization And Genetic Assimilation. Journal of Phylogenetics & Evolutionary Biology, 2017, 05, .	0.2	0
42	MADS-box genes and crop domestication: the jack of all traits. Journal of Experimental Botany, 2018, 69, 1447-1469.	2.4	83
43	COMT and GAD1 gene polymorphisms are associated with impaired antisaccade task performance in schizophrenic patients. European Archives of Psychiatry and Clinical Neuroscience, 2018, 268, 571-584.	1.8	11
44	Genetic architecture of obesity and related metabolic traits â€" recent insights from isolated populations. Current Opinion in Genetics and Development, 2018, 50, 74-78.	1.5	3
45	Society and personal genome data. Human Molecular Genetics, 2018, 27, R8-R13.	1.4	29
46	Partitioning the Pleiotropy Between Coronary Artery Disease and Body Mass Index Reveals the Importance of Low Frequency Variants and Central Nervous Systemâ€"Specific Functional Elements. Circulation Genomic and Precision Medicine, 2018, 11, e002050.	1.6	16
47	Quantitative analysis of population-scale family trees with millions of relatives. Science, 2018, 360, 171-175.	6.0	157
48	Deconstructing autism: from unitary syndrome to contributory developmental endophenotypes. International Review of Psychiatry, 2018, 30, 18-24.	1.4	51
49	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
50	Single-Cell RNA-Seq of Mouse Dopaminergic Neurons Informs Candidate Gene Selection for Sporadic Parkinson Disease. American Journal of Human Genetics, 2018, 102, 427-446.	2.6	102
51	Genome-wide association study for stayability measures in Nelloreâ€"Angus crossbred cows1. Journal of Animal Science, 2018, 96, 1205-1214.	0.2	7
52	Testing for Pathway (in)Activation by Using Gaussian Graphical Models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2018, 67, 1419-1436.	0.5	5
53	Polygenic risk score for schizophrenia is not strongly associated with the expression of specific genes or gene sets. Psychiatric Genetics, 2018, 28, 59-65.	0.6	6
54	Genetic instrumental variable regression: Explaining socioeconomic and health outcomes in nonexperimental data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4970-E4979.	3.3	59
55	Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. Nature Communications, 2018, 9, 1612.	5.8	95
56	Translating Immunology into Therapeutic Concepts for Inflammatory Bowel Disease. Annual Review of Immunology, 2018, 36, 755-781.	9.5	121

#	Article	IF	Citations
57	Biospecimens and the ABCD study: Rationale, methods of collection, measurement and early data. Developmental Cognitive Neuroscience, 2018, 32, 97-106.	1.9	88
58	Progress in the genetics of autism spectrum disorder. Developmental Medicine and Child Neurology, 2018, 60, 445-451.	1.1	116
59	Tread Lightly Interpreting Polygenic Tests of Selection. Genetics, 2018, 208, 1351-1355.	1.2	98
61	High-throughput mouse phenomics for characterizing mammalian gene function. Nature Reviews Genetics, 2018, 19, 357-370.	7.7	78
62	Success and failure in replication of genotypeâ€"phenotype associations: How does replication help in understanding the genetic basis of phenotypic variation in outbred populations?. Molecular Ecology Resources, 2018, 18, 739-754.	2.2	23
63	All for One and One for All: Mental Disorders in One Dimension. American Journal of Psychiatry, 2018, 175, 831-844.	4.0	601
64	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
65	The tales genes tell (or not): A century of exploration. American Journal of Physical Anthropology, 2018, 165, 741-753.	2.1	2
66	Genetic background effects in quantitative genetics: gene-by-system interactions. Current Genetics, 2018, 64, 1173-1176.	0.8	15
67	Genome-wide mapping of global-to-local genetic effects on human facial shape. Nature Genetics, 2018, 50, 414-423.	9.4	205
68	Idiopathic pulmonary fibrosis: idiopathic no more?. Lancet Respiratory Medicine,the, 2018, 6, 84-85.	5.2	8
69	5-HT2C Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. Cell, 2018, 172, 719-730.e14.	13.5	185
70	Evolutionary Perspectives on Genetic and Environmental Risk Factors for Psychiatric Disorders. Annual Review of Clinical Psychology, 2018, 14, 471-493.	6.3	31
71	An epigenetic basis for an omnigenic model of psychiatric disorders. Journal of Theoretical Biology, 2018, 443, 52-55.	0.8	28
72	Systems Signatures Reveal Unique Remission-path of Type 2 Diabetes Following Roux-en-Y Gastric Bypass Surgery. EBioMedicine, 2018, 28, 234-240.	2.7	5
73	Missing compared to what? Revisiting heritability, genes and culture. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170064.	1.8	55
74	Functional Variants Identified Efficiently through an Integrated Transcriptome and Epigenome Analysis. Scientific Reports, 2018, 8, 2959.	1.6	9
75	Accessing Gene Expression in Treatment-Resistant Schizophrenia. Molecular Neurobiology, 2018, 55, 7000-7008.	1.9	23

#	ARTICLE	IF	CITATIONS
76	Pathophysiological mechanisms of autoimmunity. Annals of the New York Academy of Sciences, 2018, 1413, 59-68.	1.8	20
77	Integration of Multi-omics Data from Mouse Diversity Panel Highlights Mitochondrial Dysfunction in Non-alcoholic Fatty Liver Disease. Cell Systems, 2018, 6, 103-115.e7.	2.9	124
78	Full genetic analysis for genome-wide association study of Fangji: a powerful approach for effectively dissecting the molecular architecture of personalized traditional Chinese medicine. Acta Pharmacologica Sinica, 2018, 39, 906-911.	2.8	10
79	Genetic Modifiers in Neurodegeneration. Current Genetic Medicine Reports, 2018, 6, 11-19.	1.9	11
80	How have our clocks evolved? Adaptive and demographic history of the out-of-African dispersal told by polymorphic loci in circadian genes. Chronobiology International, 2018, 35, 511-532.	0.9	7
81	Transcriptomics and Targeted Proteomics Analysis to Gain Insights Into the Immune-control Mechanisms of HIV-1 Infected Elite Controllers. EBioMedicine, 2018, 27, 40-50.	2.7	28
82	Ancient polymorphisms and divergence hitchhiking contribute to genomic islands of divergence within a poplar species complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E236-E243.	3.3	126
83	Causal relationship of hepatic fat with liver damage and insulin resistance in nonalcoholic fatty liver. Journal of Internal Medicine, 2018, 283, 356-370.	2.7	256
84	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. Plant Physiology, 2018, 176, 2133-2147.	2.3	88
85	Expanding the spectrum of CVD genetics. Nature Reviews Cardiology, 2018, 15, 77-78.	6.1	6
86	The new genetics of intelligence. Nature Reviews Genetics, 2018, 19, 148-159.	7.7	290
87	De novo mutations implicate novel genes in systemic lupus erythematosus. Human Molecular Genetics, 2018, 27, 421-429.	1.4	52
88	Polygenic influences on dyslipidemias. Current Opinion in Lipidology, 2018, 29, 133-143.	1.2	51
89	The Post-GWAS Era: From Association to Function. American Journal of Human Genetics, 2018, 102, 717-730.	2.6	626
90	Recent developments in the genetics of attentionâ€deficit hyperactivity disorder. Psychiatry and Clinical Neurosciences, 2018, 72, 654-672.	1.0	14
91	Personal Omics for Precision Health. Circulation Research, 2018, 122, 1169-1171.	2.0	54
92	Identifying causal variants at the interferon lambda locus in case-control studies: Utilizing non-synonymous variant rs117648444 to probe the role of IFN-Î»4. Gene, 2018, 664, 168-180.	1.0	9
93	Replicability and Prediction: Lessons and Challenges from GWAS. Trends in Genetics, 2018, 34, 504-517.	2.9	138

#	Article	IF	Citations
94	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. Genome Research, 2018, 28, 739-750.	2.4	324
95	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. Molecular Biology and Evolution, 2018, 35, 1489-1506.	3.5	103
96	Weighted Burden Analysis of Exome-Sequenced Case-Control Sample Implicates Synaptic Genes in Schizophrenia Aetiology. Behavior Genetics, 2018, 48, 198-208.	1.4	23
97	Polygenic Risk Scores in Clinical Psychology: Bridging Genomic Risk to Individual Differences. Annual Review of Clinical Psychology, 2018, 14, 119-157.	6.3	110
98	LSMM: a statistical approach to integrating functional annotations with genome-wide association studies. Bioinformatics, 2018, 34, 2788-2796.	1.8	18
99	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. Population Genomics, 2018, , 361-425.	0.2	6
100	The genomics of local adaptation in trees: are we out of the woods yet?. Tree Genetics and Genomes, 2018, 14, 1.	0.6	87
101	Genomic loci modulating retinal ganglion cell death following elevated IOP in the mouse. Experimental Eye Research, 2018, 169, 61-67.	1.2	9
103	A Simple Test Identifies Selection on Complex Traits. Genetics, 2018, 209, 321-333.	1.2	18
104	Evidence for a second ankylosing spondylitis-associated <i>RUNX3</i> regulatory polymorphism. RMD Open, 2018, 4, e000628.	1.8	16
105	Precision medicine screening using whole-genome sequencing and advanced imaging to identify disease risk in adults. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3686-3691.	3.3	76
106	Collective effects of common SNPs and risk prediction in lung cancer. Heredity, 2018, 121, 537-547.	1.2	9
107	Has the Gloom Lifted on Genome-wide Association Studies?. Biological Psychiatry, 2018, 83, 544-545.	0.7	1
108	Comprehensive review and annotation of susceptibility SNPs associated with obesityâ€related traits. Obesity Reviews, 2018, 19, 917-930.	3.1	31
109	Genetic analysis of deep phenotyping projects in common disorders. Schizophrenia Research, 2018, 195, 51-57.	1.1	11
110	The road less traveled: from genotype to phenotype in flies and humans. Mammalian Genome, 2018, 29, 5-23.	1.0	26
111	Genetic association studies and the risk factors for developing the â€œImmunoâ€bileâ€logicâ€•disease primary biliary cholangitis. Hepatology, 2018, 67, 1620-1622.	3.6	5
112	Neurodevelopmental disease mechanisms, primary cilia, and endosomes converge on the BLOCâ€1 and BORC complexes. Developmental Neurobiology, 2018, 78, 311-330.	1.5	21

#	ARTICLE	IF	CITATIONS
113	The genetics underlying idiopathic ventricular fibrillation: A special role for catecholaminergic polymorphic ventricular tachycardia?. International Journal of Cardiology, 2018, 250, 139-145.	0.8	42
114	Genetic architecture: the shape of the genetic contribution to human traits and disease. Nature Reviews Genetics, 2018, 19, 110-124.	7.7	335
115	Collective effects of common single nucleotide polymorphisms and genetic risk prediction in type 1 diabetes. Clinical Genetics, 2018, 93, 1069-1074.	1.0	8
116	Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in Type 2 Diabetes GWAS. , 2018, , .		2
117	Copy number variants in people with autism spectrum disorders and co-morbid psychosis. European Journal of Medical Genetics, 2018, 61, 230-234.	0.7	10
118	Identification of 64 Novel Genetic Loci Provides an Expanded View on the Genetic Architecture of Coronary Artery Disease. Circulation Research, 2018, 122, 433-443.	2.0	850
119	Genetic association of molecular traits: A help to identify causative variants in complex diseases. Clinical Genetics, 2018, 93, 520-532.	1.0	45
120	Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. Evolutionary Applications, 2018, 11, 1035-1052.	1.5	169
121	Great tits and the city: Distribution of genomic diversity and geneâ€"environment associations along an urbanization gradient. Evolutionary Applications, 2018, 11, 593-613.	1.5	42
122	Drug development in the era of precision medicine. Nature Reviews Drug Discovery, 2018, 17, 183-196.	21.5	294
123	Discovery of genetic risk factors for disease. Journal of the Royal Society of New Zealand, 2018, 48, 191-202.	1.0	0
124	The genetics of human personality. Genes, Brain and Behavior, 2018, 17, e12439.	1.1	134
125	Intellectual Investment, Dopaminergic Gene Variation, and Life Events: A Critical Examination. Personality Neuroscience, 2018, 1, e3.	1.3	0
126	Multi-OMICS analyses of frailty and chronic widespread musculoskeletal pain suggest involvement of shared neurological pathways. Pain, 2018, 159, 2565-2572.	2.0	38
127	Genetics of Alzheimer's Disease. Dementia and Neurocognitive Disorders, 2018, 17, 131.	0.4	50
128	Clinal Adaptation in the Marine Environment. Population Genomics, 2018, , 221-247.	0.2	3
129	Genome-Wide Association Analyses in the Model Rhizobium <i>Ensifer meliloti</i>. MSphere, 2018, 3, .	1.3	26
130	Quantifying how constraints limit the diversity of viable routes to adaptation. PLoS Genetics, 2018, 14, e1007717.	1.5	78

#	Article	IF	Citations
131	Comparing Genome-Wide Association Study Results from Different Measurements of an Underlying Phenotype. G3: Genes, Genomes, Genetics, 2018, 8, 3715-3722.	0.8	16
132	Large-scale associations between the leukocyte transcriptome and BOLD responses to speech differ in autism early language outcome subtypes. Nature Neuroscience, 2018, 21, 1680-1688.	7.1	69
133	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	2.6	30
134	Pipeline design to identify key features and classify the chemotherapy response on lung cancer patients using large-scale genetic data. BMC Systems Biology, 2018, 12, 97.	3.0	2
135	Exploring Coronary Artery Disease GWAs Targets With Functional Links to Immunometabolism. Frontiers in Cardiovascular Medicine, 2018, 5, 148.	1.1	10
136	Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.	6.2	97
137	Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. PLoS Genetics, 2018, 14, e1007794.	1.5	48
138	Behavior-dependent <i>cis</i> regulation reveals genes and pathways associated with bower building in cichlid fishes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11081-E11090.	3.3	42
139	Genetic Pointillism versus Physiological Form. Perspectives in Biology and Medicine, 2018, 61, 503-516.	0.3	5
140	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. SSRN Electronic Journal, 2018, , .	0.4	4
141	Into the Wild: GWAS Exploration of Non-coding RNAs. Frontiers in Cardiovascular Medicine, 2018, 5, 181.	1.1	94
142	Intensive Glucose Control Reduces the Risk Effect of TRIB3, SMARCD3, and ATF6 Genetic Variation on Diabetic Vascular Complications. Frontiers in Pharmacology, 2018, 9, 1422.	1.6	10
143	The Myocardial Infarction Associated Variant in the MIR196A2 Gene and Presumable Signaling Pathways to Involve miR-196a2 in the Pathological Phenotype. Molecular Biology, 2018, 52, 872-877.	0.4	5
144	Dopamine perturbation of gene co-expression networks reveals differential response in schizophrenia for translational machinery. Translational Psychiatry, 2018, 8, 278.	2.4	8
145	Out in the Cold: Identification of Genomic Regions Associated With Cold Tolerance in the Biocontrol Fungus Clonostachys rosea Through Genome-Wide Association Mapping. Frontiers in Microbiology, 2018, 9, 2844.	1.5	33
146	An Enrichment Analysis for Cardiometabolic Traits Suggests Non-Random Assignment of Genes to microRNAs. International Journal of Molecular Sciences, 2018, 19, 3666.	1.8	4
147	Applying Functional Genomics to Chronic Obstructive Pulmonary Disease. Annals of the American Thoracic Society, 2018, 15, S239-S242.	1.5	10
148	Genetic identification of Ly75 as a novel quantitative trait gene for resistance to obesity in mice. Scientific Reports, 2018, 8, 17658.	1.6	3

#	ARTICLE	IF	CITATIONS
149	Childhood-Onset Schizophrenia: Insights from Induced Pluripotent Stem Cells. International Journal of Molecular Sciences, 2018, 19, 3829.	1.8	24
150	Mitonuclear epistasis, genotypeâ€byâ€environment interactions, and personalized genomics of complex traits in <i>Drosophila</i>. IUBMB Life, 2018, 70, 1275-1288.	1.5	23
151	Population Genomics: Advancing Understanding of Nature. Population Genomics, 2018, , 3-79.	0.2	70
152	Toward the Language Oscillogenome. Frontiers in Psychology, 2018, 9, 1999.	1.1	28
153	Don't throw out the sympatric speciation with the crater lake water: fine-scale investigation of introgression provides equivocal support for causal role of secondary gene flow in one of the clearest examples of sympatric speciation. Evolution Letters, 2018, 2, 524-540.	1.6	35
154	Mutation pattern analysis reveals polygenic mini-drivers associated with relapse after surgery in lung adenocarcinoma. Scientific Reports, 2018, 8, 14830.	1.6	5
155	Modularity of genes involved in local adaptation to climate despite physical linkage. Genome Biology, 2018, 19, 157.	3.8	41
157	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	9.4	132
158	Pervasive Modulation of Obesity Risk by the Environment and Genomic Background. Genes, 2018, 9, 411.	1.0	16
159	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. Genomics, Proteomics and Bioinformatics, 2018, 16, 283-293.	3.0	19
160	Revisiting the evolutionary origins of obesity: lazy versus peppyâ€thrifty genotype hypothesis. Obesity Reviews, 2018, 19, 1525-1543.	3.1	19
161	The Small World of Adult Hippocampal Neurogenesis. Frontiers in Neuroscience, 2018, 12, 641.	1.4	7
162	Tracing Early Neurodevelopment in Schizophrenia with Induced Pluripotent Stem Cells. Cells, 2018, 7, 140.	1.8	35
163	Adjustment for covariates using summary statistics of genomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 812-825.	0.6	5
164	Transcription-driven genome organization: a model for chromosome structure and the regulation of gene expression tested through simulations. Nucleic Acids Research, 2018, 46, 9895-9906.	6.5	92
165	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. Neurology: Genetics, 2018, 4, e266.	0.9	12
166	Genetics of Human Longevity Within an Eco-Evolutionary Nature-Nurture Framework. Circulation Research, 2018, 123, 745-772.	2.0	75
167	Catechol-O-Methyltransferase moderates effect of stress mindset on affect and cognition. PLoS ONE, 2018, 13, e0195883.	1.1	17

#	ARTICLE	IF	CITATIONS
168	Robust Findings From 25ÂYears of PTSD Genetics Research. Current Psychiatry Reports, 2018, 20, 115.	2.1	45
169	A plant biodiversity effect resolved to a single chromosomal region. Nature Ecology and Evolution, 2018, 2, 1933-1939.	3.4	34
170	Polygenic adaptation in changing environments (a). Europhysics Letters, 2018, 123, 48002.	0.7	5
171	Large-scale genome-wide enrichment analyses identify new trait-associated genes and pathways across 31 human phenotypes. Nature Communications, 2018, 9, 4361.	5.8	88
172	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
173	Shared Biological Pathways Between Alzheimerâ€™s Disease and Ischemic Stroke. Frontiers in Neuroscience, 2018, 12, 605.	1.4	13
174	Deep learning in biomedicine. Nature Biotechnology, 2018, 36, 829-838.	9.4	409
175	Insights and Implications of Genome-Wide Association Studies of Height. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3155-3168.	1.8	31
176	Cross-tissue eQTL enrichment of associations in schizophrenia. PLoS ONE, 2018, 13, e0202812.	1.1	6
177	The Peril of Gene-Targeted Conservation. Trends in Ecology and Evolution, 2018, 33, 827-839.	4.2	104
178	Challenges and Strategies for Breeding Resistance in Capsicum annuum to the Multifarious Pathogen, Phytophthora capsici. Frontiers in Plant Science, 2018, 9, 628.	1.7	83
179	Cancer expression quantitative trait loci (eQTLs) can be determined from heterogeneous tumor gene expression data by modeling variation in tumor purity. Genome Biology, 2018, 19, 130.	3.8	27
180	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. PLoS Genetics, 2018, 14, e1007650.	1.5	43
181	Live fast, die young? A review on the developmental trajectories of ADHD across the lifespan. European Neuropsychopharmacology, 2018, 28, 1059-1088.	0.3	398
182	Insights into the Etiology of Mammalian Neural Tube Closure Defects from Developmental, Genetic and Evolutionary Studies. Journal of Developmental Biology, 2018, 6, 22.	0.9	43
183	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
184	Using mouse transgenic and human stem cell technologies to model genetic mutations associated with schizophrenia and autism. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170037.	1.8	20
185	Multitrait genome association analysis identifies new susceptibility genes for human anthropometric variation in the GCAT cohort. Journal of Medical Genetics, 2018, 55, 765-778.	1.5	28

#	Article	IF	Citations
186	The impact of genome-wide association studies on biomedical research publications. Human Genomics, 2018, 12, 38.	1.4	11
187	Perceived neighborhood social cohesion and cardiometabolic risk: a geneÂÃ—Âenvironment study. Biodemography and Social Biology, 2018, 64, 173-186.	0.4	1
188	From genome-wide associations to candidate causal variants by statistical fine-mapping. Nature Reviews Genetics, 2018, 19, 491-504.	7.7	611
189	Rare-Variant Studies to Complement Genome-Wide Association Studies. Annual Review of Genomics and Human Genetics, 2018, 19, 97-112.	2.5	34
190	Pharmacogenetic tests to guide drug treatment in depression: Comparison of the available testing kits and clinical trials. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 86, 36-44.	2.5	39
191	Some implications of an epigenetic-based omnigenic model of psychiatric disorders. Journal of Theoretical Biology, 2018, 452, 81-84.	0.8	14
192	The personal and clinical utility of polygenic risk scores. Nature Reviews Genetics, 2018, 19, 581-590.	7.7	1,102
193	Array of MADS-Box Genes: Facilitator for Rapid Adaptation?. Trends in Plant Science, 2018, 23, 563-576.	4.3	35
194	Performance of a Genomic Sequencing Classifier for the Preoperative Diagnosis of Cytologically Indeterminate Thyroid Nodules. JAMA Surgery, 2018, 153, 817.	2.2	275
195	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic Acids Research, 2018, 46, W114-W120.	6.5	69
196	Genetics of Resistant Hypertension: the Missing Heritability and Opportunities. Current Hypertension Reports, 2018, 20, 48.	1.5	9
197	Next-generation sequencing in drug development: target identification and genetically stratified clinical trials. Drug Discovery Today, 2018, 23, 1776-1783.	3.2	46
198	Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. Human Genetics, 2018, 137, 413-425.	1.8	8
199	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. British Journal of Cancer, 2018, 118, 1639-1647.	2.9	16
200	Low quality cardiovascular care is important coronary risk factor in India. Indian Heart Journal, 2018, 70, S419-S430.	0.2	17
201	Threshold for neural tube defect risk by accumulated singleton loss-of-function variants. Cell Research, 2018, 28, 1039-1041.	5.7	48
202	Genetic and evolutionary determinants of human population variation in immune responses. Current Opinion in Genetics and Development, 2018, 53, 28-35.	1.5	20
203	Genome-Wide Association Studies Identify Disease Mechanisms in Age-Related Macular Degeneration. Ophthalmology, 2018, 125, 962-964.	2.5	9

#	ARTICLE	IF	CITATIONS
204	A regulatory mutant on <i><scp>TRIM</scp>26</i> conferring the risk of nasopharyngeal carcinoma by inducing low immune response. Cancer Medicine, 2018, 7, 3848-3861.	1.3	14
205	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. Nature Communications, 2018, 9, 2526.	5.8	48
206	Weak effects of common genetic variation in oxytocin and vasopressin receptor genes on rhesus macaque social behavior. American Journal of Primatology, 2018, 80, e22873.	0.8	16
208	Connecting genetics and gene expression data for target prioritisation and drug repositioning. BioData Mining, 2018, 11, 7.	2.2	41
209	Co-regulatory networks of human serum proteins link genetics to disease. Science, 2018, 361, 769-773.	6.0	375
210	Robustness and evolvability of heterogeneous cell populations. Molecular Biology of the Cell, 2018, 29, 1400-1409.	0.9	11
211	Introgression of a Block of Genome Under Infinitesimal Selection. Genetics, 2018, 209, 1279-1303.	1.2	33
212	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. Frontiers in Cardiovascular Medicine, 2018, 5, 56.	1.1	21
213	Empirical Bayes Estimation of Semi-parametric Hierarchical Mixture Models for Unbiased Characterization of Polygenic Disease Architectures. Frontiers in Genetics, 2018, 9, 115.	1.1	10
214	Detection of Significant Association Between Variants in Cannabinoid Receptor 1 Gene (CNR1) and Personality in Africanâ€“American Population. Frontiers in Genetics, 2018, 9, 199.	1.1	13
215	Mental Illnesses-Associated Fxr1 and Its Negative Regulator Gsk3Î² Are Modulators of Anxiety and Glutamatergic Neurotransmission. Frontiers in Molecular Neuroscience, 2018, 11, 119.	1.4	24
216	Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians. BMJ: British Medical Journal, 2018, 362, k601.	2.4	1,880
217	MCRiceRepGP: a framework for the identification of genes associated with sexual reproduction in rice. Plant Journal, 2018, 96, 188-202.	2.8	13
218	Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073.	2.0	5
219	NKG2D gene variation and susceptibility to viral bronchiolitis in childhood. Pediatric Research, 2018, 84, 451-457.	1.1	3
220	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. Current Atherosclerosis Reports, 2018, 20, 47.	2.0	24
221	Enabling Precision Medicine through Integrative Network Models. Journal of Molecular Biology, 2018, 430, 2913-2923.	2.0	15
222	Analysis of causal effect of <i>APOA5</i> variants on premature coronary artery disease. Annals of Human Genetics, 2018, 82, 437-447.	0.3	8

#	Article	IF	Citations
223	Stem Cells to Inform the Neurobiology of Mental Illness. Current Topics in Behavioral Neurosciences, 2018, 40, 13-43.	0.8	4
224	An update on the genetics of hyperuricaemia and gout. Nature Reviews Rheumatology, 2018, 14, 341-353.	3.5	186
225	Identification of usual interstitial pneumonia pattern using RNA-Seq and machine learning: challenges and solutions. BMC Genomics, 2018, 19, 101.	1.2	23
226	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
227	A multi-trait Bayesian method for mapping QTL and genomic prediction. Genetics Selection Evolution, 2018, 50, 10.	1.2	32
228	Single-cell RNA-seq of human induced pluripotent stem cells reveals cellular heterogeneity and cell state transitions between subpopulations. Genome Research, 2018, 28, 1053-1066.	2.4	102
229	Environmental history impacts gene expression during diapause development in the alfalfa leafcutting bee, <i>Megachile rotundata</i>. Journal of Experimental Biology, 2018, 221, .	0.8	17
230	Genome-wide studies of heart failure and endophenotypes: lessons learned and future directions. Cardiovascular Research, 2018, 114, 1209-1225.	1.8	18
231	Towards a more predictable plant breeding pipeline with CRISPR/Cas-induced allelic series to optimize quantitative and qualitative traits. Current Opinion in Plant Biology, 2018, 45, 218-225.	3.5	46
232	Divergent brain gene expression profiles between alternative behavioural helper types in a cooperative breeder. Molecular Ecology, 2018, 27, 4136-4151.	2.0	11
233	Experimental Planning and Execution. , 2018, , 67-106.		1
234	Genetic Regulatory Mechanisms of Smooth Muscle Cells Map to Coronary Artery Disease Risk Loci. American Journal of Human Genetics, 2018, 103, 377-388.	2.6	76
235	Application of Causal Inference to Genomic Analysis: Advances in Methodology. Frontiers in Genetics, 2018, 9, 238.	1.1	20
236	Allele distribution and testing for association between an oxygen dependent degradation domain SNP in EPAS1 and pulmonary arterial pressures in yearling Angus cattle. Agri Gene, 2018, 9, 27-31.	1.9	1
237	Human cardiac <i>cis</i>-regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. Genome Research, 2018, 28, 1577-1588.	2.4	25
238	Turning omics data into therapeutic insights. Current Opinion in Pharmacology, 2018, 42, 95-101.	1.7	9
239	Coadapted genomes and selection on hybrids: Fisher's geometric model explains a variety of empirical patterns. Evolution Letters, 2018, 2, 472-498.	1.6	57
240	Genetic variations in the SNP rs850807 reflect a trade-off between autism and paranoia symptom expressions: a comment on Crespi et al . 2018. Biology Letters, 2018, 14, 20180108.	1.0	3

#	Article	IF	Citations
241	Gene editing in the context of an increasingly complex genome. BMC Genomics, 2018, 19, 595.	1.2	8
242	Genome-wide map of proximity linkage to renin proximal promoter in rat. Physiological Genomics, 2018, 50, 323-331.	1.0	6
243	Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. Translational Psychiatry, 2018, 8, 158.	2.4	15
244	Evolutionary diversity as a catalyst for biological discovery. Integrative Zoology, 2018, 13, 616-633.	1.3	22
245	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
246	Visible Machine Learning for Biomedicine. Cell, 2018, 173, 1562-1565.	13.5	115
247	Landscape, bifurcations, geometry for development. Current Opinion in Systems Biology, 2018, 11, 129-136.	1.3	7
248	Host genetics and microbiome associations through the lens of genome wide association studies. Current Opinion in Microbiology, 2018, 44, 9-19.	2.3	33
249	Human Genetics of Obesity and Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2018, 11, e002090.	1.6	58
250	Recent insights into the evolution of quantitative traits in non-human primates. Current Opinion in Genetics and Development, 2018, 53, 15-20.	1.5	1
251	Whole Exome Sequencing of Patients from Multicase Families with Systemic Lupus Erythematosus Identifies Multiple Rare Variants. Scientific Reports, 2018, 8, 8775.	1.6	32
252	Williams Syndrome neuroanatomical score associates with GTF2IRD1 in large-scale magnetic resonance imaging cohorts: a proof of concept for multivariate endophenotypes. Translational Psychiatry, 2018, 8, 114.	2.4	6
253	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
254	Genetic Network Complexity Shapes Background-Dependent Phenotypic Expression. Trends in Genetics, 2018, 34, 578-586.	2.9	35
255	Targeting the FKBP51/GR/Hsp90 Complex to Identify Functionally Relevant Treatments for Depression and PTSD. ACS Chemical Biology, 2018, 13, 2288-2299.	1.6	29
256	Metaâ€Analysis of Publicly Available Chinese Hamster Ovary (CHO) Cell Transcriptomic Datasets for Identifying Engineering Targets to Enhance Recombinant Protein Yields. Biotechnology Journal, 2018, 13, e1800066.	1.8	10
257	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. Nature Communications, 2018, 9, 2427.	5.8	159
258	Population genetics and GWAS: A primer. PLoS Biology, 2018, 16, e2005485.	2.6	36

#	Article	IF	Citations
259	Leveraging GWAS for complex traits to detect signatures of natural selection in humans. Current Opinion in Genetics and Development, 2018, 53, 9-14.	1.5	22
260	The genetic architecture of type 1 diabetes mellitus. Molecular and Cellular Endocrinology, 2018, 477, 70-80.	1.6	51
261	Concepts About VË™O2max and Trainability Are Context Dependent. Exercise and Sport Sciences Reviews, 2018, 46, 138-143.	1.6	42
262	Grimon: graphical interface to visualize multi-omics networks. Bioinformatics, 2018, 34, 3934-3936.	1.8	11
263	Using tree-based methods for detection of geneâ€"gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. Bioinformatics, 2019, 35, 181-188.	1.8	10
264	Genetics of attention deficit hyperactivity disorder. Molecular Psychiatry, 2019, 24, 562-575.	4.1	614
265	Evaluating the Prediction of Brain Maturity From Functional Connectivity After Motion Artifact Denoising. Cerebral Cortex, 2019, 29, 2455-2469.	1.6	73
266	Artificial Intelligence and Machine Learning in Bioinformatics. , 2019, , 272-286.		11
267	Disease classification: from phenotypic similarity to integrative genomics and beyond. Briefings in Bioinformatics, 2019, 20, 1769-1780.	3.2	19
268	Rediscovering the value of families for psychiatric genetics research. Molecular Psychiatry, 2019, 24, 523-535.	4.1	43
269	The influence of the serotonin transporter gene 5-HTTLPR polymorphism on suicidal behaviors: a meta-analysis. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 88, 375-387.	2.5	35
270	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. Cerebral Cortex, 2019, 29, 2904-2914.	1.6	36
271	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	9.4	774
272	Biological Relativity Requires Circular Causality but Not Symmetry of Causation: So, Where, What and When Are the Boundaries?. Frontiers in Physiology, 2019, 10, 827.	1.3	57
273	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	2.6	175
274	Genomic and epigenomic bases of transgressive segregation â€" New breeding paradigm for novel plant phenotypes. Plant Science, 2019, 288, 110213.	1.7	39
275	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. National Science Review, 2019, 6, 1201-1222.	4.6	30
276	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.	1.8	51

#	Article	IF	Citations
277	Unifying Theoretical and Empirical Perspectives on Genomic Differentiation. Trends in Ecology and Evolution, 2019, 34, 987-995.	4.2	11
278	Computer Optimized Microscopy. Methods in Molecular Biology, 2019, , .	0.4	4
279	Genome-wide association studies of severe P. falciparum malaria susceptibility: progress, pitfalls and prospects. BMC Medical Genomics, 2019, 12, 120.	0.7	28
281	Making DEEP Sense of Lifestyle Risk and Resilience. Frontiers in Aging Neuroscience, 2019, 11, 171.	1.7	3
282	A Cell Segmentation/Tracking Tool Based on Machine Learning. Methods in Molecular Biology, 2019, 2040, 399-422.	0.4	12
283	Network-Based Integrative Analysis of Genomics, Epigenomics and Transcriptomics in Autism Spectrum Disorders. International Journal of Molecular Sciences, 2019, 20, 3363.	1.8	8
284	Family Clustering of Autoimmune Vitiligo Results Principally from Polygenic Inheritance of Common Risk Alleles. American Journal of Human Genetics, 2019, 105, 364-372.	2.6	21
285	A gene regulatory network explains RETâ€“EDNRB epistasis in Hirschsprung disease. Human Molecular Genetics, 2019, 28, 3137-3147.	1.4	25
286	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. Science, 2019, 365, .	6.0	152
287	Crickâ€™s sequence hypothesis - a review. Communicative and Integrative Biology, 2019, 12, 59-64.	0.6	7
288	Swede midge (Diptera: Cecidomyiidae) diapause initiation under stable conditions: not a family affair. Canadian Entomologist, 2019, 151, 465-474.	0.4	18
289	The potential of genomics for restoring ecosystems and biodiversity. Nature Reviews Genetics, 2019, 20, 615-628.	7.7	142
290	Using natural variation to understand the evolutionary pressures on plant photosynthesis. Current Opinion in Plant Biology, 2019, 49, 68-73.	3.5	9
291	Linking Delay Discounting and Substance Use Disorders: Genotypes and Phenotypes. Perspectives on Behavior Science, 2019, 42, 419-432.	1.1	12
292	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. Molecular Ecology, 2019, 28, 3544-3560.	2.0	32
293	Thinking About the Evolution of Complex Traits in the Era of Genome-Wide Association Studies. Annual Review of Genomics and Human Genetics, 2019, 20, 461-493.	2.5	186
294	How humans can contribute to Mendelian randomization analyses. International Journal of Epidemiology, 2019, 48, 661-664.	0.9	23
295	Robust Candidates for Language Development and Evolution Are Significantly Dysregulated in the Blood of People With Williams Syndrome. Frontiers in Neuroscience, 2019, 13, 258.	1.4	1

#	ARTICLE	IF	CITATIONS
296	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. Genome Medicine, 2019, 11, 47.	3.6	68
297	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. Nature Genetics, 2019, 51, 1137-1148.	9.4	208
298	Exploratory locomotion, a predictor of addiction vulnerability, is oligogenic in rats selected for this phenotype. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13107-13115.	3.3	33
299	Molecular pharmacology of metabotropic receptors targeted by neuropsychiatric drugs. Nature Structural and Molecular Biology, 2019, 26, 535-544.	3.6	45
300	A subset of topologically associating domains fold into mesoscale core-periphery networks. Scientific Reports, 2019, 9, 9526.	1.6	9
301	Enhanced Molecular Appreciation of Psychiatric Disorders Through High-Dimensionality Data Acquisition and Analytics. Methods in Molecular Biology, 2019, 2011, 671-723.	0.4	13
302	Characterization of DSM-IV Opioid Dependence Among Individuals of European Ancestry. Journal of Studies on Alcohol and Drugs, 2019, 80, 319-330.	0.6	11
303	Sexual selection and the evolution of male and female cognition: A test using experimental evolution in seed beetles*. Evolution; International Journal of Organic Evolution, 2019, 73, 2390-2400.	1.1	18
304	Association Mapping and Disease: Evolutionary Perspectives. Methods in Molecular Biology, 2019, 1910, 533-553.	0.4	0
305	An omnidirectional visualization model of personalized gene regulatory networks. Npj Systems Biology and Applications, 2019, 5, 38.	1.4	20
306	Genes, depressive symptoms, and chronic stressors: A nationally representative longitudinal study in the United States. Social Science and Medicine, 2019, 242, 112586.	1.8	1
307	Somatic maintenance impacts the evolution of mutation rate. BMC Evolutionary Biology, 2019, 19, 172.	3.2	9
308	Update on the Role of the Non-Canonical Wnt/Planar Cell Polarity Pathway in Neural Tube Defects. Cells, 2019, 8, 1198.	1.8	55
309	Rare-variant collapsing analyses for complex traits: guidelines and applications. Nature Reviews Genetics, 2019, 20, 747-759.	7.7	147
310	Genetic factors define CPO and CLO subtypes of nonsyndromicorofacial cleft. PLoS Genetics, 2019, 15, e1008357.	1.5	70
311	Review article: the genetics of the human leucocyte antigen region in inflammatory bowel disease. Alimentary Pharmacology and Therapeutics, 2019, 50, 885-900.	1.9	18
312	Genomeâ€wide association analyses reveal polygenic genomic architecture underlying divergent shell morphology in Spanish Littorina saxatilis ecotypes. Ecology and Evolution, 2019, 9, 9427-9441.	0.8	13
313	Compensatory<i>trans</i>-regulatory alleles minimizing variation in<i>TDH3</i>expression are common within<i>Saccharomyces cerevisiae</i>. Evolution Letters, 2019, 3, 448-461.	1.6	21

#	Article	IF	Citations
314	Genetic and epigenetic determinants of muscle mass. , 2019, , 251-272.		0
315	How to Investigate the Origins of Novelty: Insights Gained from Genetic, Behavioral, and Fitness Perspectives. Integrative Organismal Biology, 2019, 1, obz018.	0.9	10
316	Genetic Approaches for Sports Performance: How Far Away Are We?. Sports Medicine, 2019, 49, 199-204.	3.1	20
317	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nâ€‰=â€‰17,706). Molecular Psychiatry, 2021, 26, 3943-3955.	4.1	100
318	Genome-wide association analysis of 19,629 individuals identifies variants influencing regional brain volumes and refines their genetic co-architecture with cognitive and mental health traits. Nature Genetics, 2019, 51, 1637-1644.	9.4	186
319	Advances in asthma and allergic disease genetics: Is bigger always better?. Journal of Allergy and Clinical Immunology, 2019, 144, 1495-1506.	1.5	61
320	Generating an Artificial Nest Building Pufferfish in a Cellular Automaton Through Behavior Decomposition. International Journal of Artificial Intelligence and Machine Learning, 2019, 9, 1-12.	0.4	2
321	Genome-Wide Association Study on the Early-Phase Insulin Response to a Liquid Mixed Meal: Results From the NEO Study. Diabetes, 2019, 68, 2327-2336.	0.3	9
322	Genome-wide association studies and genetic testing: understanding the science, success, and future of a rapidly developing field. Journal of the American Veterinary Medical Association, 2019, 255, 1126-1136.	0.2	10
323	Quantifying the polygenic contribution to variable expressivity in eleven rare genetic disorders. Nature Communications, 2019, 10, 4897.	5.8	89
324	Systems genetics applications in metabolism research. Nature Metabolism, 2019, 1, 1038-1050.	5.1	35
325	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.	3.8	47
326	Polygenic selection drives the evolution of convergent transcriptomic landscapes across continents within a Nearctic sister species complex. Molecular Ecology, 2019, 28, 4388-4403.	2.0	38
327	Preparing biomedical students for the unknown. EMBO Reports, 2019, 20, e49004.	2.0	1
328	SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. BMC Genomics, 2019, 20, 694.	1.2	13
329	The Wiring of Intelligence. Perspectives on Psychological Science, 2019, 14, 1034-1061.	5.2	39
330	Biologie und Mathematik. , 2019, , .		6
331	Network modeling of single-cell omics data: challenges, opportunities, and progresses. Emerging Topics in Life Sciences, 2019, 3, 379-398.	1.1	48

#	ARTICLE	IF	CITATIONS
332	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	9.0	213
333	Complex Phenotypes: Mechanisms Underlying Variation in Human Stature. Current Osteoporosis Reports, 2019, 17, 301-323.	1.5	11
334	The dark genome and pleiotropy: challenges for precision medicine. Mammalian Genome, 2019, 30, 212-216.	1.0	16
335	Identifying and exploiting gene-pathway interactions from RNA-seq data for binary phenotype. BMC Genetics, 2019, 20, 36.	2.7	2
336	Mitochondrial genomic variation drives differential nuclear gene expression in discrete regions of Drosophila gene and protein interaction networks. BMC Genomics, 2019, 20, 691.	1.2	15
337	Social and non-social autism symptoms and trait domains are genetically dissociable. Communications Biology, 2019, 2, 328.	2.0	57
338	Getting to the Cores of Autism. Cell, 2019, 178, 1287-1298.	13.5	204
339	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. Nature Communications, 2019, 10, 4064.	5.8	48
340	Ultrarare variants drive substantial cis heritability of human gene expression. Nature Genetics, 2019, 51, 1349-1355.	9.4	98
341	Dark-matter matters: Discriminating subtle blood cancers using the darkest DNA. PLoS Computational Biology, 2019, 15, e1007332.	1.5	7
342	Benchmarking network propagation methods for disease gene identification. PLoS Computational Biology, 2019, 15, e1007276.	1.5	30
343	Deconvolution of transcriptional networks identifies TCF4 as a master regulator in schizophrenia. Science Advances, 2019, 5, eaau4139.	4.7	59
344	Estimation of variance components, heritability and the ridge penalty in high-dimensional generalized linear models. Communications in Statistics Part B: Simulation and Computation, 2019, , 1-19.	0.6	5
345	Association genetics of bunch weight and its component traits in East African highland banana (Musa) Tj ETQq1 1 0.784314 rgBT /Over	1.8	17
346	Finding New Cell Wall Regulatory Genes in Populus trichocarpa Using Multiple Lines of Evidence. Frontiers in Plant Science, 2019, 10, 1249.	1.7	13
347	Microbiome composition shapes rapid genomic adaptation of<i>Drosophila melanogaster</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20025-20032.	3.3	103
348	Oligogenic Effects of 16p11.2 Copy-Number Variation on Craniofacial Development. Cell Reports, 2019, 28, 3320-3328.e4.	2.9	34
349	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. Current Biology, 2019, 29, 2926-2935.e4.	1.8	40

#	Article	IF	Citations
350	Verifying Feighnerâ€™s Hypothesis; Anorexia Nervosa Is Not a Psychiatric Disorder. Frontiers in Psychology, 2019, 10, 2110.	1.1	7
351	The future of rodent models in depression research. Nature Reviews Neuroscience, 2019, 20, 686-701.	4.9	178
352	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
353	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	2.6	36
354	The challenges of primary biliary cholangitis: What is new and what needs to be done. Journal of Autoimmunity, 2019, 105, 102328.	3.0	86
355	Exploring genetic variation that influences brain methylation in attention-deficit/hyperactivity disorder. Translational Psychiatry, 2019, 9, 242.	2.4	21
356	Why and how to study genetic changes with context-dependent effects. Current Opinion in Genetics and Development, 2019, 58-59, 95-102.	1.5	20
357	Synergistic effects of common schizophrenia risk variants. Nature Genetics, 2019, 51, 1475-1485.	9.4	184
358	The Human Cell Atlas: making â€˜cell spaceâ€™ for disease. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	9
359	A Microglial Signature Directing Human Aging and Neurodegeneration-Related Gene Networks. Frontiers in Neuroscience, 2019, 13, 2.	1.4	63
360	The obesity transition: stages of the global epidemic. Lancet Diabetes and Endocrinology,the, 2019, 7, 231-240.	5.5	662
361	Environmental and Evolutionary Drivers of the Modular Gene Regulatory Network Underlying Phenotypic Plasticity for Stress Resistance in the Nematode <i>Caenorhabditis remanei</i>. G3: Genes, Genomes, Genetics, 2019, 9, 969-982.	0.8	22
362	The virtuous cycle of human genetics and mouse models in drug discovery. Nature Reviews Drug Discovery, 2019, 18, 255-272.	21.5	44
363	Differential vulnerability to neighbourhood disorder: a geneÃ—environment interaction study. Journal of Epidemiology and Community Health, 2019, 73, 388-392.	2.0	14
364	Developing individual differences in primate behavior: the role of genes, environment, and their interplay. Behavioral Ecology and Sociobiology, 2019, 73, 1.	0.6	11
365	Disentangling polygenic associations between attention-deficit/hyperactivity disorder, educational attainment, literacy and language. Translational Psychiatry, 2019, 9, 35.	2.4	25
366	Comprehensive functional annotation of susceptibility SNPs prioritized 10 genes for schizophrenia. Translational Psychiatry, 2019, 9, 56.	2.4	20
367	CLOCK Polymorphisms in Attention-Deficit/Hyperactivity Disorder (ADHD): Further Evidence Linking Sleep and Circadian Disturbances and ADHD. Genes, 2019, 10, 88.	1.0	19

#	ARTICLE	IF	CITATIONS
368	The Effects of Epistasis and Pleiotropy on Genome-Wide Scans for Adaptive Outlier Loci. Journal of Heredity, 2019, 110, 494-513.	1.0	3
369	Adaptive Landscapes in the Age of Synthetic Biology. Molecular Biology and Evolution, 2019, 36, 890-907.	3.5	25
370	An interaction-based model for neuropsychiatric features of copy-number variants. PLoS Genetics, 2019, 15, e1007879.	1.5	39
371	Genetic correlations in the dental dimensions of Saguinus fuscicollis. American Journal of Physical Anthropology, 2019, 169, 557-566.	2.1	12
372	Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. Communications Biology, 2019, 2, 186.	2.0	20
373	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle. Epigenomes, 2019, 3, 10.	0.8	12
374	Evidence for the genetic basis and epistatic interactions underlying oceanâ€•and riverâ€•maturing ecotypes of Pacific Lamprey (<i>Entosphenus tridentatus</i>) returning to the Klamath River, California. Molecular Ecology, 2019, 28, 3171-3185.	2.0	15
375	Genomic medicine in Chagas disease. Acta Tropica, 2019, 197, 105062.	0.9	20
376	Genome-wide association meta-analysis of cocaine dependence: Shared genetics with comorbid conditions. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 94, 109667.	2.5	48
377	An evaluation of noncoding genome annotation tools through enrichment analysis of 15 genome-wide association studies. Briefings in Bioinformatics, 2019, 20, 995-1003.	3.2	3
378	Searching for Sympatric Speciation in the Genomic Era. BioEssays, 2019, 41, e1900047.	1.2	61
379	Clinical-pathological correlations of BAV and the attendant thoracic aortopathies. Part 2: Pluridisciplinary perspective on their genetic and molecular origins. Journal of Molecular and Cellular Cardiology, 2019, 133, 233-246.	0.9	3
380	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180248.	1.8	32
381	Host Genetic Characters of Acute Exacerbation of Chronic Hepatitis B (AECHB). , 2019, , 159-221.		0
382	Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. Genetics, 2019, 212, 919-929.	1.2	12
383	Exome sequencing of cases with neural tube defects identifies candidate genes involved in one-carbon/vitamin B12 metabolisms and Sonic Hedgehog pathway. Human Genetics, 2019, 138, 703-713.	1.8	13
384	Oligogenic inheritance of a human heart disease involving a genetic modifier. Science, 2019, 364, 865-870.	6.0	142
386	Genome Wide Association Study and Next Generation Sequencing: A Glimmer of Light Toward New Possible Horizons in Frontotemporal Dementia Research. Frontiers in Neuroscience, 2019, 13, 506.	1.4	23

#	ARTICLE	IF	CITATIONS
388	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
389	Exploring the use of molecular dynamics in assessing protein variants for phenotypic alterations. Human Mutation, 2019, 40, 1424-1435.	1.1	10
390	Admixture mapping in interspecific <i>Populus</i> hybrids identifies classes of genomic architectures for phytochemical, morphological and growth traits. New Phytologist, 2019, 223, 2076-2089.	3.5	21
391	Benefits and limitations of genome-wide association studies. Nature Reviews Genetics, 2019, 20, 467-484.	7.7	1,226
392	Drug discovery for psychiatric disorders using high-content single-cell screening of signaling network responses ex vivo. Science Advances, 2019, 5, eaau9093.	4.7	22
393	Genetic Insights Into Smooth Muscle Cell Contributions to Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1006-1017.	1.1	26
394	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10636-10645.	3.3	22
395	The role of polygenic risk score gene-set analysis in the context of the omnigenic model of schizophrenia. Neuropsychopharmacology, 2019, 44, 1562-1569.	2.8	44
396	A systems biology approach uncovers cell-specific gene regulatory effects of genetic associations in multiple sclerosis. Nature Communications, 2019, 10, 2236.	5.8	65
397	Bioinformatic Analysis of Gene Variants from Gastroschisis Recurrence Identifies Multiple Novel Pathogenetic Pathways: Implication for the Closure of the Ventral Body Wall. International Journal of Molecular Sciences, 2019, 20, 2295.	1.8	10
398	Molecular Origins of Complex Heritability in Natural Genotype-to-Phenotype Relationships. Cell Systems, 2019, 8, 363-379.e3.	2.9	26
399	â€˜Artificial spermatidâ€™-mediated genome editingâ€. Biology of Reproduction, 2019, 101, 538-548.	1.2	8
401	Polygenic adaptation: From sweeps to subtle frequency shifts. PLoS Genetics, 2019, 15, e1008035.	1.5	113
402	Role of Mitochondrial DNA Damage in ROS-Mediated Pathogenesis of Age-Related Macular Degeneration (AMD). International Journal of Molecular Sciences, 2019, 20, 2374.	1.8	121
403	RWâ€2018â€”Research Workshop: The Effect of Nutrition on Epigenetic Status, Growth, and Health. Journal of Parenteral and Enteral Nutrition, 2019, 43, 627-637.	1.3	6
404	<i>np</i>²<scp>QTL</scp>: networking phenotypic plasticity quantitative trait loci across heterogeneous environments. Plant Journal, 2019, 99, 796-806.	2.8	7
405	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. ELife, 2019, 8, .	2.8	276
406	Transcriptome Changes in Relation to Manic Episode. Frontiers in Psychiatry, 2019, 10, 280.	1.3	18

#	Article	IF	Citations
407	Bioactive Ingredients in Chinese Herbal Medicines That Target Non-coding RNAs: Promising New Choices for Disease Treatment. Frontiers in Pharmacology, 2019, 10, 515.	1.6	40
408	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	2.6	46
409	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. Cell, 2019, 177, 1022-1034.e6.	13.5	385
410	Pathway centrality in protein interaction networks identifies putative functional mediating pathways in pulmonary disease. Scientific Reports, 2019, 9, 5863.	1.6	7
411	Clinical Genetic Testing and Counseling in Psychiatry. , 2019, , 181-202.		0
412	Cross-species alcohol dependence-associated gene networks: Co-analysis of mouse brain gene expression and human genome-wide association data. PLoS ONE, 2019, 14, e0202063.	1.1	14
413	Pleiotropy Informed Adaptive Association Test of Multiple Traits Using Genome-Wide Association Study Summary Data. Biometrics, 2019, 75, 1076-1085.	0.8	13
414	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. Communications Biology, 2019, 2, 100.	2.0	41
415	HLAâ€associated antiepileptic drugâ€induced cutaneous adverse reactions. Hla, 2019, 93, 417-435.	0.4	52
416	The genetics of depression: successful genome-wide association studies introduce new challenges. Translational Psychiatry, 2019, 9, 114.	2.4	75
417	Pervasive function and evidence for selection across standing genetic variation in S. cerevisiae. Nature Communications, 2019, 10, 1222.	5.8	10
418	The Genetic Variability of APOE in Different Human Populations and Its Implications for Longevity. Genes, 2019, 10, 222.	1.0	96
419	Polygenic Risk Scores in Neurodegenerative Diseases: a Review. Current Genetic Medicine Reports, 2019, 7, 22-29.	1.9	23
420	Multitrait genomeâ€wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. New Phytologist, 2019, 223, 293-309.	3.5	85
421	A data-driven interactome of synergistic genes improves network-based cancer outcome prediction. PLoS Computational Biology, 2019, 15, e1006657.	1.5	13
422	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. Epigenetics, 2019, 14, 260-276.	1.3	25
423	Population genomics of rapid evolution in natural populations: polygenic selection in response to power station thermal effluents. BMC Evolutionary Biology, 2019, 19, 61.	3.2	67
424	Primary Immunodeficiency and Cancer Predisposition Revisited: Embedding Two Closely Related Concepts Into an Integrative Conceptual Framework. Frontiers in Immunology, 2018, 9, 3136.	2.2	47

#	Article	IF	Citations
425	Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breederâ€™s equation. Theoretical and Applied Genetics, 2019, 132, 627-645.	1.8	219
426	Genetics and Education: Recent Developments in the Context of an Ugly History and an Uncertain Future. AERA Open, 2019, 5, 233285841881051.	1.3	39
427	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
428	Genomic Medicineâ€"Progress, Pitfalls, and Promise. Cell, 2019, 177, 45-57.	13.5	143
429	The Genetic Basis of Metabolic Disease. Cell, 2019, 177, 146-161.	13.5	104
430	Gene-Environment Interaction in the Era of Precision Medicine. Cell, 2019, 177, 38-44.	13.5	73
431	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
432	Identification of Shared Genes Between Ischemic Stroke and Parkinson's Disease Using Genome-Wide Association Studies. Frontiers in Neurology, 2019, 10, 297.	1.1	18
433	Genomic basis of delayed reward discounting. Behavioural Processes, 2019, 162, 157-161.	0.5	10
434	ANGPTL4 gene E40K variation protects against obesityâ€associated dyslipidemia in participants with obesity. Obesity Science and Practice, 2019, 5, 83-90.	1.0	13
435	Shared genes between Alzheimerâ€™s disease and ischemic stroke. CNS Neuroscience and Therapeutics, 2019, 25, 855-864.	1.9	36
436	Dissection of Complex, Fitness-Related Traits in Multiple<i>Drosophila</i>Mapping Populations Offers Insight into the Genetic Control of Stress Resistance. Genetics, 2019, 211, 1449-1467.	1.2	22
437	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. Cell Systems, 2019, 8, 122-135.e7.	2.9	45
438	Prefrontal Coexpression of Schizophrenia Risk Genes Is Associated With Treatment Response in Patients. Biological Psychiatry, 2019, 86, 45-55.	0.7	27
439	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. Annual Review of Genomics and Human Genetics, 2019, 20, 181-200.	2.5	33
441	The Orexin System and Nicotine Addiction: Preclinical Insights. , 2019, , 509-517.		1
442	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
443	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. Genome Medicine, 2019, 11, 19.	3.6	33

#	Article	IF	Citations
444	Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. Frontiers in Cardiovascular Medicine, 2019, 6, 21.	1.1	15
445	Integrative Approach to Reveal Cell Type Specificity and Gene Candidates for Psoriatic Arthritis Outside the MHC. Frontiers in Genetics, 2019, 10, 304.	1.1	6
446	Williams Syndrome, Human Self-Domestication, and Language Evolution. Frontiers in Psychology, 2019, 10, 521.	1.1	26
447	Genotypes identified by genome-wide association analyses influence yearling pulmonary arterial pressure and growth traits in Angus heifers from a high-altitude beef production system. Livestock Science, 2019, 224, 75-86.	0.6	5
448	Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. PLoS Genetics, 2019, 15, e1007973.	1.5	5
449	Imputed gene associations identify replicable <i>trans</i>â€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608.	0.6	19
450	Heritability and genetic variance of dementia with Lewy bodies. Neurobiology of Disease, 2019, 127, 492-501.	2.1	29
451	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	9.4	262
452	Genome-wide association mapping of grain yield in a diverse collection of spring wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	108
453	Mouse Skull Mean Shape and Shape Robustness Rely on Different Genetic Architectures and Different Loci. Frontiers in Genetics, 2019, 10, 64.	1.1	12
454	Evolutionary highways to persistent bacterial infection. Nature Communications, 2019, 10, 629.	5.8	89
456	S-CAP extends pathogenicity prediction to genetic variants that affect RNA splicing. Nature Genetics, 2019, 51, 755-763.	9.4	56
457	Exploiting the Power of Group Differences: Using Patterns to Solve Data Analysis Problems. Synthesis Lectures on Data Mining and Knowledge Discovery, 2019, 11, 1-146.	0.5	5
458	The Challenges and Opportunities of Small Effects. JAMA Psychiatry, 2019, 76, 353.	6.0	83
459	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. American Journal of Human Genetics, 2019, 104, 503-519.	2.6	21
460	The Effects of Demography and Genetics on the Neutral Distribution of Quantitative Traits. Genetics, 2019, 211, 1371-1394.	1.2	6
461	Treating the â€œEâ€•in â€œG Ã— Eâ€ Trauma-Informed Approaches and Psychological Therapy Interventions in Psychosis. Frontiers in Psychiatry, 2019, 10, 9.	1.3	12
462	African American ancestry contribution to asthma and atopic dermatitis. Annals of Allergy, Asthma and Immunology, 2019, 122, 456-462.	0.5	33

#	Article	IF	Citations
463	Rejoinder: â€˜Gene hunting with hidden Markov model knockoffsâ€™. Biometrika, 2019, 106, 35-45.	1.3	15
464	Herb Target Prediction Based on Representation Learning of Symptom related Heterogeneous Network. Computational and Structural Biotechnology Journal, 2019, 17, 282-290.	1.9	26
465	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. Journal of the American Society of Nephrology: JASN, 2019, 30, 421-441.	3.0	27
466	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	5.8	98
467	Multiple Changes Underlie Allelic Divergence of<i>CUP2</i>Between<i>Saccharomyces</i>Species. G3: Genes, Genomes, Genetics, 2019, 9, 3595-3600.	0.8	5
468	Association Mapping Based on a Common-Garden Migration Experiment Reveals Candidate Genes for Migration Tendency in Brown Trout. G3: Genes, Genomes, Genetics, 2019, 9, 2887-2896.	0.8	18
469	Multi-trait Improvement by Predicting Genetic Correlations in Breeding Crosses. G3: Genes, Genomes, Genetics, 2019, 9, 3153-3165.	0.8	34
470	High-Dimensional Bayesian Network Inference From Systems Genetics Data Using Genetic Node Ordering. Frontiers in Genetics, 2019, 10, 1196.	1.1	14
471	The Search for the Genes of Vasovagal Syncope. Frontiers in Cardiovascular Medicine, 2019, 6, 175.	1.1	18
472	Tightly linked antagonistic-effect loci underlie polygenic phenotypic variation in<i>C. elegans</i>. Evolution Letters, 2019, 3, 462-473.	1.6	37
473	Assessing the potential for assisted gene flow using past introduction of Norway spruce in southern Sweden: Local adaptation and genetic basis of quantitative traits in trees. Evolutionary Applications, 2019, 12, 1946-1959.	1.5	36
474	DNA variants affecting the expression of numerous genes in trans have diverse mechanisms of action and evolutionary histories. PLoS Genetics, 2019, 15, e1008375.	1.5	34
475	Ecological genomics of adaptation to unpredictability in experimental rotifer populations. Scientific Reports, 2019, 9, 19646.	1.6	2
476	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. BMC Genomics, 2019, 20, 929.	1.2	6
477	Understanding Is a Design Problem: Cognizing from a Designerly Thinking Perspective. Part 2. She Ji, 2019, 5, 327-342.	0.6	1
478	Genetic risk scores in lipid disorders. Current Opinion in Cardiology, 2019, 34, 406-412.	0.8	7
479	Benchmarking machine learning models for late-onset alzheimerâ€™s disease prediction from genomic data. BMC Bioinformatics, 2019, 20, 709.	1.2	41
480	Minor alleles are associated with white rust (Albugo occidentalis) susceptibility in spinach (Spinacia) Tj ETQq1 1 0.784314 rgBT /Overlo	2.9	6

#	Article	IF	Citations
481	The great hairball gambit. PLoS Genetics, 2019, 15, e1008519.	1.5	34
482	Network Modeling Approaches and Applications to Unravelling Non-Alcoholic Fatty Liver Disease. Genes, 2019, 10, 966.	1.0	26
483	Effectiveness of Genomic Selection by Response to Selection for Winter Wheat Variety Improvement. Plant Genome, 2019, 12, 1-15.	1.6	18
484	Low coverage whole genome sequencing enables accurate assessment of common variants and calculation of genome-wide polygenic scores. Genome Medicine, 2019, 11, 74.	3.6	70
485	Three geneticâ€"environmental networks for human personality. Molecular Psychiatry, 2021, 26, 3858-3875.	4.1	58
486	What Is Karyotype Coding and Why Is Genomic Topology Important for Cancer and Evolution?. Frontiers in Genetics, 2019, 10, 1082.	1.1	41
487	Genetics and Omics Analysis of Autoimmune Skin Blistering Diseases. Frontiers in Immunology, 2019, 10, 2327.	2.2	24
488	Genetic Risk Scores. Current Protocols in Human Genetics, 2019, 104, e95.	3.5	69
489	Genes, Gender Inequality, and Educational Attainment. American Sociological Review, 2019, 84, 1069-1098.	2.8	49
490	Choroidal Neovascularization: Mechanisms of Endothelial Dysfunction. Frontiers in Pharmacology, 2019, 10, 1363.	1.6	57
491	Implications of juvenile idiopathic arthritis genetic risk variants for disease pathogenesis and classification. Current Opinion in Rheumatology, 2019, 31, 401-410.	2.0	24
492	Genetic dissection of canine hip dysplasia phenotypes and osteoarthritis reveals three novel loci. BMC Genomics, 2019, 20, 1027.	1.2	13
493	The evolution of genetic-based risk scores for lipids and cardiovascular disease. Current Opinion in Lipidology, 2019, 30, 71-81.	1.2	49
494	Landscape of stimulation-responsive chromatin across diverse human immune cells. Nature Genetics, 2019, 51, 1494-1505.	9.4	196
495	A perturbed gene network containing PI3Kâ€"AKT, RASâ€"ERK and WNTâ€"Î²-catenin pathways in leukocytes is linked to ASD genetics and symptom severity. Nature Neuroscience, 2019, 22, 1624-1634.	7.1	71
496	Brain-derived neurotrophic factor and schizophrenia. Psychiatric Genetics, 2019, 29, 200-210.	0.6	69
497	The Genetic Relevance of Human Induced Pluripotent Stem Cell-Derived Microglia to Alzheimerâ€™s Disease and Major Neuropsychiatric Disorders. Molecular Neuropsychiatry, 2019, 5, 85-96.	3.0	9
498	Comprehensive identification of pleiotropic loci for body fat distribution using the NHGRIâ€EBI Catalog of published genomeâ€wide association studies. Obesity Reviews, 2019, 20, 385-406.	3.1	10

#	ARTICLE	IF	CITATIONS
499	Back to the future: revisiting MAS as a tool for modern plant breeding. Theoretical and Applied Genetics, 2019, 132, 647-667.	1.8	130
500	Evidence for Weak Selective Constraint on Human Gene Expression. Genetics, 2019, 211, 757-772.	1.2	48
501	The structure of cognition in 9 and 10 year-old children and associations with problem behaviors: Findings from the ABCD studyâ€™s baseline neurocognitive battery. Developmental Cognitive Neuroscience, 2019, 36, 100606.	1.9	128
502	Thinking About Schizophrenia in an Era of Genomic Medicine. American Journal of Psychiatry, 2019, 176, 12-20.	4.0	45
503	Dissection of Leaf Angle Variation in Maize through Genetic Mapping and Metaâ€Analysis. Plant Genome, 2019, 12, 180024.	1.6	26
504	Earlyâ€onset inflammatory bowel disease as a model disease to identify key regulators of immune homeostasis mechanisms. Immunological Reviews, 2019, 287, 162-185.	2.8	60
505	HPA-axis multilocus genetic variation moderates associations between environmental stress and depressive symptoms among adolescents. Development and Psychopathology, 2019, 31, 1339-1352.	1.4	27
507	Genomic updates in understanding PTSD. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 90, 197-203.	2.5	23
508	Dissecting the Genetics of Osteoporosis using Systems Approaches. Trends in Genetics, 2019, 35, 55-67.	2.9	43
509	A rare regulatory variant in the MEF2D gene affects gene regulation and splicing and is associated with a SLE sub-phenotype in Swedish cohorts. European Journal of Human Genetics, 2019, 27, 432-441.	1.4	12
510	Genetic rescue and the maintenance of native ancestry. Conservation Genetics, 2019, 20, 59-64.	0.8	37
511	Longevity defined as top 10% survivors and beyond is transmitted as a quantitative genetic trait. Nature Communications, 2019, 10, 35.	5.8	62
512	Mapping of quantitative trait loci for life history traits segregating within common frog populations. Heredity, 2019, 122, 800-808.	1.2	5
513	CRISPR/Cas9-mediated targeted T-DNA integration in rice. Plant Molecular Biology, 2019, 99, 317-328.	2.0	37
514	Genetic Association Study in Multigenerational Kindreds With Vasovagal Syncope. Circulation: Arrhythmia and Electrophysiology, 2019, 12, e006884.	2.1	22
515	Phenotypic Annotation: Using Polygenic Scores to Translate Discoveries From Genome-Wide Association Studies From the Top Down. Current Directions in Psychological Science, 2019, 28, 82-90.	2.8	49
516	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. American Journal of Respiratory Cell and Molecular Biology, 2019, 60, 388-398.	1.4	15
517	Genomic index selection provides a pragmatic framework for setting and refining multi-objective breeding targets in Miscanthus. Annals of Botany, 2019, 124, 521-529.	1.4	10

#	Article	IF	Citations
518	Exome sequencing in families with severe mental illness identifies novel and rare variants in genes implicated in Mendelian neuropsychiatric syndromes. Psychiatry and Clinical Neurosciences, 2019, 73, 11-19.	1.0	31
519	Systems-Wide Approaches in Induced Pluripotent Stem Cell Models. Annual Review of Pathology: Mechanisms of Disease, 2019, 14, 395-419.	9.6	24
520	Early behavioral indices of inherited liability to autism. Pediatric Research, 2019, 85, 127-133.	1.1	13
521	From the Past to the Future: Considering the Value and Limits of Evolutionary Prediction. American Naturalist, 2019, 193, 1-10.	1.0	43
522	Optimising the identification of causal variants across varying genetic architectures in crops. Plant Biotechnology Journal, 2019, 17, 893-905.	4.1	29
523	Post-GWAS in prostate cancer: from genetic association to biological contribution. Nature Reviews Cancer, 2019, 19, 46-59.	12.8	73
524	Independent and Jointâ€•GWAS for growth traits in Eucalyptus by assembling genomeâ€wide data for 3373 individuals across four breeding populations. New Phytologist, 2019, 221, 818-833.	3.5	62
525	Genetics of Hyperuricemia and Gout. , 2019, , 9-27.		0
526	A quantitative approach to neuropsychiatry: The why and the how. Neuroscience and Biobehavioral Reviews, 2019, 97, 3-9.	2.9	63
527	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. Molecular Psychiatry, 2019, 24, 182-197.	4.1	47
528	New considerations for hiPSC-based models of neuropsychiatric disorders. Molecular Psychiatry, 2019, 24, 49-66.	4.1	64
529	The Genetics of Treatment-Resistant Depression: A Critical Review and Future Perspectives. International Journal of Neuropsychopharmacology, 2019, 22, 93-104.	1.0	32
530	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1707-1719.	4.1	59
531	Mutations in MERTK are not associated with age-related macular degeneration. International Ophthalmology, 2019, 39, 63-67.	0.6	2
532	Psychiatric genetics and the structure of psychopathology. Molecular Psychiatry, 2019, 24, 409-420.	4.1	281
533	Beyond genomeâ€wide significance: integrative approaches to the interpretation and extension of GWAS findings for alcohol use disorder. Addiction Biology, 2019, 24, 275-289.	1.4	15
534	â€œCrossoverâ€•in Depressive Symptoms Among Older Couples: Are Previous Findings Artifactual?. Journal of Aging and Health, 2020, 32, 3-13.	0.9	2
535	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain. Molecular Psychiatry, 2020, 25, 791-804.	4.1	86

#	ARTICLE	IF	CITATIONS
536	Genome-wide significant regions in 43 Utah high-risk families implicate multiple genes involved in risk for completed suicide. Molecular Psychiatry, 2020, 25, 3077-3090.	4.1	40
537	A joint study of whole exome sequencing and structural MRI analysis in major depressive disorder. Psychological Medicine, 2020, 50, 384-395.	2.7	19
538	Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. Human Genetics, 2020, 139, 5-21.	1.8	37
539	Integrative analysis of rare copy number variants and gene expression data in alopecia areata implicates an aetiological role for autophagy. Experimental Dermatology, 2020, 29, 243-253.	1.4	21
540	Missing heritability of complex diseases: case solved?. Human Genetics, 2020, 139, 103-113.	1.8	109
541	The abiding relevance of mouse models of rare mutations to psychiatric neuroscience and therapeutics. Schizophrenia Research, 2020, 217, 37-51.	1.1	9
542	A Genetics Perspective on the Role of the (Neuro)Immune System in Schizophrenia. Schizophrenia Research, 2020, 217, 105-113.	1.1	43
543	Uncovering the complex genetics of human personality: response from authors on the PGMRA Model. Molecular Psychiatry, 2020, 25, 2210-2213.	4.1	17
544	Social Integration, Self-Rated Health . . . and Genes?. Journal of Aging and Health, 2020, 32, 462-471.	0.9	3
545	Clinical application of antidepressant pharmacogenetics: Considerations for the design of future studies. Neuroscience Letters, 2020, 726, 133651.	1.0	14
546	Genetic basis for postpartum psychosis. , 2020, , 149-158.		0
547	The E Is in the G: Geneâ€"Environmentâ€"Trait Correlations and Findings From Genome-Wide Association Studies. Perspectives on Psychological Science, 2020, 15, 81-89.	5.2	28
548	Joint utilization of genetic analysis and semi-cloning technology reveals a digenic etiology of MÃ¼llerian anomalies. Cell Research, 2020, 30, 91-94.	5.7	10
549	The proteome and its dynamics: A missing piece for integrative multi-omics in schizophrenia. Schizophrenia Research, 2020, 217, 148-161.	1.1	16
550	The spectral condition number plot for regularization parameter evaluation. Computational Statistics, 2020, 35, 629-646.	0.8	3
551	CRISPR-based functional evaluation of schizophrenia risk variants. Schizophrenia Research, 2020, 217, 26-36.	1.1	10
553	Divergence of an association between depressive symptoms and a dopamine polygenic score in Caucasians and Asians. European Archives of Psychiatry and Clinical Neuroscience, 2020, 270, 229-235.	1.8	14
554	Neuropsychiatric â€œComorbidityâ€•as Causal Influence in Autism. Journal of the American Academy of Child and Adolescent Psychiatry, 2020, 59, 229-235.	0.3	21

#	ARTICLE	IF	CITATIONS
555	Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. Human Genetics, 2020, 139, 23-41.	1.8	72
556	Moonshots for aging. Nutrition and Healthy Aging, 2020, 5, 239-246.	0.5	1
557	Gene Expression Modularity Reveals Footprints of Polygenic Adaptation in Theobroma cacao. Molecular Biology and Evolution, 2020, 37, 110-123.	3.5	22
558	Epilepsy genetics: clinical impacts and biological insights. Lancet Neurology, The, 2020, 19, 93-100.	4.9	75
559	Genetics of COPD. Annual Review of Physiology, 2020, 82, 413-431.	5.6	104
560	Archaic hominin introgression into modern human genomes. American Journal of Physical Anthropology, 2020, 171, 60-73.	2.1	33
561	Editorial: How to review an article for a research journalâ€"And what to expect as an author. International Journal of Auditing, 2020, 24, 1-2.	0.9	0
562	Genomics of major depressive disorder. , 2020, , 187-200.		0
563	Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. Trends in Molecular Medicine, 2020, 26, 232-241.	3.5	31
564	Developmental structuring of phenotypic variation: A case study with a cellular automata model of ontogeny. Evolution & Development, 2020, 22, 20-34.	1.1	4
565	Diseaseâ€associated polymorphisms within the conserved ECR1 enhancer differentially regulate the tissueâ€specific activity of the cannabinoidâ€1 receptor gene promoter; implications for cannabinoid pharmacogenetics. Human Mutation, 2020, 41, 291-298.	1.1	9
566	Polygenic risk scores outperform machine learning methods in predicting coronary artery disease status. Genetic Epidemiology, 2020, 44, 125-138.	0.6	29
567	Towards chamber specific heart-on-a-chip for drug testing applications. Advanced Drug Delivery Reviews, 2020, 165-166, 60-76.	6.6	52
568	An Intraocular Pressure Polygenic Risk Score Stratifies Multiple Primary Open-Angle Glaucoma Parameters Including Treatment Intensity. Ophthalmology, 2020, 127, 901-907.	2.5	37
569	Construction of a High-Density Genetic Linkage Map and QTL Mapping for Growth-Related Traits in Takifugu bimaculatus. Marine Biotechnology, 2020, 22, 130-144.	1.1	19
570	Reproducible Genetic Risk Loci for Anxiety: Results From â^¼200,000 Participants in the Million Veteran Program. American Journal of Psychiatry, 2020, 177, 223-232.	4.0	185
571	The genetics of bipolar disorder. Molecular Psychiatry, 2020, 25, 544-559.	4.1	161
572	Mechanisms of tissue and cell-type specificity in heritable traits andÂdiseases. Nature Reviews Genetics, 2020, 21, 137-150.	7.7	105

#	ARTICLE	IF	CITATIONS
573	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	13.7	441
574	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. Lancet Rheumatology, The, 2020, 2, e50-e62.	2.2	17
575	Geneticsâ€™ Piece of the PI: Inferring the Origin of Complex Traits and Diseases from Proteomeâ€Wide Proteinâ€"Protein Interaction Dynamics. BioEssays, 2020, 42, 1900169.	1.2	0
576	The Neurodevelopment of Autism from Infancy Through Toddlerhood. Neuroimaging Clinics of North America, 2020, 30, 97-114.	0.5	33
577	Bayesian shrinkage estimation of high dimensional causal mediation effects in omics studies. Biometrics, 2020, 76, 700-710.	0.8	39
578	Searching for parent-of-origin effects on cardiometabolic traits in imprinted genomic regions. European Journal of Human Genetics, 2020, 28, 646-655.	1.4	5
579	Cardioinformatics: the nexus of bioinformatics and precision cardiology. Briefings in Bioinformatics, 2020, 21, 2031-2051.	3.2	15
580	Forest genomics: Advancing climate adaptation, forest health, productivity, and conservation. Evolutionary Applications, 2020, 13, 3-10.	1.5	108
581	High-dimensionality Data Analysis of Pharmacological Systems Associated with Complex Diseases. Pharmacological Reviews, 2020, 72, 191-217.	7.1	17
582	Mitonuclear conflict and cooperation govern the integration of genotypes, phenotypes and environments. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190188.	1.8	43
583	Molecular systems in inflammatory bowel disease. , 2020, , 367-388.		1
584	Functional testing of ASD-associated genes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26-28.	3.3	17
585	Overlapping genetic architecture between Parkinson disease and melanoma. Acta Neuropathologica, 2020, 139, 347-364.	3.9	23
586	PACSIN2 rs2413739 influence on thiopurine pharmacokinetics: validation studies in pediatric patients. Pharmacogenomics Journal, 2020, 20, 415-425.	0.9	15
587	A road map for understanding molecular and genetic determinants of osteoporosis. Nature Reviews Endocrinology, 2020, 16, 91-103.	4.3	200
588	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. Nature Biotechnology, 2020, 38, 56-65.	9.4	188
589	Mental health is biological health: Why tackling â€œdiseases of the mindâ€• is an imperative for biological anthropology in the 21st century. American Journal of Physical Anthropology, 2020, 171, 87-117.	2.1	38
590	Genes dysregulated in the blood of people with Williams syndrome are enriched in protein-coding genes positively selected in humans. European Journal of Medical Genetics, 2020, 63, 103828.	0.7	6

#	Article	IF	Citations
591	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. Nucleic Acids Research, 2020, 48, e109-e109.	6.5	15
592	Shortâ€term heritable variation overwhelms 200 generations of mutational variance for metabolic traits in<i>Caenorhabditis elegans</i>. Evolution; International Journal of Organic Evolution, 2020, 74, 2451-2464.	1.1	3
593	Influence of multiple apolipoprotein A-I and B genetic variations on insulin resistance and metabolic syndrome in obstructive sleep apnea. Nutrition and Metabolism, 2020, 17, 83.	1.3	6
594	Genome-Wide Association Study of Wood Anatomical and Morphological Traits in Populus trichocarpa. Frontiers in Plant Science, 2020, 11, 545748.	1.7	21
595	Patient-Derived Midbrain Organoids to Explore the Molecular Basis of Parkinson's Disease. Frontiers in Neurology, 2020, 11, 1005.	1.1	26
596	Evolutionary rate and genetic load in an emblematic Mediterranean tree following an ancient and prolonged population collapse. Molecular Ecology, 2020, 29, 4797-4811.	2.0	15
597	Many functionally connected loci foster adaptive diversification along a neotropical hybrid zone. Science Advances, 2020, 6, .	4.7	18
598	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
599	Functional genomics, genetic risk profiling and cell phenotypes in neurodegenerative disease. Neurobiology of Disease, 2020, 146, 105088.	2.1	3
600	Microanatomy of the Human Atherosclerotic Plaque by Single-Cell Transcriptomics. Circulation Research, 2020, 127, 1437-1455.	2.0	283
601	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. PLoS Genetics, 2020, 16, e1009025.	1.5	42
602	Identification of a Core Module for Bone Mineral Density through the Integration of a Co-expression Network and GWAS Data. Cell Reports, 2020, 32, 108145.	2.9	21
603	The shaping of immunological responses through natural selection after the Roma Diaspora. Scientific Reports, 2020, 10, 16134.	1.6	2
604	Commentary: Mendelian randomization and educationâ€"Challenges remain. International Journal of Epidemiology, 2020, 49, 1193-1206.	0.9	11
605	Practicing precision medicine with intelligently integrative clinical and multi-omics data analysis. Human Genomics, 2020, 14, 35.	1.4	58
606	Varmole: a biologically drop-connect deep neural network model for prioritizing disease risk variants and genes. Bioinformatics, 2021, 37, 1772-1775.	1.8	12
607	Origins and Consequences of Chromosomal Instability: From Cellular Adaptation to Genome Chaos-Mediated System Survival. Genes, 2020, 11, 1162.	1.0	26
608	The role of stochasticity in biological communication processes. Progress in Biophysics and Molecular Biology, 2021, 162, 122-128.	1.4	20

#	Article	IF	Citations
609	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. Nature Communications, 2020, 11, 4930.	5.8	20
610	VariantSpark: Cloud-based machine learning for association study of complex phenotype and large-scale genomic data. GigaScience, 2020, 9, .	3.3	10
611	Special Article: Translational Science Update. Pharmacological Implications of Emerging Schizophrenia Genetics. Journal of Clinical Psychopharmacology, 2020, 40, 323-329.	0.7	10
612	Genomic Chaos Begets Psychiatric Disorder. Complex Psychiatry, 2020, 6, 20-29.	1.3	6
613	Womenâ€™s greater late-life depression: Traumatic experiences or GxE?. Advances in Life Course Research, 2020, 45, 100341.	0.8	2
614	Leveraging existing GWAS summary data of genetically correlated and uncorrelated traits to improve power for a new GWAS. Genetic Epidemiology, 2020, 44, 717-732.	0.6	2
615	Protein-Protein interactions uncover candidate â€˜core genesâ€™ within omnigenic disease networks. PLoS Genetics, 2020, 16, e1008903.	1.5	16
616	Genomic variability. , 2020, , 63-75.		0
617	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. BMC Genomics, 2020, 21, 754.	1.2	3
618	Modern Strategies to Assess and Breed Forest Tree Adaptation to Changing Climate. Frontiers in Plant Science, 2020, 11, 583323.	1.7	95
619	Contributions of Adaptive Plant Architecture to Transgressive Salinity Tolerance in Recombinant Inbred Lines of Rice: Molecular Mechanisms Based on Transcriptional Networks. Frontiers in Genetics, 2020, 11, 594569.	1.1	7
620	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
621	Leaf shape in Populus tremula is a complex, omnigenic trait. Ecology and Evolution, 2020, 10, 11922-11940.	0.8	19
622	An Imperative Need for Further Genetic Studies of Alopecia Areata. Journal of Investigative Dermatology Symposium Proceedings, 2020, 20, S22-S27.	0.8	8
623	Influence of Genetic Interactions on Polygenic Prediction. G3: Genes, Genomes, Genetics, 2020, 10, 109-115.	0.8	19
624	Computational Identification of Gene Networks as a Biomarker of Neuroblastoma Risk. Cancers, 2020, 12, 2086.	1.7	8
625	The Jaw Epidemic: Recognition, Origins, Cures, and Prevention. BioScience, 2020, 70, 759-771.	2.2	17
626	Clinical psychology is an applied evolutionary science. Clinical Psychology Review, 2020, 81, 101892.	6.0	14

#	ARTICLE	IF	CITATIONS
627	Multiscale causal networks identify VGF as a key regulator of Alzheimerâ€™s disease. Nature Communications, 2020, 11, 3942.	5.8	94
628	Genome-wide association studies of callus differentiation for the desert tree,<i>Populus euphratica</i>. Tree Physiology, 2020, 40, 1762-1777.	1.4	18
629	Character identity mechanisms: a conceptual model for comparative-mechanistic biology. Biology and Philosophy, 2020, 35, 1.	0.7	37
630	Conserved mammalian modularity of quantitative trait loci revealed human functional orthologs in blood pressure control. PLoS ONE, 2020, 15, e0235756.	1.1	2
631	Tutorial: a guide to performing polygenic risk score analyses. Nature Protocols, 2020, 15, 2759-2772.	5.5	918
632	Heat Diffusion Kernel Algorithm-Based Interpretation of the Disease Intervention Mechanism for DHA. Genes, 2020, 11, 754.	1.0	0
633	Entity Focus: Applied Genetic Science at Different Levels. , 2020, , 521-544.		3
634	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
635	The Spruce Genome. Compendium of Plant Genomes, 2020, , .	0.3	0
636	Polygenic inheritance, GWAS, polygenic risk scores, and the search for functional variants. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18924-18933.	3.3	95
637	Functional Captures of Multiple Human Quantitative Trait Loci Regulating Blood Pressure with the Use of Orthologs in Genetically Defined Rat Models. Canadian Journal of Cardiology, 2020, 36, 756-763.	0.8	1
638	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. Nature Machine Intelligence, 2020, 2, 447-456.	8.3	6
639	Genetics of Obesity in East Asians. Frontiers in Genetics, 2020, 11, 575049.	1.1	19
640	C3: connect separate connected components to form a succinct disease module. BMC Bioinformatics, 2020, 21, 433.	1.2	6
641	Genotype by environment interaction for gene expression in Drosophila melanogaster. Nature Communications, 2020, 11, 5451.	5.8	30
642	Genetic Influences on Disease Subtypes. Annual Review of Genomics and Human Genetics, 2020, 21, 413-435.	2.5	23
643	A mega-analysis of expression quantitative trait loci in retinal tissue. PLoS Genetics, 2020, 16, e1008934.	1.5	22
644	Canalization and Robustness in Human Genetics and Disease. Annual Review of Genetics, 2020, 54, 189-211.	3.2	22

#	ARTICLE	IF	CITATIONS
645	Combined Analyses of Phenotype, Genotype and Climate Implicate Local Adaptation as a Driver of Diversity in Eucalyptus microcarpa (Grey Box). Forests, 2020, 11, 495.	0.9	6
646	Leveraging correlations between variants in polygenic risk scores to detect heterogeneity in GWAS cohorts. PLoS Genetics, 2020, 16, e1009015.	1.5	4
647	The statistical practice of the GTEx Project: from single to multiple tissues. Quantitative Biology, 2021, 9, 151-167.	0.3	1
648	Genes, Personality and Personality Disorders. , 2020, , 111-129.		0
649	Genes and Human Identity. , 2020, , 196-214.		0
651	Whole-genome analysis of noncoding genetic variations identifies multiscale regulatory element perturbations associated with Hirschsprung disease. Genome Research, 2020, 30, 1618-1632.	2.4	13
653	Genetic Confusion. , 2020, , 1-16.		0
654	Genetic Information and How It Flows. , 2020, , 17-35.		0
655	Genes and Environments in Human Development. , 2020, , 36-54.		0
656	What Is Behavioural Genetics?. , 2020, , 55-73.		0
657	Genes and Mental Health. , 2020, , 74-93.		0
658	Genes, Education and Intelligence. , 2020, , 94-110.		0
659	Genes, Food, Exercise and Weight. , 2020, , 130-142.		0
660	Genes, Religiosity and Political Commitment. , 2020, , 143-154.		0
661	Gay Genes? Genetics and Sexual Orientation. , 2020, , 155-177.		0
662	Are We Slaves to Our Genes?. , 2020, , 178-195.		0
666	Detecting selection with a genetic cross. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22323-22330.	3.3	18
667	Genetic modifiers of longâ€term survival in sickle cell anemia. Clinical and Translational Medicine, 2020, 10, e152.	1.7	21

#	Article	IF	Citations
668	AI Enabled Precision Medicine: Patient Stratification, Drug Repurposing and Combination Therapies. , 0, , .		5
669	Multi-locus interactions and the build-up of reproductive isolation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190543.	1.8	34
670	What Has a Century of Quantitative Genetics Taught Us About Nature's Genetic Tool Kit?. Annual Review of Genetics, 2020, 54, 439-464.	3.2	11
671	Decoding Susceptibility to Respiratory Viral Infections and Asthma Inception in Children. International Journal of Molecular Sciences, 2020, 21, 6372.	1.8	11
672	Plant science decadal vision 2020â€“2030: Reimagining the potential of plants for a healthy and sustainable future. Plant Direct, 2020, 4, e00252.	0.8	26
673	Genome-wide variation and transcriptional changes in diverse developmental processes underlie the rapid evolution of seasonal adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23960-23969.	3.3	53
674	Extent and context dependence of pleiotropy revealed by high-throughput single-cell phenotyping. PLoS Biology, 2020, 18, e3000836.	2.6	27
675	Omics Application in Animal Scienceâ€"A Special Emphasis on Stress Response and Damaging Behaviour in Pigs. Genes, 2020, 11, 920.	1.0	31
676	Genetic Inheritance and Its Contribution to Tinnitus. Current Topics in Behavioral Neurosciences, 2020, 51, 29-47.	0.8	6
677	Epigeneticâ€“smoking interaction reveals histologically heterogeneous effects of TRIM27 DNA methylation on overall survival among earlyâ€stage NSCLC patients. Molecular Oncology, 2020, 14, 2759-2774.	2.1	13
678	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	7.7	118
679	A heuristic model of the effects of phenotypic robustness in adaptive evolution. Theoretical Population Biology, 2020, 136, 22-30.	0.5	0
680	Networks of Physiological Adjustments and Defenses, and Their Synergy With Sodium (Na+) Homeostasis Explain the Hidden Variation for Salinity Tolerance Across the Cultivated Gossypium hirsutum Germplasm. Frontiers in Plant Science, 2020, 11, 588854.	1.7	4
681	Evidence for the placenta-brain axis: multi-omic kernel aggregation predicts intellectual and social impairment in children born extremely preterm. Molecular Autism, 2020, 11, 97.	2.6	26
682	The Autism Palette: Combinations of Impairments Explain the Heterogeneity in ASD. Frontiers in Psychiatry, 2020, 11, 503462.	1.3	5
683	Editorial: 2020 â€“ The year of viruses. Progress in Biophysics and Molecular Biology, 2020, 158, 1-3.	1.4	2
684	Higher-order interactions in statistical physics and machine learning: A model-independent solution to the inverse problem at equilibrium. Physical Review E, 2020, 102, 053314.	0.8	14
686	Perspective: Quality Versus Quantity; Is It Important to Assess the Role of Enhancers in Complex Disease from an In Vivo Perspective?. International Journal of Molecular Sciences, 2020, 21, 7856.	1.8	1

#	ARTICLE	IF	CITATIONS
687	Publicly Available hiPSC Lines with Extreme Polygenic Risk Scores for Modeling Schizophrenia. Complex Psychiatry, 2020, 6, 68-82.	1.3	18
688	Leveraging Multiple Layers of Data To Predict <i>Drosophila</i> Complex Traits. G3: Genes, Genomes, Genetics, 2020, 10, 4599-4613.	0.8	21
689	Single-cell RNA-seq analysis of the brainstem of mutant SOD1 mice reveals perturbed cell types and pathways of amyotrophic lateral sclerosis. Neurobiology of Disease, 2020, 141, 104877.	2.1	48
690	Noncoding regions underpin avian bill shape diversification at macroevolutionary scales. Genome Research, 2020, 30, 553-565.	2.4	24
691	Genes and genomes and unnecessary complexity in precision medicine. Npj Genomic Medicine, 2020, 5, 21.	1.7	12
692	Genome-Wide Association Studies of CKD and Related Traits. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 1643-1656.	2.2	28
693	Evo-Devo Path as a Bridge between Evolution, Morphological Disparity, and Medicine with Comments on â€œHopeful Monstersâ€•in the Age of Genomics. Current Molecular Biology Reports, 2020, 6, 79-90.	0.8	1
694	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. Genome Research, 2020, 30, 790-801.	2.4	97
695	Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. JCO Clinical Cancer Informatics, 2020, 4, 399-411.	1.0	13
696	Beyond SNP heritability: Polygenicity and discoverability of phenotypes estimated with a univariate Gaussian mixture model. PLoS Genetics, 2020, 16, e1008612.	1.5	120
697	Molecular design of hypothalamus development. Nature, 2020, 582, 246-252.	13.7	105
698	The metabolome as a link in the genotype-phenotype map for peroxide resistance in the fruit fly, Drosophila melanogaster. BMC Genomics, 2020, 21, 341.	1.2	14
699	Sociology, Genetics, and the Coming of Age of Sociogenomics. Annual Review of Sociology, 2020, 46, 553-581.	3.1	52
700	Dynamic genetic architecture of yeast response to environmental perturbation shed light on origin of cryptic genetic variation. PLoS Genetics, 2020, 16, e1008801.	1.5	15
701	p53: 800 million years of evolution and 40 years of discovery. Nature Reviews Cancer, 2020, 20, 471-480.	12.8	421
702	The quest for genetic sequence variants conferring risk of endometriosis. , 2020, , 91-109.		2
703	Trade-offs, Pleiotropy, and Shared Molecular Pathways: A Unified View of Constraints on Adaptation. Integrative and Comparative Biology, 2020, 60, 332-347.	0.9	30
704	Pathway Analysis of Genes Identified through Post-GWAS to Underpin Prostate Cancer Aetiology. Genes, 2020, 11, 526.	1.0	2

#	ARTICLE	IF	CITATIONS
705	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. Frontiers in Genetics, 2020, 11, 424.	1.1	335
706	A practical view of fine-mapping and gene prioritization in the post-genome-wide association era. Open Biology, 2020, 10, 190221.	1.5	88
707	Drug repositioning for psychiatric and neurological disorders through a network medicine approach. Translational Psychiatry, 2020, 10, 141.	2.4	24
708	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. American Journal of Human Genetics, 2020, 107, 46-59.	2.6	30
709	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	1.4	7
710	Approaches to studying the genomic architecture of complex birth defects. Prenatal Diagnosis, 2020, 40, 1047-1055.	1.1	5
711	Co-localization between Sequence Constraint and Epigenomic Information Improves Interpretation of Whole-Genome Sequencing Data. American Journal of Human Genetics, 2020, 106, 513-524.	2.6	3
712	Facilitating Complex Trait Analysis via Reduced Complexity Crosses. Trends in Genetics, 2020, 36, 549-562.	2.9	35
713	Heterogeneity and Polygenicity in Psychiatric Disorders: A Genome-Wide Perspective. Chronic Stress, 2020, 4, 247054702092484.	1.7	26
714	Re-evaluating the relationship between missing heritability and the microbiome. Microbiome, 2020, 8, 87.	4.9	17
715	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. Computational and Structural Biotechnology Journal, 2020, 18, 1429-1439.	1.9	91
716	Functional genomics of parental care of insects. Hormones and Behavior, 2020, 122, 104756.	1.0	5
717	A selective inference approach for false discovery rate control using multiomics covariates yields insights into disease risk. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15028-15035.	3.3	16
718	Effects of Phenotypic Robustness on Adaptive Evolutionary Dynamics. Evolutionary Biology, 2020, 47, 233-239.	0.5	4
719	Transcriptomeâ€wide association studies: a view from Mendelian randomization. Quantitative Biology, 2021, 9, 107-121.	0.3	22
720	Identification of therapeutic targets from genetic association studies using hierarchical component analysis. BioData Mining, 2020, 13, 6.	2.2	3
721	Distinct subtypes of polycystic ovary syndrome with novel genetic associations: An unsupervised, phenotypic clustering analysis. PLoS Medicine, 2020, 17, e1003132.	3.9	134
722	Adaptation via pleiotropy and linkage: Association mapping reveals a complex genetic architecture within the stickleback<i>Eda</i>locus. Evolution Letters, 2020, 4, 282-301.	1.6	34

#	ARTICLE	IF	CITATIONS
723	Origins and characterization of variants shared between databases of somatic and germline human mutations. BMC Bioinformatics, 2020, 21, 227.	1.2	14
724	Genomic resources for dissecting the role of non-protein coding variation in gene-environment interactions. Toxicology, 2020, 441, 152505.	2.0	2
725	Polygenic risk scores: pleiotropy and the effect of environment. GeroScience, 2020, 42, 1635-1647.	2.1	5
726	Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. PLoS Genetics, 2020, 16, e1008855.	1.5	9
727	Genomics of Clinal Local Adaptation in<i>Pinus sylvestris</i>Under Continuous Environmental and Spatial Genetic Setting. G3: Genes, Genomes, Genetics, 2020, 10, 2683-2696.	0.8	24
728	Natural Selection Shapes Codon Usage in the Human Genome. American Journal of Human Genetics, 2020, 107, 83-95.	2.6	44
729	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. PLoS ONE, 2020, 15, e0232201.	1.1	28
730	CRISPR disruption and UK Biobank analysis of a highly conserved polymorphic enhancer suggests a role in male anxiety and ethanol intake. Molecular Psychiatry, 2021, 26, 2263-2276.	4.1	9
731	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. Frontiers in Genetics, 2020, 11, 106.	1.1	21
732	Evolutionary Physiology and Genomics in the Highly Adaptable Killifish (<i>Fundulus heteroclitus</i>) Tj ETQq1 1 0.784314 rgBT /Overl		18
733	Whole exome sequencing identifies multiple novel candidate genes in familial gastroschisis. Molecular Genetics & Genomic Medicine, 2020, 8, e1176.	0.6	10
734	Perceived neighborhood social cohesion and cardiometabolic risk: a gene Ã— environment study. Biodemography and Social Biology, 2020, 65, 1-15.	0.4	7
735	Gene expression networks in the <i>Drosophila</i> Genetic Reference Panel. Genome Research, 2020, 30, 485-496.	2.4	55
736	The Resurgence of Introgression Breeding, as Exemplified in Wheat Improvement. Frontiers in Plant Science, 2020, 11, 252.	1.7	66
737	Transposable elements contribute to the genomic response to insecticides in <i>Drosophila melanogaster</i>. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190341.	1.8	27
738	Emerging phenotyping strategies will advance our understanding of psychiatric genetics. Nature Neuroscience, 2020, 23, 475-480.	7.1	41
739	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	7.7	78
740	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. PLoS Genetics, 2020, 16, e1008686.	1.5	8

#	ARTICLE	IF	CITATIONS
741	How to link genomics to physiology through epigenomics. Epigenomics, 2020, 12, 285-287.	1.0	17
742	Progress in Genetic Polymorphisms Related to Lipid Disturbances Induced by Atypical Antipsychotic Drugs. Frontiers in Pharmacology, 2019, 10, 1669.	1.6	14
743	Functionally Enigmatic Genes in Cancer: Using TCGA Data to Map the Limitations of Annotations. Scientific Reports, 2020, 10, 4106.	1.6	14
744	An atlas of evidence-based phenotypic associations across the mouse phenome. Scientific Reports, 2020, 10, 3957.	1.6	3
745	Polygenic adaptation: a unifying framework to understand positive selection. Nature Reviews Genetics, 2020, 21, 769-781.	7.7	238
746	Exploring the Genomic Architectures of Health, Physical Traits and Antisocial Behavioral Outcomes: A Brief Report. Frontiers in Psychiatry, 2020, 11, 539.	1.3	4
747	Harnessing protein posttranslational modifications for plant improvement. , 2020, , 385-401.		3
748	Meeting Report: 68th Montagna Symposium on the Biology of Skin â€œDecoding Complex Skin Diseases: Integrating Genetics, Genomics, and Disease Biologyâ€• Journal of Investigative Dermatology, 2020, 140, 2105-2110.	0.3	0
749	Translating genomic insights into cardiovascular medicine: Opportunities and challenges of CRISPR-Cas9. Trends in Cardiovascular Medicine, 2021, 31, 341-348.	2.3	5
750	The three dimensions of somatic evolution: Integrating the role of genetic damage, lifeâ€•history traits, and aging in carcinogenesis. Evolutionary Applications, 2020, 13, 1569-1580.	1.5	5
751	Gene expression predictions and networks in natural populations supports the omnigenic theory. BMC Genomics, 2020, 21, 416.	1.2	26
752	Statistical methods for SNP heritability estimation and partition: A review. Computational and Structural Biotechnology Journal, 2020, 18, 1557-1568.	1.9	41
753	Whole genome sequencing of familial isolated oesophagus atresia uncover shared structural variants. BMC Medical Genomics, 2020, 13, 85.	0.7	2
754	Genetic Underpinnings of Increased BMI and Its Association With Late Midlife Cognitive Abilities. Gerontology and Geriatric Medicine, 2020, 6, 233372142092526.	0.8	1
755	Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17135-17141.	3.3	24
756	Mouse Systems Genetics as a Prelude to Precision Medicine. Trends in Genetics, 2020, 36, 259-272.	2.9	41
757	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. Molecular Biology and Evolution, 2020, 37, 1604-1614.	3.5	19
758	Quantitative trait variation in ASD probands and toddler sibling outcomes at 24â€‰months. Journal of Neurodevelopmental Disorders, 2020, 12, 5.	1.5	18

#	Article	IF	Citations
759	Neurofibromatosis Type 1 Implicates Ras Pathways in the Genetic Architecture of Neurodevelopmental Disorders. Behavior Genetics, 2020, 50, 191-202.	1.4	14
760	Artificial Intelligence for Cardiac Imaging-Genetics Research. Frontiers in Cardiovascular Medicine, 2020, 6, 195.	1.1	16
761	Intolerance of loud sounds in childhood: Is there an intergenerational association with grandmaternal smoking in pregnancy?. PLoS ONE, 2020, 15, e0229323.	1.1	4
762	Multi-resolution localization of causal variants across the genome. Nature Communications, 2020, 11, 1093.	5.8	37
763	How to interpret and integrate multi-omics data at systems level. Animal Cells and Systems, 2020, 24, 1-7.	0.8	23
764	Prostate cancer risk SNP rs10993994 is a trans-eQTL for SNHG11 mediated through MSMB. Human Molecular Genetics, 2020, 29, 1581-1591.	1.4	8
765	One-carbon metabolism and folate transporter genes: Do they factor prominently in the genetic etiology of neural tube defects?. Biochimie, 2020, 173, 27-32.	1.3	23
766	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. Genome Biology, 2020, 21, 42.	3.8	60
767	Genomic Regions Associated With Skeletal Type Traits in Beef and Dairy Cattle Are Common to Regions Associated With Carcass Traits, Feed Intake and Calving Difficulty. Frontiers in Genetics, 2020, 11, 20.	1.1	21
768	Towards attaining a quantitative and mechanistic model of a cell. Nature Reviews Molecular Cell Biology, 2020, 21, 301-302.	16.1	1
769	Opinion: Is gene mapping in wild populations useful for understanding and predicting adaptation to global change?. Global Change Biology, 2020, 26, 2737-2749.	4.2	8
770	Genetics of ADHD: What Should the Clinician Know?. Current Psychiatry Reports, 2020, 22, 18.	2.1	43
771	The Contextualized Genetics of HumanÂLongevity. Journal of the American College of Cardiology, 2020, 75, 968-979.	1.2	25
772	GWAS in cancer: progress and challenges. Molecular Genetics and Genomics, 2020, 295, 537-561.	1.0	53
773	Meta-analysis and systematic review of ADGRL3 (LPHN3) polymorphisms in ADHD susceptibility. Molecular Psychiatry, 2021, 26, 2277-2285.	4.1	22
774	Minor Effects of 11 Dof Family Genes Contribute to the Missing Heritability of Heading Date in Rice (Oryza sativa L.). Frontiers in Plant Science, 2020, 10, 1739.	1.7	11
775	Beyond large-effect loci: large-scale GWAS reveals a mixed large-effect and polygenic architecture for age at maturity of Atlantic salmon. Genetics Selection Evolution, 2020, 52, 9.	1.2	62
776	Association between polygenic liability for schizophrenia and substance involvement: A nationwide populationâ€based study in Taiwan. Genes, Brain and Behavior, 2020, 19, e12639.	1.1	9

#	Article	IF	Citations
777	Comments on: Hierarchical inference for genome-wide association studies by Jelle J. Goeman and Stefan BÃ¶hringer. Computational Statistics, 2020, 35, 41-45.	0.8	1
778	Functional analysis of candidate genes from genome-wide association studies of hearing. Hearing Research, 2020, 387, 107879.	0.9	13
779	Atypical lateralization in neurodevelopmental and psychiatric disorders: What is the role of stress?. Cortex, 2020, 125, 215-232.	1.1	75
780	Learning to collaborate: bringing together behavior and quantitative genomics. Journal of Neurogenetics, 2020, 34, 28-35.	0.6	0
781	Next-generation drug repurposing using human genetics and network biology. Current Opinion in Pharmacology, 2020, 51, 78-92.	1.7	61
782	The relationship between the minor allele content and Alzheimer's disease. Genomics, 2020, 112, 2426-2432.	1.3	4
783	Towards a comprehensive catalogue of validated and target-linked human enhancers. Nature Reviews Genetics, 2020, 21, 292-310.	7.7	229
784	Genomic inbreeding trends, influential sire lines and selection in the global Thoroughbred horse population. Scientific Reports, 2020, 10, 466.	1.6	33
785	Glycosyltransferase OsUGT90A1 helps protect the plasma membrane during chilling stress in rice. Journal of Experimental Botany, 2020, 71, 2723-2739.	2.4	36
786	Developmental Genes and Regulatory Proteins, Domains of Cognitive Impairment in Schizophrenia Spectrum Psychosis and Implications for Antipsychotic Drug Discovery: The Example of Dysbindin-1 Isoforms and Beyond. Frontiers in Pharmacology, 2019, 10, 1638.	1.6	13
787	CRISPR-mediated gene correction links the ATP7A M1311V mutations with amyotrophic lateral sclerosis pathogenesis in one individual. Communications Biology, 2020, 3, 33.	2.0	6
788	Elusive vehicles of genetic representation. Biology and Philosophy, 2020, 35, 1.	0.7	0
789	Statistical Methods in Genome-Wide Association Studies. Annual Review of Biomedical Data Science, 2020, 3, 265-288.	2.8	6
790	Research advances in the genomics and applications for molecular breeding of aquaculture animals. Aquaculture, 2020, 526, 735357.	1.7	80
791	Alzheimerâ€™s disease beyond amyloid: Can the repetitive failures of amyloid-targeted therapeutics inform future approaches to dementia drug discovery?. Biochemical Pharmacology, 2020, 177, 113945.	2.0	62
792	The contribution of rare genetic variants to the pathogenesis of polycystic ovary syndrome. Current Opinion in Endocrine and Metabolic Research, 2020, 12, 26-32.	0.6	21
793	Modularity/non-cumulativity of quantitative trait loci on blood pressure. Journal of Human Hypertension, 2020, 34, 432-439.	1.0	1
794	Phylotranscriptomics of the Pentapetalae Reveals Frequent Regulatory Variation in Plant Local Responses to the Fungal Pathogen <i>Sclerotinia sclerotiorum</i>. Plant Cell, 2020, 32, 1820-1844.	3.1	21

#	ARTICLE	IF	CITATIONS
795	Genomic release-recapture experiment in the wild reveals within-generation polygenic selection in stickleback fish. Nature Communications, 2020, 11, 1928.	5.8	21
796	Accurate and Scalable Construction of Polygenic Scores in Large Biobank Data Sets. American Journal of Human Genetics, 2020, 106, 679-693.	2.6	80
797	On the diagnostic and neurobiological origins of bipolar disorder. Translational Psychiatry, 2020, 10, 118.	2.4	7
798	Prenatal Origins of ASD: The When, What, and How of ASD Development. Trends in Neurosciences, 2020, 43, 326-342.	4.2	100
799	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. PLoS Genetics, 2020, 16, e1008720.	1.5	180
800	The Evolutionary Forces Shaping Cis- and Trans-Regulation of Gene Expression within a Population of Outcrossing Plants. Molecular Biology and Evolution, 2020, 37, 2386-2393.	3.5	13
801	A parallelized strategy for epistasis analysis based on Empirical Bayesian Elastic Net models. Bioinformatics, 2020, 36, 3803-3810.	1.8	4
802	Dynamic effects of interacting genes underlying rice flowering-time phenotypic plasticity and global adaptation. Genome Research, 2020, 30, 673-683.	2.4	46
803	Leveraging gene co-expression patterns to infer trait-relevant tissues in genome-wide association studies. PLoS Genetics, 2020, 16, e1008734.	1.5	25
804	Detecting Shared Genetic Architecture Among Multiple Phenotypes by Hierarchical Clustering of Gene-Level Association Statistics. Genetics, 2020, 215, 511-529.	1.2	13
805	Network Structure Analysis Identifying Key Genes of Autism and Its Mechanism. Computational and Mathematical Methods in Medicine, 2020, 2020, 1-9.	0.7	6
806	Pathological mechanism and antisense oligonucleotide-mediated rescue of a non-coding variant suppressing factor 9 RNA biogenesis leading to hemophilia B. PLoS Genetics, 2020, 16, e1008690.	1.5	4
807	Convergence and Divergence in the Genetics of Psychiatric Disorders From Pathways to Developmental Stages. Biological Psychiatry, 2021, 89, 32-40.	0.7	11
808	Dissecting the heritable risk of breast cancer: From statistical methods to susceptibility genes. Seminars in Cancer Biology, 2021, 72, 175-184.	4.3	10
809	Two sides of the same medal: Noncoding mutations reveal new pathological mechanisms and insights into the regulation of gene expression. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1616.	3.2	1
810	Translational and interdisciplinary insights into presbyacusis: A multidimensional disease. Hearing Research, 2021, 402, 108109.	0.9	21
811	Autism and Williams syndrome: Dissimilar socio-cognitive profiles with similar patterns of abnormal gene expression in the blood. Autism, 2021, 25, 464-489.	2.4	6
812	Graduate Student Literature Review: Understanding the genetic mechanisms underlying mastitis. Journal of Dairy Science, 2021, 104, 1183-1191.	1.4	14

#	ARTICLE	IF	CITATIONS
813	Precision medicine and therapies of the future. Epilepsia, 2021, 62, S90-S105.	2.6	39
814	Signature-based approaches for informed drug repurposing: targeting CNS disorders. Neuropsychopharmacology, 2021, 46, 116-130.	2.8	38
815	Where Are the Disease-Associated eQTLs?. Trends in Genetics, 2021, 37, 109-124.	2.9	163
816	Itâ€™s in Our Blood: A Glimpse of Personalized Medicine. Trends in Molecular Medicine, 2021, 27, 20-30.	3.5	26
817	Asthma in farm children is more determined by genetic polymorphisms and in nonâ€farm children by environmental factors. Pediatric Allergy and Immunology, 2021, 32, 295-304.	1.1	17
818	Pleiotropy and Cross-Disorder Genetics Among Psychiatric Disorders. Biological Psychiatry, 2021, 89, 20-31.	0.7	75
819	Isolated dystonia: clinical and genetic updates. Journal of Neural Transmission, 2021, 128, 405-416.	1.4	18
820	Molecular and evolutionary processes generating variation in gene expression. Nature Reviews Genetics, 2021, 22, 203-215.	7.7	154
821	The Population-Specific Impact of Neandertal Introgression on Human Disease. Genome Biology and Evolution, 2021, 13, .	1.1	24
822	Host genetics and infectious disease: new tools, insights and translational opportunities. Nature Reviews Genetics, 2021, 22, 137-153.	7.7	98
823	Retroelement-derived RNA and its role in the brain. Seminars in Cell and Developmental Biology, 2021, 114, 68-80.	2.3	10
824	Genomics of hypertension: the road to precision medicine. Nature Reviews Cardiology, 2021, 18, 235-250.	6.1	99
825	Discover novel disease-associated genes based on regulatory networks of long-range chromatin interactions. Methods, 2021, 189, 22-33.	1.9	8
826	Systems biology in cardiovascular disease: a multiomics approach. Nature Reviews Cardiology, 2021, 18, 313-330.	6.1	134
827	Can Reasons and Values Influence Action: How Might Intentional Agency Work Physiologically?. Journal for General Philosophy of Science, 2021, 52, 277-295.	0.7	14
828	Causal Inference Methods to Integrate Omics and Complex Traits. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a040493.	2.9	9
829	Few Fixed Variants between Trophic Specialist Pupfish Species Reveal Candidate<i>Cis</i>-Regulatory Alleles Underlying Rapid Craniofacial Divergence. Molecular Biology and Evolution, 2021, 38, 405-423.	3.5	18
830	Effect Sizes of Deletions and Duplications on Autism Risk Across the Genome. American Journal of Psychiatry, 2021, 178, 87-98.	4.0	50

#	ARTICLE	IF	CITATIONS
831	Fast hybrid Bayesian integrative learning of multiple gene regulatory networks for type 1 diabetes. Biostatistics, 2021, 22, 233-249.	0.9	2
832	Clustering suicidal phenotypes and genetic associations with brain-derived neurotrophic factor in patients with substance use disorders. Translational Psychiatry, 2021, 11, 72.	2.4	4
834	DOMINO: a networkâ€based active module identification algorithm with reduced rate of false calls. Molecular Systems Biology, 2021, 17, e9593.	3.2	36
835	Genetic mapping of developmental trajectories for complex traits and diseases. Computational and Structural Biotechnology Journal, 2021, 19, 3458-3469.	1.9	1
836	Fitness maps to a large-effect locus in introduced stickleback populations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	45
837	Independent evolution toward larger body size in the distinctive Faroe Island mice. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	0
838	Genome diversity in Ukraine. GigaScience, 2021, 10, .	3.3	9
839	Network propagation of rare variants in Alzheimerâ€™s disease reveals tissue-specific hub genes and communities. PLoS Computational Biology, 2021, 17, e1008517.	1.5	1
840	Short loop functional commonality identified in leukaemia proteome highlights crucial protein sub-networks. NAR Genomics and Bioinformatics, 2021, 3, lqab010.	1.5	0
841	Rehabilitation of Karl Popperâ€™s Ideas on Evolutionary Biology and the Nature of Biological Science. , 2021, , 193-209.		3
842	Introduction to epigenetics in psychiatry. , 2021, , 3-24.		1
843	Genomic Variation, Evolvability, and the Paradox of Mental Illness. Frontiers in Psychiatry, 2020, 11, 593233.	1.3	2
844	STOX1 deficiency is associated with renin-mediated gestational hypertension and placental defects. JCI Insight, 2021, 6, .	2.3	4
845	Genetic loci shared between major depression and intelligence with mixed directions of effect. Nature Human Behaviour, 2021, 5, 795-801.	6.2	23
846	Best Practices for Binary and Ordinal Data Analyses. Behavior Genetics, 2021, 51, 204-214.	1.4	21
848	Insulinâ€™s Discovery: New Insights on Its Hundredth Birthday: From Insulin Action and Clearance to Sweet Networks. International Journal of Molecular Sciences, 2021, 22, 1030.	1.8	2
849	Genetics and Epigenetics of Addiction. , 2021, , .		0
850	Variation in Pleiotropic Hub Gene Expression Is Associated with Interspecific Differences in Head Shape and Eye Size in <i>Drosophila</i>. Molecular Biology and Evolution, 2021, 38, 1924-1942.	3.5	14

#	ARTICLE	IF	CITATIONS
852	How Well Can Multivariate and Univariate GWAS Distinguish Between True and Spurious Pleiotropy?. Frontiers in Genetics, 2020, 11, 602526.	1.1	12
853	Molecular Pathways within Autism Spectrum Disorder Endophenotypes. Journal of Molecular Neuroscience, 2021, 71, 1357-1367.	1.1	3
854	Allele-specific expression of Parkinsonâ€™s disease susceptibility genes in human brain. Scientific Reports, 2021, 11, 504.	1.6	10
855	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.	1.9	40
856	Genes, depression, and nuclear DNA. , 2021, , 15-23.		0
857	Schizophrenia polygenic risk is associated with child mental health problems through early childhood adversity: evidence for a geneâ€"environment correlation. European Child and Adolescent Psychiatry, 2022, 31, 529-539.	2.8	7
858	An Academic Clinicianâ€™s Road Map to Hypertension Genomics. Hypertension, 2021, 77, 284-295.	1.3	9
859	Complex pleiotropic genetic architecture of evolved heat stress and oxidative stress resistance in the nematode<i>Caenorhabditis remanei</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	4
860	Genome-Wide Association Analysis Reveals the Genetic Architecture of Parasite (Cryptocaryon) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 242-254.	1.1	16
861	The Role of Genetic Ancestry as a Risk Factor for Primary Open-angle Glaucoma in African Americans. , 2021, 62, 28.		18
862	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. Communications Biology, 2021, 4, 185.	2.0	59
863	Evolvability and evolutionary rescue. Evolution & Development, 2021, 23, 308-319.	1.1	15
865	Genome sequences of Tropheus moorii and Petrochromis trewavasae, two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. Scientific Reports, 2021, 11, 4309.	1.6	4
866	Emergence and propagation of epistasis in metabolic networks. ELife, 2021, 10, .	2.8	25
868	The data-hypothesis relationship. Genome Biology, 2021, 22, 57.	3.8	7
869	Data bias. Genome Biology, 2021, 22, 59.	3.8	5
870	Variantâ€•set association test for generalized linear mixed model. Genetic Epidemiology, 2021, 45, 402-412.	0.6	2
872	Predicting the Future of Genetic Risk Profiling of Glaucoma. JAMA Ophthalmology, 2021, 139, 224.	1.4	15

#	Article	IF	Citations
873	Genetics and Epigenetics in Asthma. International Journal of Molecular Sciences, 2021, 22, 2412.	1.8	74
874	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. ELife, 2021, 10, .	2.8	77
875	Disentangling selection on genetically correlated polygenic traits via whole-genome genealogies. American Journal of Human Genetics, 2021, 108, 219-239.	2.6	48
877	Novel and Transgressive Salinity Tolerance in Recombinant Inbred Lines of Rice Created by Physiological Coupling-Uncoupling and Network Rewiring Effects. Frontiers in Plant Science, 2021, 12, 615277.	1.7	15
878	<i>Trans</i>-acting genetic variation affects the expression of adjacent genes. Genetics, 2021, 217, .	1.2	4
880	An epigenetic pathway in rice connects genetic variation to anaerobic germination and seedling establishment. Plant Physiology, 2021, 186, 1042-1059.	2.3	12
881	CRISPR-Cas technology in corn: a new key to unlock genetic knowledge and create novel products. Molecular Breeding, 2021, 41, 1.	1.0	13
882	The clinical applicability of polygenic risk scores for LDL-cholesterol: considerations, current evidence and future perspectives. Current Opinion in Lipidology, 2021, 32, 112-116.	1.2	16
884	Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. Human Molecular Genetics, 2021, 30, 294-304.	1.4	17
885	Low-pass sequencing increases the power of GWAS and decreases measurement error of polygenic risk scores compared to genotyping arrays. Genome Research, 2021, 31, 529-537.	2.4	66
886	Artificial intelligence in drug discovery: what is realistic, what are illusions? Part 1: Ways to make an impact, and why we are not there yet. Drug Discovery Today, 2021, 26, 511-524.	3.2	136
888	A Complex Systems Perspective on Neuroimaging Studies of Behavior and Its Disorders. Neuroscientist, 2022, 28, 382-399.	2.6	39
889	Grandchildâ€™s IQ is associated with grandparental environments prior to the birth of the parents. Wellcome Open Research, 2020, 5, 198.	0.9	3
890	Multi-Omics Data Analysis Uncovers Molecular Networks and Gene Regulators for Metabolic Biomarkers. Biomolecules, 2021, 11, 406.	1.8	1
891	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. PLoS Genetics, 2021, 17, e1009398.	1.5	46
893	Association between complement component 4A expression, cognitive performance and brain imaging measures in UK Biobank. Psychological Medicine, 2022, 52, 3497-3507.	2.7	13
894	Boosting GWAS using biological networks: A study on susceptibility to familial breast cancer. PLoS Computational Biology, 2021, 17, e1008819.	1.5	4
895	Aptardi predicts polyadenylation sites in sample-specific transcriptomes using high-throughput RNA sequencing and DNA sequence. Nature Communications, 2021, 12, 1652.	5.8	18

#	ARTICLE	IF	CITATIONS
896	Improving gene function predictions using independent transcriptional components. Nature Communications, 2021, 12, 1464.	5.8	20
900	The Role of White Matter Dysfunction and Leukoencephalopathy/Leukodystrophy Genes in the Aetiology of Frontotemporal Dementias: Implications for Novel Approaches to Therapeutics. International Journal of Molecular Sciences, 2021, 22, 2541.	1.8	7
901	Population Genetics: How Many Variable Genes Affect Variable Traits?. Current Biology, 2021, 31, R248-R250.	1.8	1
902	To Be a Champion of the 24-h Ultramarathon Race. If Not the Heart ... Mosaic Theory?. International Journal of Environmental Research and Public Health, 2021, 18, 2371.	1.2	6
903	The Illusions of the Modern Synthesis. Biosemiotics, 2021, 14, 5-24.	0.8	51
909	Testing Implications of the Omnigenic Model for the Genetic Analysis of Loci Identified through Genome-wide Association. Current Biology, 2021, 31, 1092-1098.e6.	1.8	15
911	Social epigenomics: are we at an impasse?. Epigenomics, 2021, 13, 1747-1759.	1.0	16
912	Natural variation in the regulation of neurodevelopmental genes modifies flight performance in Drosophila. PLoS Genetics, 2021, 17, e1008887.	1.5	10
913	Nonparallel transcriptional divergence during parallel adaptation. Molecular Ecology, 2021, 30, 1516-1530.	2.0	14
914	Identification of disease treatment mechanisms through the multiscale interactome. Nature Communications, 2021, 12, 1796.	5.8	72
915	Pharmacogenomics applied to recombinant human growth hormone responses in children with short stature. Reviews in Endocrine and Metabolic Disorders, 2021, 22, 135-143.	2.6	5
917	Phenotypic and genetic markers of psychopathology in a population-based sample of older adults. Translational Psychiatry, 2021, 11, 239.	2.4	2
919	Comparative regulomics supports pervasive selection on gene dosage following whole genome duplication. Genome Biology, 2021, 22, 103.	3.8	54
920	A model and test for coordinated polygenic epistasis in complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
921	The impact of identity by descent on fitness and disease in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	17
923	Fatigue in Women with Fibromyalgia: A Gene-Physical Activity Interaction Study. Journal of Clinical Medicine, 2021, 10, 1902.	1.0	2
924	Using CRISPR to understand and manipulate gene regulation. Development (Cambridge), 2021, 148, .	1.2	9
925	MeSCoT: the tool for quantitative trait simulation through the mechanistic modeling of genesâ€™ regulatory interactions. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3

#	ARTICLE	IF	CITATIONS
926	Geographic variation in the polygenic score of height in Japan. Human Genetics, 2021, 140, 1097-1108.	1.8	6
928	Evidence of an interaction between <i>FXR1</i> and <i>GSK3Î²</i> polymorphisms on levels of Negative Symptoms of Schizophrenia and their response to antipsychotics. European Psychiatry, 2021, 64, e39.	0.1	6
929	Harnessing pluripotent stem cells as models to decipher human evolution. FEBS Journal, 2022, 289, 2992-3010.	2.2	11
930	Identifying therapeutic drug targets using bidirectional effect genes. Nature Communications, 2021, 12, 2224.	5.8	11
931	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.	2.3	4
932	Common and Rare Variant Prediction and Penetrance of IBD in a Large, Multi-ethnic, Health System-based Biobank Cohort. Gastroenterology, 2021, 160, 1546-1557.	0.6	43
934	Transhumanist Genetic Enhancement: Creation of a â€˜New Manâ€™ Through Technological Innovation. New Bioethics, 2021, 27, 105-126.	0.5	2
935	Complex evolution of novel red floral color in<i>Petunia</i>. Plant Cell, 2021, 33, 2273-2295.	3.1	44
936	Spurious regulatory connections dictate the expressionâ€fitness landscape of translation factors. Molecular Systems Biology, 2021, 17, e10302.	3.2	8
937	Toward a Theory of Homology: Development and the De-Coupling of Morphological and Molecular Evolution. British Journal for the Philosophy of Science, 2023, 74, 771-810.	1.4	7
938	Genetic basis of offspring numberâ€“body weight tradeoff in <i>Drosophila melanogaster</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
939	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	3.8	2
940	Growth genes are implicated in the evolutionary divergence of sympatric piscivorous and insectivorous rainbow trout (Oncorhynchus mykiss). Bmc Ecology and Evolution, 2021, 21, 63.	0.7	2
942	Detecting local genetic correlations with scan statistics. Nature Communications, 2021, 12, 2033.	5.8	23
943	KnetMiner: a comprehensive approach for supporting evidenceâ€based gene discovery and complex trait analysis across species. Plant Biotechnology Journal, 2021, 19, 1670-1678.	4.1	50
946	On polygenic risk scores for complex traits prediction. Biometrics, 2022, 78, 499-511.	0.8	2
947	Public attitudes toward genetic risk scoring in medicine and beyond. Social Science and Medicine, 2021, 274, 113796.	1.8	7
948	Twelve years of GWAS discoveries for osteoporosis and related traits: advances, challenges and applications. Bone Research, 2021, 9, 23.	5.4	85

#	Article	IF	Citations
949	A robust twoâ€sample transcriptomeâ€wide Mendelian randomization method integrating GWAS with multiâ€tissue eQTL summary statistics. Genetic Epidemiology, 2021, 45, 353-371.	0.6	11
950	Differential Regulation of Maize and Sorghum Orthologs in Response to the Fungal Pathogen Exserohilum turcicum. Frontiers in Plant Science, 2021, 12, 675208.	1.7	6
951	Identification of two novel bullous pemphigoid- associated alleles, HLA-DQA1*05:05 and -DRB1*07:01, in Germans. Orphanet Journal of Rare Diseases, 2021, 16, 228.	1.2	16
952	Predicting Individual Differences in Cognitive Ability from Brain Imaging and Genetics. , 2021, , 327-348.		0
953	False and true positives in arthropod thermal adaptation candidate gene lists. Genetica, 2021, 149, 143-153.	0.5	9
954	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. ELife, 2021, 10, .	2.8	41
955	Recovering dynamic networks in big static datasets. Physics Reports, 2021, 912, 1-57.	10.3	29
956	Gene-to-trait knowledge graphs show association of plant photoreceptors with physiological and developmental processes that can confer agronomic benefits. Genetic Resources and Crop Evolution, 2021, 68, 2727-2735.	0.8	2
957	Modeling genome-wide by environment interactions through omnigenic interactome networks. Cell Reports, 2021, 35, 109114.	2.9	20
959	Cultural evolution of genetic heritability. Behavioral and Brain Sciences, 2022, 45, 1-147.	0.4	26
960	Harnessing Crop Wild Diversity for Climate Change Adaptation. Genes, 2021, 12, 783.	1.0	73
962	Folk Classification and Factor Rotations: Whales, Sharks, and the Problems With the Hierarchical Taxonomy of Psychopathology (HiTOP). Clinical Psychological Science, 2022, 10, 259-278.	2.4	26
963	Personalized Medicine Using Cutting Edge Technologies for Genetic Epilepsies. Current Neuropharmacology, 2021, 19, 813-831.	1.4	3
964	Importance of GWAS in finding un-targeted genetic association of sporadic Alzheimerâ€™s disease. Molecular and Cellular Toxicology, 2021, 17, 233.	0.8	6
965	On Genetic Correlation Estimation With Summary Statistics From Genome-Wide Association Studies. Journal of the American Statistical Association, 2022, 117, 1-11.	1.8	4
966	Mergeomics 2.0: a web server for multi-omics data integration to elucidate disease networks and predict therapeutics. Nucleic Acids Research, 2021, 49, W375-W387.	6.5	46
967	Risk Stratification and Clinical Utility of Polygenic Risk Scores in Ophthalmology. Translational Vision Science and Technology, 2021, 10, 14.	1.1	14
969	Characterization and comparison of gene-centered human interactomes. Briefings in Bioinformatics, 2021, 22, .	3.2	9

#	ARTICLE	IF	CITATIONS
970	Impact of rare and common genetic variation in the interleukin-1 pathway on human cytokine responses. Genome Medicine, 2021, 13, 94.	3.6	5
972	Back to the future: implications of genetic complexity for the structure of hybrid breeding programs. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	13
973	Unoccupied aerial systems discovered overlooked loci capturing the variation of entire growing period in maize. Plant Genome, 2021, 14, e20102.	1.6	16
975	A fast wavelet-based functional association analysis replicates several susceptibility loci for birth weight in a Norwegian population. BMC Genomics, 2021, 22, 321.	1.2	0
978	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. Nature Communications, 2021, 12, 2878.	5.8	25
979	Recombinant Inbred Mice as Models for Experimental Precision Medicine and Biology. , 0, , .		2
980	A vertebrate adaptive radiation is assembled from an ancient and disjunct spatiotemporal landscape. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
981	A parallel algorithm for ridge-penalized estimation of the multivariate exponential family from data of mixed types. Statistics and Computing, 2021, 31, 1.	0.8	0
982	The peripheral and core regions of virus-host network of COVID-19. Briefings in Bioinformatics, 2021, 22, .	3.2	3
984	Fast Cross-validation for Multi-penalty High-dimensional Ridge Regression. Journal of Computational and Graphical Statistics, 2021, 30, 835-847.	0.9	11
985	Integrative genomic analysis of blood pressure and related phenotypes in rats. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	6
988	Tejaas: reverse regression increases power for detecting trans-eQTLs. Genome Biology, 2021, 22, 142.	3.8	4
989	Schizophrenia: a classic battle ground of nature versus nurture debate. Science Bulletin, 2021, 66, 1037-1046.	4.3	4
990	Identification of a Novel Genetic Marker for Risk of Degenerative Rotator Cuff Disease Surgery in the UK Biobank. Journal of Bone and Joint Surgery - Series A, 2021, 103, 1259-1267.	1.4	9
991	The Genetic Architecture of Fitness Drives Population Viability during Rapid Environmental Change. American Naturalist, 2021, 197, 511-525.	1.0	32
992	Allelic polymorphism at <i>foxo</i> contributes to local adaptation in <i>Drosophila melanogaster</i>. Molecular Ecology, 2021, 30, 2817-2830.	2.0	7
993	Gene Environment Interactions in the Etiology of Neural Tube Defects. Frontiers in Genetics, 2021, 12, 659612.	1.1	49
996	Forecasting cellular states: from descriptive to predictive biology via single-cell multiomics. Current Opinion in Systems Biology, 2021, 26, 24-32.	1.3	10

#	ARTICLE	IF	CITATIONS
997	Genome-enabled discovery of evolutionary divergence in brains and behavior. Scientific Reports, 2021, 11, 13016.	1.6	5
998	Can Blockchain Solve the Dilemma in the Ethics of Genomic Biobanks?. Science and Engineering Ethics, 2021, 27, 35.	1.7	4
999	Leveraging breeding programs and genomic data in Norway spruce (Picea abies L. Karst) for GWAS analysis. Genome Biology, 2021, 22, 179.	3.8	29
1000	Cellular Darwinism: Regulatory networks, stochasticity, and selection in cancer development. Progress in Biophysics and Molecular Biology, 2021, 165, 66-71.	1.4	14
1001	Integrative omics of schizophrenia: from genetic determinants to clinical classification and risk prediction. Molecular Psychiatry, 2022, 27, 113-126.	4.1	33
1003	Causal inference for heritable phenotypic risk factors using heterogeneous genetic instruments. PLoS Genetics, 2021, 17, e1009575.	1.5	36
1004	Body Mass Index and Birth Weight Improve Polygenic Risk Score for Type 2 Diabetes. Journal of Personalized Medicine, 2021, 11, 582.	1.1	12
1006	Frequency distribution and association of Fat-mass and obesity (FTO) gene SNP rs-9939609 variant with Diabetes Mellitus Type-II population of Hyderabad, Sindh, Pakistan. Saudi Journal of Biological Sciences, 2021, 28, 4183-4190.	1.8	6
1008	Capturing the rapidly evolving study of adaptation. Journal of Evolutionary Biology, 2021, 34, 856-865.	0.8	3
1009	Polygenic prediction of atopic dermatitis improves with atopic training and filaggrin factors. Journal of Allergy and Clinical Immunology, 2022, 149, 145-155.	1.5	11
1010	Statistical mechanics of clock gene networks underlying circadian rhythms. Applied Physics Reviews, 2021, 8, .	5.5	14
1012	Animal models of stress and stress-related neurocircuits: A comprehensive review. Stress and Brain, 2021, 1, 108-127.	0.3	11
1013	Mental health and music engagement: review, framework, and guidelines for future studies. Translational Psychiatry, 2021, 11, 370.	2.4	23
1014	Taking risks to feel excitement: Detailed personality profile and genetic associations. European Journal of Personality, 0, , 089020702110192.	1.9	2
1015	Evaluating marginal genetic correlation of associated loci for complex diseases and traits between European and East Asian populations. Human Genetics, 2021, 140, 1285-1297.	1.8	12
1018	Shifting epigenetic contexts influence regulatory variation and disease risk. Aging, 2021, 13, 15699-15749.	1.4	2
1020	Advancing clinical genomics and precision medicine with GVViZ: FAIR bioinformatics platform for variable gene-disease annotation, visualization, and expression analysis. Human Genomics, 2021, 15, 37.	1.4	15
1021	Associations of genetic risk and smoking with incident COPD. European Respiratory Journal, 2022, 59, 2101320.	3.1	13

#	ARTICLE	IF	CITATIONS
1022	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. Molecular Plant, 2021, 14, 874-887.	3.9	56
1023	ANNORE: genetic fine-mapping with functional annotation. Human Molecular Genetics, 2021, 31, 32-40.	1.4	0
1025	Annual and perennial Medicago show signatures of parallel adaptation to climate and soil in highly conserved genes. Molecular Ecology, 2021, 30, 4448-4465.	2.0	9
1026	The neural crest cell hypothesis: no unified explanation for domestication. Genetics, 2021, 219, .	1.2	19
1028	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits. Nature Communications, 2021, 12, 4481.	5.8	39
1029	A generative network model of neurodevelopmental diversity in structural brain organization. Nature Communications, 2021, 12, 4216.	5.8	34
1033	Dissecting the shared genetic basis of migraine and mental disorders using novel statistical tools. Brain, 2022, 145, 142-153.	3.7	27
1034	Characterization of the genetic basis of local adaptation of wheat landraces from Iran and Pakistan using genomeâ€wide association study. Plant Genome, 2021, 14, e20096.	1.6	8
1035	Unraveling the genetics of tomato fruit weight during crop domestication and diversification. Theoretical and Applied Genetics, 2021, 134, 3363-3378.	1.8	12
1036	Revisiting a GWAS peak in Arabidopsis thaliana reveals possible confounding by genetic heterogeneity. Heredity, 2021, 127, 245-252.	1.2	8
1037	Small Effects: The Indispensable Foundation for a Cumulative Psychological Science. Perspectives on Psychological Science, 2022, 17, 205-215.	5.2	196
1038	Sources of Individual Differences in Pain. Annual Review of Neuroscience, 2021, 44, 1-25.	5.0	23
1039	Highly pleiotropic variants of human traits are enriched in genomic regions with strong background selection. Human Genetics, 2021, 140, 1343-1351.	1.8	3
1040	Effects of eight neuropsychiatric copy number variants on human brain structure. Translational Psychiatry, 2021, 11, 399.	2.4	18
1041	Genetics of substance use disorders in the era of big data. Nature Reviews Genetics, 2021, 22, 712-729.	7.7	60
1042	Transcriptional-regulatory convergence across functional MDD risk variants identified by massively parallel reporter assays. Translational Psychiatry, 2021, 11, 403.	2.4	11
1044	An Integrative Genomic Strategy Identifies sRAGE as a Causal and Protective Biomarker of Lung Function. Chest, 2022, 161, 76-84.	0.4	5
1045	Genetic drivers of m6A methylation in human brain, lung, heart and muscle. Nature Genetics, 2021, 53, 1156-1165.	9.4	57

#	ARTICLE	IF	CITATIONS
1046	The distribution of common-variant effect sizes. Nature Genetics, 2021, 53, 1243-1249.	9.4	37
1048	Genetic prediction of complex traits with polygenic scores: a statistical review. Trends in Genetics, 2021, 37, 995-1011.	2.9	55
1050	Machine learning based disease prediction from genotype data. Biological Chemistry, 2021, 402, 871-885.	1.2	7
1051	A Single-Step Genome Wide Association Study on Body Size Traits Using Imputation-Based Whole-Genome Sequence Data in Yorkshire Pigs. Frontiers in Genetics, 2021, 12, 629049.	1.1	18
1054	Genetic Variations in the Transforming Growth Factor-Î²1 Pathway May Improve Predictive Power for Overall Survival in Non-small Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 599719.	1.3	4
1055	Untangling the genetic link between type 1 and type 2 diabetes using functional genomics. Scientific Reports, 2021, 11, 13871.	1.6	6
1056	Found in translationâ€"core network preservation across liver diseases and species. Cell Reports Medicine, 2021, 2, 100347.	3.3	1
1057	Increased burden of rare variants in genes of the endosomal Toll-like receptor pathway in patients with systemic lupus erythematosus. Lupus, 2021, 30, 1756-1763.	0.8	2
1058	Accelerated deciphering of the genetic architecture of agricultural economic traits in pigs using a low-coverage whole-genome sequencing strategy. GigaScience, 2021, 10, .	3.3	34
1060	Selection for environmental variance of litter size in rabbits involves genes in pathways controlling animal resilience. Genetics Selection Evolution, 2021, 53, 59.	1.2	8
1061	Searching for improvements in predicting human eye colour from DNA. International Journal of Legal Medicine, 2021, 135, 2175-2187.	1.2	5
1063	Polygenic Adaptation: Integrating Population Genetics and Gene Regulatory Networks. Trends in Genetics, 2021, 37, 631-638.	2.9	41
1064	Prioritization of disease genes from GWAS using ensemble-based positive-unlabeled learning. European Journal of Human Genetics, 2021, 29, 1527-1535.	1.4	19
1065	Unveiling the Pathogenesis of Psychiatric Disorders Using Network Models. Genes, 2021, 12, 1101.	1.0	10
1066	Systems Pharmacology-Based Precision Therapy and Drug Combination Discovery for Breast Cancer. Cancers, 2021, 13, 3586.	1.7	4
1067	Cell type-specific and cross-population polygenic risk score analyses of MIR137 gene pathway in schizophrenia. IScience, 2021, 24, 102785.	1.9	15
1069	Gentamicin-induced hearing loss: A retrospective study using the Food and Drug Administration Adverse Event Reporting System and a toxicological study using drugâ^'gene network analysis. Heliyon, 2021, 7, e07429.	1.4	2
1070	Whole-exome imputation within UK Biobank powers rare coding variant association and fine-mapping analyses. Nature Genetics, 2021, 53, 1260-1269.	9.4	88

#	ARTICLE	IF	CITATIONS
1072	Posthumanism: Creation of â€˜New Menâ€™ Through Technological Innovation. New Bioethics, 2021, 27, 197-218.	0.5	1
1073	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. Nature Neuroscience, 2021, 24, 1313-1323.	7.1	44
1074	Genetic Prioritization, Therapeutic Repositioning and Cross-Disease Comparisons Reveal Inflammatory Targets Tractable for Kidney Stone Disease. Frontiers in Immunology, 2021, 12, 687291.	2.2	6
1075	Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation. ELife, 2021, 10, .	2.8	10
1076	Cis-regulatory variants affect gene expression dynamics in yeast. ELife, 2021, 10, .	2.8	6
1077	Assigning function to SNPs: Considerations when interpreting genetic variation. Seminars in Cell and Developmental Biology, 2022, 121, 135-142.	2.3	13
1078	Enhancers in disease: molecular basis and emerging treatment strategies. Trends in Molecular Medicine, 2021, 27, 1060-1073.	3.5	84
1080	Flexible coâ€data learning for highâ€dimensional prediction. Statistics in Medicine, 2021, 40, 5910-5925.	0.8	8
1081	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	11.8	529
1082	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
1084	Decoding disease: from genomes to networks to phenotypes. Nature Reviews Genetics, 2021, 22, 774-790.	7.7	46
1085	Application of Genetic Studies to Flow Cytometry Data and Its Impact on Therapeutic Intervention for Autoimmune Disease. Frontiers in Immunology, 2021, 12, 714461.	2.2	2
1087	Genomeâ€environment association methods comparison supports omnigenic adaptation to ecological niche in malaria vector mosquitoes. Molecular Ecology, 2021, 30, 6468-6485.	2.0	11
1089	Environmentally induced ribosomal DNA (rDNA) instability in human cells and populations exposed to hexavalent chromium [Cr (VI)]. Environment International, 2021, 153, 106525.	4.8	20
1090	From variant to function in human disease genetics. Science, 2021, 373, 1464-1468.	6.0	75
1091	Specialty Grand Challenge: Systems Genetics. Frontiers in Systems Biology, 2021, 1, .	0.5	0
1092	Genetic predisposition to tinnitus in the UK Biobank population. Scientific Reports, 2021, 11, 18150.	1.6	5
1096	Atypical genomic cortical patterning in autism with poor early language outcome. Science Advances, 2021, 7, eabh1663.	4.7	21

#	Article	IF	Citations
1097	The identification of grain size genes by RapMap reveals directional selection during rice domestication. Nature Communications, 2021, 12, 5673.	5.8	19
1099	Bridging Tumorigenesis and Therapy Resistance With a Non-Darwinian and Non-Lamarckian Mechanism of Adaptive Evolution. Frontiers in Oncology, 2021, 11, 732081.	1.3	3
1100	Hypothesis-driven science in large-scale studies: the case of GWAS. Biology and Philosophy, 2021, 36, 1.	0.7	1
1101	Inferring multilayer interactome networks shaping phenotypic plasticity and evolution. Nature Communications, 2021, 12, 5304.	5.8	13
1102	Enhancing genetic gains through marker-assisted recurrent selection: from phenotyping to genotyping. Cereal Research Communications, 2022, 50, 523-538.	0.8	5
1103	Molecular Biology Networks and Key Gene Regulators for Inflammatory Biomarkers Shared by Breast Cancer Development: Multi-Omics Systems Analysis. Biomolecules, 2021, 11, 1379.	1.8	2
1104	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. Genome Biology, 2021, 22, 262.	3.8	56
1105	Adolescent cannabis use and adult psychoticism: A longitudinal co-twin control analysis using data from two cohorts.. Journal of Abnormal Psychology, 2021, 130, 691-701.	2.0	5
1106	Mitigating tradeoffs in plant breeding. IScience, 2021, 24, 102965.	1.9	28
1109	Evolving networks of human intelligence. Intelligence, 2021, 88, 101567.	1.6	8
1110	The omnigenic model and polygenic prediction of complex traits. American Journal of Human Genetics, 2021, 108, 1558-1563.	2.6	61
1111	Discovery and implications of polygenicity of common diseases. Science, 2021, 373, 1468-1473.	6.0	80
1114	Pleiotropy or linkage? Their relative contributions to the genetic correlation of quantitative traits and detection by multitrait GWA studies. Genetics, 2021, 219, .	1.2	24
1115	Genetic architecture and major genes for backfat thickness in pig lines of diverse genetic backgrounds. Genetics Selection Evolution, 2021, 53, 76.	1.2	35
1116	Integrative Pre-Breeding for Biotic Resistance in Forest Trees. Plants, 2021, 10, 2022.	1.6	16
1120	Common host variation drives malaria parasite fitness in healthy human red cells. ELife, 2021, 10, .	2.8	17
1121	From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics. Physics of Life Reviews, 2021, 38, 55-106.	1.5	49
1122	From GWAS to Gene: Transcriptome-Wide Association Studies and Other Methods to Functionally Understand GWAS Discoveries. Frontiers in Genetics, 2021, 12, 713230.	1.1	55

#	ARTICLE	IF	CITATIONS
1124	Polygenic Risk Scores for Kidney Function and Their Associations with Circulating Proteome, and Incident Kidney Diseases. Journal of the American Society of Nephrology: JASN, 2021, 32, 3161-3173.	3.0	27
1125	Integration of functional genomics data to uncover cell type-specific pathways affected in Parkinson's disease. Biochemical Society Transactions, 2021, 49, 2091-2100.	1.6	1
1126	A computational approach for identification of core modules from a co-expression network and GWAS data. STAR Protocols, 2021, 2, 100768.	0.5	0
1127	RARG variant predictive of doxorubicin-induced cardiotoxicity identifies a cardioprotective therapy. Cell Stem Cell, 2021, 28, 2076-2089.e7.	5.2	36
1129	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
1130	Generating novel plant genetic variation via genome editing to escape the breeding lottery. In Vitro Cellular and Developmental Biology - Plant, 2021, 57, 627.	0.9	3
1131	Genetics on the neurodiversity spectrum: Genetic, phenotypic and endophenotypic continua in autism and ADHD. Studies in History and Philosophy of Science Part A, 2021, 89, 52-62.	0.6	28
1132	Wisdom of the crowds: A suggested polygenic plan for small-RNA-mediated regulation in bacteria. IScience, 2021, 24, 103096.	1.9	7
1133	Problems and promises: How to tell the story of a Genome Wide Association Study?. Studies in History and Philosophy of Science Part A, 2021, 89, 1-10.	0.6	4
1134	Meaningful associations in the adolescent brain cognitive development study. NeuroImage, 2021, 239, 118262.	2.1	108
1135	Crossing design shapes patterns of genetic variation in synthetic recombinant populations of Saccharomyces cerevisiae. Scientific Reports, 2021, 11, 19551.	1.6	5
1136	Complex small-world regulatory networks emerge from the 3D organisation of the human genome. Nature Communications, 2021, 12, 5756.	5.8	15
1137	From QTL to gene: C. elegans facilitates discoveries of the genetic mechanisms underlying natural variation. Trends in Genetics, 2021, 37, 933-947.	2.9	37
1138	Karyotype coding: The creation and maintenance of system information for complexity and biodiversity. BioSystems, 2021, 208, 104476.	0.9	15
1139	Genetic markers of vasovagal syncope. Autonomic Neuroscience: Basic and Clinical, 2021, 235, 102871.	1.4	6
1140	A candidate biological network formed by genes from genomic and hypothesis-free scans of suicide. Preventive Medicine, 2021, 152, 106604.	1.6	4
1141	The salmon louse genome: Copepod features and parasitic adaptations. Genomics, 2021, 113, 3666-3680.	1.3	17
1142	Combinatorial analytics: An essential tool for the delivery of precision medicine and precision agriculture. Artificial Intelligence in the Life Sciences, 2021, 1, 100003.	1.6	6

#	ARTICLE	IF	CITATIONS
1143	COPD Genetics. , 2022, , 503-514.		0
1144	Network Analysis Reveals Proteins Associated with Aortic Dilatation in Mucopolysaccharidoses. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 34-43.	2.2	3
1145	Comparison between instrumental variable and mediation-based methods for reconstructing causal gene networks in yeast. Molecular Omics, 2021, 17, 241-251.	1.4	4
1146	Genome-wide analysis of gene dosage in 24,092 individuals estimates that 10,000 genes modulate cognitive ability. Molecular Psychiatry, 2021, 26, 2663-2676.	4.1	33
1147	Accumulation of<i>cis</i>- and<i>trans</i>-regulatory variations is associated with phenotypic divergence of a complex trait between yeast species. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	6
1148	Advances and challenges in quantitative delineation of the genetic architecture of complex traits. Quantitative Biology, 2021, 9, 168-184.	0.3	0
1149	The evolution of group differences in changing environments. PLoS Biology, 2021, 19, e3001072.	2.6	37
1150	A modular master regulator landscape controls cancer transcriptional identity. Cell, 2021, 184, 334-351.e20.	13.5	78
1151	Proteome-wide Systems Genetics to Identify Functional Regulators of Complex Traits. Cell Systems, 2021, 12, 5-22.	2.9	19
1152	Genes, Environments, and Time: The Biology of Adversity and Resilience. Pediatrics, 2021, 147, .	1.0	96
1153	Zinc-Biofortified Rice: A Sustainable Food-Based Product for Fighting Zinc Malnutrition. , 2021, , 449-470.		10
1154	Analysis framework and experimental design for evaluating synergy-driving gene expression. Nature Protocols, 2021, 16, 812-840.	5.5	8
1156	Evolution of Holobionts: The Hologenome Concept. The Microbiomes of Humans, Animals, Plants, and the Environment, 2021, , 317-352.	0.2	1
1157	Do Genes Explain Sexual Minority Mental Health Disparities?. Archives of Sexual Behavior, 2021, 50, 731-737.	1.2	17
1158	Mendelian randomization under the omnigenic architecture. Briefings in Bioinformatics, 2021, 22, .	3.2	9
1160	Status and prospects of genomeâ€wide association studies in plants. Plant Genome, 2021, 14, e20077.	1.6	200
1161	Nonsparse Learning with Latent Variables. Operations Research, 2021, 69, 346-359.	1.2	9
1162	Limits and constraints to crop domestication. American Journal of Botany, 2020, 107, 1617-1621.	0.8	7

#	Article	IF	Citations
1163	Current Perspectives on Nasopharyngeal Carcinoma. Advances in Experimental Medicine and Biology, 2019, 1164, 11-34.	0.8	135
1164	Applications of Developmental Psychopathology. Advances in Experimental Medicine and Biology, 2019, 1192, 429-451.	0.8	1
1165	Multitissue Multiomics Systems Biology to Dissect Complex Diseases. Trends in Molecular Medicine, 2020, 26, 718-728.	3.5	39
1166	The Importance of Genetic Redundancy in Evolution. Trends in Ecology and Evolution, 2020, 35, 809-822.	4.2	99
1167	Genetics of nurture: A test of the hypothesis that parentsâ€™ genetics predict their observed caregiving.. Developmental Psychology, 2019, 55, 1461-1472.	1.2	51
1168	New concerns raised over value of genome-wide disease studies. Nature, 2017, 546, 463-463.	13.7	21
1169	Discovering the genes mediating the interactions between chronic respiratory diseases in the human interactome. Nature Communications, 2020, 11, 811.	5.8	25
1170	Challenges and future of precision medicine strategies for breast cancer based on a database on drug reactions. Bioscience Reports, 2019, 39, .	1.1	12
1171	Massively parallel discovery of human-specific substitutions that alter enhancer activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	67
1172	Implicit Realism Impedes Progress in Psychology: Comment on Fried (2020). Psychological Inquiry, 2020, 31, 326-333.	0.4	13
1173	A Connectomic Hypothesis for the Hominization of the Brain. Cerebral Cortex, 2021, 31, 2425-2449.	1.6	47
1174	Low-density lipoproteins cause atherosclerotic cardiovascular disease: pathophysiological, genetic, and therapeutic insights: a consensus statement from the European Atherosclerosis Society Consensus Panel. European Heart Journal, 2020, 41, 2313-2330.	1.0	776
1175	A Role for Somatostatin-Positive Interneurons in Neuro-Oscillatory and Information Processing Deficits in Schizophrenia. Schizophrenia Bulletin, 2021, 47, 1385-1398.	2.3	21
1319	Selective trade-offs maintain alleles underpinning complex trait variation in plants. Science, 2018, 361, 475-478.	6.0	94
1320	Enhancer Predictions and Genome-Wide Regulatory Circuits. Annual Review of Genomics and Human Genetics, 2020, 21, 37-54.	2.5	18
1321	Genome-Wide Polygenic Score and the Risk of Ischemic Stroke in a Prospective Cohort. Stroke, 2020, 51, 759-765.	1.0	25
1322	Genetic basis of human congenital anomalies of the kidney and urinary tract. Journal of Clinical Investigation, 2018, 128, 4-15.	3.9	91
1323	Host genetic variability and pneumococcal disease: a systematic review and meta-analysis. BMC Medical Genomics, 2019, 12, 130.	0.7	11

#	Article	IF	Citations
1324	Statistical inference in two-sample summary-data Mendelian randomization using robust adjusted profile score. Annals of Statistics, 2020, 48, .	1.4	333
1325	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. F1000Research, 2018, 7, 121.	0.8	4
1326	Grandchildâ€™s IQ is associated with grandparental environments prior to the birth of the parents. Wellcome Open Research, 2020, 5, 198.	0.9	3
1327	A population genetic interpretation of GWAS findings for human quantitative traits. PLoS Biology, 2018, 16, e2002985.	2.6	291
1328	Network approaches and applications in biology. PLoS Computational Biology, 2017, 13, e1005771.	1.5	40
1329	Natural variation in the sequestosome-related gene, sqst-5, underlies zinc homeostasis in Caenorhabditis elegans. PLoS Genetics, 2020, 16, e1008986.	1.5	24
1330	Unique genetic signatures of local adaptation over space and time for diapause, an ecologically relevant complex trait, in Drosophila melanogaster. PLoS Genetics, 2020, 16, e1009110.	1.5	48
1331	Enrichment of minor allele of SNPs and genetic prediction of type 2 diabetes risk in British population. PLoS ONE, 2017, 12, e0187644.	1.1	17
1332	Transcription factor Runx1 is pro-neurogenic in adult hippocampal precursor cells. PLoS ONE, 2018, 13, e0190789.	1.1	13
1333	Psychiatric genetics â€" Does diagnosis matter?. Journal of Psychiatry and Neuroscience, 2017, 42, 291-293.	1.4	2
1334	Interactions between Polygenic Scores and Environments: Methodological and Conceptual Challenges. Sociological Science, 0, 7, 365-386.	2.0	33
1335	The fog of genetics: what is known, unknown and unknowable in the genetics of complex traits and diseases. EMBO Reports, 2019, 20, e48054.	2.0	11
1336	A Novel Mapping Strategy Utilizing Mouse Chromosome Substitution Strains Identifies Multiple Epistatic Interactions That Regulate Complex Traits. G3: Genes, Genomes, Genetics, 2020, 10, 4553-4563.	0.8	4
1337	The polygenic nature of rheumatoid arthritis. Ecological Genetics, 2019, 17, 77-90.	0.1	1
1338	FOXO3 cell resilience gene neighborhood. Aging, 2017, 9, 2467-2468.	1.4	8
1339	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
1340	The potential of translational research in dogs in human medicine. Translational and Regulatory Sciences, 2019, 1, 31-36.	0.2	3
1341	Social and Reproductive Success in the United States: The Roles of Income, Education and Cognition. Mankind Quarterly, 2019, 59, 357-393.	0.1	5

#	Article	IF	Citations
1342	Phenotype inference in an Escherichia coli strain panel. ELife, 2017, 6, .	2.8	38
1343	Genetics of trans-regulatory variation in gene expression. ELife, 2018, 7, .	2.8	146
1344	Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. ELife, 2018, 7, .	2.8	121
1345	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. ELife, 2019, 8, .	2.8	14
1346	Variable prediction accuracy of polygenic scores within an ancestry group. ELife, 2020, 9, .	2.8	268
1347	Asymmetrical diversification of the receptor-ligand interaction controlling self-incompatibility in Arabidopsis. ELife, 2019, 8, .	2.8	11
1348	A broad mutational target explains a fast rate of phenotypic evolution. ELife, 2020, 9, .	2.8	13
1349	A trans-eQTL network regulates osteoclast multinucleation and bone mass. ELife, 2020, 9, .	2.8	24
1350	Genetic mapping of etiologic brain cell types for obesity. ELife, 2020, 9, .	2.8	79
1351	KDM5A mutations identified in autism spectrum disorder using forward genetics. ELife, 2020, 9, .	2.8	27
1352	Fitness variation across subtle environmental perturbations reveals local modularity and global pleiotropy of adaptation. ELife, 2020, 9, .	2.8	69
1353	Genomic analysis of variability in Delta-toxin levels between <i>Staphylococcus aureus</i> strains. PeerJ, 2020, 8, e8717.	0.9	12
1354	An integrated approach to identify bimodal genes associated with prognosis in cÃ¢ncer. Genetics and Molecular Biology, 2021, 44, e20210109.	0.6	3
1355	Priority index: database of genetic targets in immune-mediated disease. Nucleic Acids Research, 2022, 50, D1358-D1367.	6.5	16
1356	Mitochondria as environments for the nuclear genome in Drosophila: mitonuclear GÃ—GÃ—E. Journal of Heredity, 2022, 113, 37-47.	1.0	11
1357	What Future for Evolutionary Biology? Response to Commentaries on â€œThe Illusions of the Modern Synthesisâ€. Biosemiotics, 2021, 14, 683-695.	0.8	5
1358	Using phenotypic plasticity to understand the structure and evolution of the genotypeâ€“phenotype map. Genetica, 2022, 150, 209-221.	0.5	16
1359	Biodiversity, resilience and the stability of evolutionary systems. Current Biology, 2021, 31, R1149-R1153.	1.8	3

#	ARTICLE	IF	CITATIONS
1360	Natural selection drives genomeâ€wide evolution via chance genetic associations. Molecular Ecology, 2022, 31, 467-481.	2.0	5
1362	Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits. PLoS Computational Biology, 2021, 17, e1009483.	1.5	16
1364	Combinatorial patterns of gene expression changes contribute to variable expressivity of the developmental delay-associated 16p12.1 deletion. Genome Medicine, 2021, 13, 163.	3.6	5
1366	Genome-wide scans for signatures of selection in Mangalarga Marchador horses using high-throughput SNP genotyping. BMC Genomics, 2021, 22, 737.	1.2	5
1367	Wavelet Screening: a novel approach to analyzing GWAS data. BMC Bioinformatics, 2021, 22, 484.	1.2	2
1368	A Computational Atlas of Tissue-specific Regulatory Networks. Frontiers in Systems Biology, 2021, 1, .	0.5	3
1369	Associations between polygenic risk of substance use and use disorder and alcohol, cannabis, and nicotine use in adolescence and young adulthood in a longitudinal twin study. Psychological Medicine, 2023, 53, 2296-2306.	2.7	7
1370	Generalizability of GWA-Identified Genetic Risk Variants for Metabolic Traits to Populations from the Arabian Peninsula. Genes, 2021, 12, 1637.	1.0	2
1371	Associating complex traits with genetic variants: polygenic risk scores, pleiotropy and endophenotypes. Genetica, 2021, , 1.	0.5	0
1372	Phenotypic and genotypic parallel evolution in parapatric ecotypes of<i>Senecio</i>. Evolution; International Journal of Organic Evolution, 2021, 75, 3115-3131.	1.1	22
1374	Novel QTL identification and candidate gene analysis for enhancing salt tolerance in soybean (Glycine) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	14
1399	MOLECULAR GENETIC FACTORS OF THE SKELETAL MUSCLE HYPERTROPHY. Bulletin of Problems Biology and Medicine, 2018, 2, 15.	0.0	0
1401	Immune System Promiscuity in Human and Nonhuman Primate Evolution. Human Biology, 2018, 90, 251.	0.4	4
1430	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. , 2018, , .		3
1444	From Schizophrenia Genetics to Disease Biology: Harnessing New Concepts and Technologies. Journal of Psychiatry and Brain Science, 2019, 4, .	0.3	3
1445	Molecular Basis of Complex Heritability in Natural Genotype-to-Phenotype Relationships. SSRN Electronic Journal, 0, , .	0.4	0
1448	From the neo-Kraepelinian framework to the new mechanical philosophy of psychiatry: regaining common sense. Journal of Psychiatry and Neuroscience, 2019, 44, 3-7.	1.4	3
1449	Oligogenic Effects of 16p11.2 Copy Number Variation on Craniofacial Development. SSRN Electronic Journal, 0, , .	0.4	1

#	Article	IF	Citations
1450	On the Role of Hub and Orphan Genes in the Diagnosis of Breast Invasive Carcinoma. Lecture Notes in Computer Science, 2019, , 631-642.	1.0	0
1451	Psychiatric Genetics, Epigenetics, and Cellular Models in Coming Years. Journal of Psychiatry and Brain Science, 2019, 4, .	0.3	1
1487	Transcriptomic Analysis of Left Ventricle Myocardium in an SHR Congenic Line With Ameliorated Cardiac Fibrosis. Physiological Research, 2019, 68, 747-755.	0.4	1
1496	Differential admixture in Latin American populations and its impact on the study of colorectal cancer. Genetics and Molecular Biology, 2020, 43, e20200143.	0.6	0
1506	Current state and problems of poultry breeding in Russia (review). Agricultural Science Euro-North-East, 2020, 21, 217-232.	0.2	3
1515	Genomeâ€'wide association study and genomic prediction for growth traits in yellow-plumage chicken using genotyping-by-sequencing. Genetics Selection Evolution, 2021, 53, 82.	1.2	5
1516	Common and Distinct Disruptions of Cortical Surface Morphology Between Autism Spectrum Disorder Children With and Without SHANK3 Deficiency. Frontiers in Neuroscience, 2021, 15, 751364.	1.4	4
1517	Local Adaptation in the Interior Spruce Hybrid Complex. Compendium of Plant Genomes, 2020, , 155-176.	0.3	5
1518	Polygenic Selection within a Single Generation Leads to Subtle Divergence among Ecological Niches. Genome Biology and Evolution, 2021, 13, .	1.1	8
1520	Characterizing the genetic basis of copper toxicity in <i>Drosophila</i> reveals a complex pattern of allelic, regulatory, and behavioral variation. Genetics, 2021, 217, 1-20.	1.2	14
1522	Energy plants (crops): potential natural and future designer plants. , 2022, , 73-114.		1
1523	Identification of genetic variants influencing methylation in brain with pleiotropic effects on psychiatric disorders. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2022, 113, 110454.	2.5	8
1525	Genetic dissection of growth trajectories in forest trees: From FunMap to FunGraph. Forestry Research, 2021, 1, 1-10.	0.5	4
1526	The golden mean: A systems biology approach to development language disorders. PragmalingÃ¼Ãstica, 2020, , 30-44.	0.1	4
1527	RNA and aging. , 2020, , 349-370.		0
1528	Chemoprevention of Cancer: Past, Present, and Future. , 2020, , 1-18.		1
1543	Genomically correlated trait combinations and antagonistic selection contributing to counterintuitive genetic patterns of adaptive diapause divergence in <i>Rhagoletis</i> flies. Journal of Evolutionary Biology, 2022, 35, 146-163.	0.8	11
1544	Evolvability: A Quantitative-Genetics Perspective. Annual Review of Ecology, Evolution, and Systematics, 2021, 52, 153-175.	3.8	36

#	Article	IF	Citations
1545	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. Nature Metabolism, 2021, 3, 1476-1483.	5.1	43
1546	Network-Driven Drug Discovery. Methods in Molecular Biology, 2022, 2390, 177-190.	0.4	1
1547	Polygenic risk for aggressive behavior from late childhood through early adulthood. European Child and Adolescent Psychiatry, 2023, 32, 651-660.	2.8	6
1548	Evidence of the folateâ€mediated oneâ€carbon metabolism pathway genes in controlling the nonâ€syndromic oral clefts risks. Oral Diseases, 2023, 29, 1080-1088.	1.5	1
1550	What is a phenotype? History and new developments of the concept. Genetica, 2022, 150, 153-158.	0.5	4
1560	A larger target leads to faster evolution. ELife, 2020, 9, .	2.8	0
1564	Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. PLoS Computational Biology, 2020, 16, e1008354.	1.5	6
1566	Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in Type 2 Diabetes GWAS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 548-558.	0.7	2
1567	Optic nerve regeneration in the mouse is a complex trait modulated by genetic background. Molecular Vision, 2018, 24, 174-186.	1.1	12
1568	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 308-319.	0.7	5
1569	Cardiology Meets Personalized Lifestyle Medicine. Integrative Medicine, 2017, 16, 12-16.	0.1	0
1570	Making Genetic Testing More Clinically Valuable. Integrative Medicine, 2018, 17, 8-12.	0.1	0
1571	Facing the Methodological Challenge in Dissecting the Genetics of ADHD: A Case for Deep Phenotyping and Heterogeneity Reduction. Journal of the Canadian Academy of Child and Adolescent Psychiatry, 2020, 29, 188-201.	0.7	3
1572	Looking back at the first twenty years of genomics. Quantitative Biology, 2022, 10, 6-16.	0.3	0
1573	Individual variations in â€˜brain ageâ€™ relate to early-life factors more than to longitudinal brain change. ELife, 2021, 10, .	2.8	71
1574	A Core Omnigenic Non-coding Trait Governing Dex-Induced Osteoporotic Effects Identified Without DEXA. Frontiers in Pharmacology, 2021, 12, 750959.	1.6	1
1575	A Multilayer Interactome Network Constructed in a Forest Poplar Population Mediates the Pleiotropic Control of Complex Traits. Frontiers in Genetics, 2021, 12, 769688.	1.1	0
1576	Evolution and development: From the pet shop to the pelagic zone. Current Biology, 2021, 31, R1469-R1471.	1.8	0

#	Article	IF	Citations
1577	The nature of coxofemoral joint pathology across family Canidae. Anatomical Record, 2022, 305, 2119-2136.	0.8	1
1578	Using Genomic Techniques in Sports and Exercise Science: Current Status and Future Opportunities. Current Sports Medicine Reports, 2021, 20, 617-623.	0.5	2
1579	Multiple epistatic DNA variants in a single gene affect gene expression in <i>trans</i>. Genetics, 2022, 220, .	1.2	6
1580	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. Nature Communications, 2021, 12, 6972.	5.8	14
1581	Genome-wide association study of periodontal pocketing in Finnish adults. BMC Oral Health, 2021, 21, 611.	0.8	2
1582	<i>DECUSSATE</i>network with flowering genes explains the variable effects of<i>qDTY12.1</i>to rice yield under drought across genetic backgrounds. Plant Genome, 2022, 15, e20168.	1.6	0
1583	A Unifying Theory for Autism: The Pathogenetic Triad as a Theoretical Framework. Frontiers in Psychiatry, 2021, 12, 767075.	1.3	6
1584	The crucial role of genome-wide genetic variation in conservation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	196
1585	Maintenance of Complex Trait Variation: Classic Theory and Modern Data. Frontiers in Genetics, 2021, 12, 763363.	1.1	11
1586	A familiar study on self-limited childhood epilepsy patients using hIPSC-derived neurons shows a bias towards immaturity at the morphological, electrophysiological and gene expression levels. Stem Cell Research and Therapy, 2021, 12, 590.	2.4	3
1588	Bench Research Informed by GWAS Results. Cells, 2021, 10, 3184.	1.8	5
1589	Regulatory SNP of RREB1 is Associated With Bone Mineral Density in Chinese Postmenopausal Osteoporosis Patients. Frontiers in Genetics, 2021, 12, 756957.	1.1	2
1590	Drug Design: Where We Are and Future Prospects. Molecules, 2021, 26, 7061.	1.7	5
1591	Using sibling models to unpack the relationship between education and cognitive functioning in later life. SSM - Population Health, 2021, 17, 100960.	1.3	1
1592	Complex adaptive architecture underlies adaptation to quantitative host resistance in a fungal plant pathogen. Molecular Ecology, 2021, , .	2.0	0
1593	We Know Even More Things: A Decade Review of Parenting Research. Journal of Research on Adolescence, 2021, 31, 870-888.	1.9	26
1594	Using singleton densities to detect recent selection in<i>Bos taurus</i>. Evolution Letters, 2021, 5, 595-606.	1.6	4
1595	Genome-wide association mapping of transcriptome variation in <i>Mimulus guttatus</i> indicates differing patterns of selection on <i>cis</i>- versus <i>trans</i>-acting mutations. Genetics, 2022, 220, .	1.2	5

#	Article	IF	Citations
1596	Excess Heritability Contribution of Alcohol Consumption Variants in the â€œMissing Heritabilityâ€•of Type 2 Diabetes Mellitus. International Journal of Molecular Sciences, 2021, 22, 12318.	1.8	0
1597	A holistic perspective on species conservation. Biological Conservation, 2021, 264, 109375.	1.9	1
1599	Germline breast cancer susceptibility genes, tumor characteristics, and survival. Genome Medicine, 2021, 13, 185.	3.6	3
1600	Emerging Insights Into Chronic Renal Disease Pathogenesis in Hypertension From Human and Animal Genomic Studies. Hypertension, 2021, 78, 1689-1700.	1.3	3
1601	New insights into genetics underlying of plumage color. Animal Genetics, 2022, 53, 80-93.	0.6	12
1602	FunGraph: A statistical protocol to reconstruct omnigenic multilayer interactome networks for complex traits. STAR Protocols, 2021, 2, 100985.	0.5	5
1603	OUP accepted manuscript. Biostatistics, 2022, , .	0.9	0
1604	Uncovering the Genetic Architecture of Replicated Adaptation. SSRN Electronic Journal, 0, , .	0.4	2
1605	Evolution of polygenic traits under global <i>vs</i> local adaptation. Genetics, 2022, 220, .	1.2	42
1606	Comprehensive exploration of the genetic contribution of the dopaminergic and serotonergic pathways to psychiatric disorders. Translational Psychiatry, 2022, 12, 11.	2.4	17
1607	Artificial Intelligence and Precision Medicine: A Perspective. Advances in Experimental Medicine and Biology, 2021, , 1-11.	0.8	6
1608	Lamin A/C missense variants: from discovery to functional validation. Npj Genomic Medicine, 2021, 6, 102.	1.7	6
1609	Biomedical data, computational methods and tools for evaluating diseaseâ€“disease associations. Briefings in Bioinformatics, 2022, 23, .	3.2	12
1610	Genome-Wide Association Analysis Reveals Genetic Loci and Candidate Genes for Chest, Abdominal, and Waist Circumferences in Two Duroc Pig Populations. Frontiers in Veterinary Science, 2021, 8, 807003.	0.9	7
1611	A genome-wide association study of serum proteins reveals shared loci with common diseases. Nature Communications, 2022, 13, 480.	5.8	79
1612	Genomeâ€wide pleiotropy analysis identifies novel blood pressure variants and improves its polygenic risk scores. Genetic Epidemiology, 2022, 46, 105-121.	0.6	6
1613	Epigenetics and the city: Nonâ€parallel DNA methylation modifications across pairs of urbanâ€forest Great tit populations. Evolutionary Applications, 2022, 15, 149-165.	1.5	15
1614	Genetic Factors in the Etiology of Preeclampsia/Eclampsia. , 2022, , 45-69.		4

#	Article	IF	Citations
1615	Developmental disorders caused by haploinsufficiency of transcriptional regulators: a perspective based on cell fate determination. Biology Open, 2022, 11, .	0.6	16
1617	Complexity against current cancer research: Are we on the wrong track?. International Journal of Cancer, 2022, 150, 1569-1578.	2.3	7
1618	Evolution in small steps and giant leaps. Evolution; International Journal of Organic Evolution, 2022, 76, 67-77.	1.1	5
1619	Profileâ€likelihood Bayesian model averaging for twoâ€sample summary data Mendelian randomization in the presence of horizontal pleiotropy. Statistics in Medicine, 2022, 41, 1100-1119.	0.8	7
1621	The regulatory network architecture of cardiometabolic diseases. Nature Genetics, 2022, 54, 2-3.	9.4	5
1622	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2022, 14, 7.	3.0	42
1623	Revisiting the malaria hypothesis: accounting for polygenicity and pleiotropy. Trends in Parasitology, 2022, 38, 290-301.	1.5	5
1624	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome Biology, 2022, 23, 13.	3.8	19
1625	Heritability: What's the point? What is it not for? A human genetics perspective. Genetica, 2022, 150, 199-208.	0.5	4
1626	Polygenic adaptation and negative selection across traits, years and environments in a longâ€lived plant species (<i>Pinus pinaster</i> Ait., Pinaceae). Molecular Ecology, 2022, 31, 2089-2105.	2.0	21
1627	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. Endocrine Reviews, 2022, 43, 927-965.	8.9	75
1628	The mutation effect reaction norm (muâ€rn) highlights environmentally dependent mutation effects and epistatic interactions. Evolution; International Journal of Organic Evolution, 2022, 76, 37-48.	1.1	12
1629	Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptomeÂwide association studies. Human Molecular Genetics, 2022, , .	1.4	3
1631	Placental genomics mediates genetic associations with complex health traits and disease. Nature Communications, 2022, 13, 706.	5.8	20
1632	Systemic lupus erythematosus as a genetic disease. Clinical Immunology, 2022, 236, 108953.	1.4	18
1633	Barcoded bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast. ELife, 2022, 11, .	2.8	33
1635	Polygenic routes lead to parallel altitudinal adaptation in <i>Heliosperma pusillum</i> (Caryophyllaceae). Molecular Ecology, 2023, 32, 1832-1847.	2.0	13
1636	The utility of a closed breeding colony of <i>Peromyscus leucopus</i> for dissecting complex traits. Genetics, 2022, 221, .	1.2	5

#	Article	IF	Citations
1637	Selection of both habitat and genes in specialized and endangered caribou. Conservation Biology, 2022, 36, .	2.4	1
1638	Use of â€˜omics for endometrial timing: the cycle moves on. Human Reproduction, 2022, 37, 644-650.	0.4	8
1639	Mendelian Randomization: A Review of Methods for the Prevention, Assessment, and Discussion of Pleiotropy in Studies Using the Fat Mass and Obesity-Associated Gene as an Instrument for Adiposity. Frontiers in Genetics, 2022, 13, 803238.	1.1	2
1640	Partitioning gene-mediated disease heritability without eQTLs. American Journal of Human Genetics, 2022, 109, 405-416.	2.6	8
1641	The role of alternative splicing in adaptation and evolution. Trends in Ecology and Evolution, 2022, 37, 299-308.	4.2	56
1642	Mutations du mythe de lâ€™ADN, Ã©tapes de matÃ©rialisation du gÃ¨ne. TracÃ©s, 2021, , 85-107.	0.1	0
1643	Circadian-Period Variation Underlies the Local Adaptation of Photoperiodism in the Short-Day Plant <i>Lemna aequinoctialis</i>. SSRN Electronic Journal, 0, , .	0.4	0
1646	Molecular parallelism in signaling function across different sexually selected ornaments in a warbler. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
1647	Targeted Re-Sequencing of the 2p21 Locus Identifies Non-Syndromic Cleft Lip Only Novel Susceptibility Gene ZFP36L2. Frontiers in Genetics, 2022, 13, 802229.	1.1	2
1648	Artificial Intelligence and Cardiovascular Genetics. Life, 2022, 12, 279.	1.1	13
1650	Predicting genotype-specific gene regulatory networks. Genome Research, 2022, 32, 524-533.	2.4	9
1654	Wheat Breeding, Transcription Factories, and Genetic Interactions: New Perspectives. Frontiers in Plant Science, 2022, 13, 807884.	1.7	0
1655	Functional network motifs defined through integration of protein-protein and genetic interactions. PeerJ, 2022, 10, e13016.	0.9	4
1656	Genetic variants associated with sepsis. PLoS ONE, 2022, 17, e0265052.	1.1	3
1659	Incorporating regulatory interactions into gene-set analyses for GWAS data: A controlled analysis with the MAGMA tool. PLoS Computational Biology, 2022, 18, e1009908.	1.5	3
1660	Technological Approach to Mind Everywhere: An Experimentally-Grounded Framework for Understanding Diverse Bodies and Minds. Frontiers in Systems Neuroscience, 2022, 16, 768201.	1.2	44
1661	Which field of research would Gregor Mendel choose in the 21st century?. Plant Cell, 2022, 34, 2462-2465.	3.1	5
1662	Embodied Prevention. Frontiers in Psychology, 2022, 13, 841393.	1.1	8

#	ARTICLE	IF	CITATIONS
1665	The ease and complexity of identifying and using specialized metabolites for crop engineering. Emerging Topics in Life Sciences, 2022, 6, 153-162.	1.1	3
1666	Protein interaction networks provide insight into fetal origins of chronic obstructive pulmonary disease. Respiratory Research, 2022, 23, 69.	1.4	7
1667	Simulated nonlinear genetic and environmental dynamics of complex traits. Development and Psychopathology, 2022, , 1-16.	1.4	0
1668	Evaluation of Genetic Kidney Diseases in Living Donor Kidney Transplantation: Towards Precision Genomic Medicine in Donor Risk Assessment. Current Transplantation Reports, 2022, 9, 127-142.	0.9	8
1670	Common genetic variants do not predict recurrent events in coronary heart disease patients. BMC Cardiovascular Disorders, 2022, 22, 96.	0.7	0
1671	Body mass index and healthcare costs: using genetic variants from the HUNT study as instrumental variables. BMC Health Services Research, 2022, 22, 396.	0.9	0
1672	The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross. Nature Communications, 2022, 13, 1463.	5.8	19
1673	Direct observation of adaptive tracking on ecological time scales in <i>Drosophila</i>. Science, 2022, 375, eabj7484.	6.0	71
1674	Mutation, selection, and the prevalence of the <i>Caenorhabditis elegans</i> heat-sensitive mortal germline phenotype. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	4
1675	BrainDevo: Spatio-Temporal Gene Regulation Repository of Brain Development. Frontiers in Molecular Neuroscience, 2022, 15, 799801.	1.4	0
1676	Enrichment analyses identify shared associations for 25 quantitative traits in over 600,000 individuals from seven diverse ancestries. American Journal of Human Genetics, 2022, 109, 871-884.	2.6	6
1677	Genetics as a key to improving crop photosynthesis. Journal of Experimental Botany, 2022, 73, 3122-3137.	2.4	25
1678	Testability of high-dimensional linear models with nonsparse structures. Annals of Statistics, 2022, 50, .	1.4	0
1679	From pharmacogenetics to pharmaco-omics: Milestones and future directions. Human Genetics and Genomics Advances, 2022, 3, 100100.	1.0	14
1680	Reframing research on evolutionary novelty and co-option: Character identity mechanisms versus deep homology. Seminars in Cell and Developmental Biology, 2023, 145, 3-12.	2.3	15
1681	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. American Journal of Human Genetics, 2022, 109, 692-709.	2.6	2
1682	Context-dependant enhancers as a reservoir of functional polymorphisms and epigenetic markers linked to alcohol use disorders and comorbidities. Addiction Neuroscience, 2022, 2, 100014.	0.4	0
1683	Overlapping association signals in the genetics of hair-related phenotypes in humans and their relevance to predictive DNA analysis. Forensic Science International: Genetics, 2022, 59, 102693.	1.6	5

#	ARTICLE	IF	CITATIONS
1685	Barcoded reciprocal hemizygosity analysis <i>via</i> sequencing illuminates the complex genetic basis of yeast thermotolerance. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
1688	Phenotypic plasticity in plant height shaped by interaction between genetic loci and diurnal temperature range. New Phytologist, 2022, 233, 1768-1779.	3.5	25
1691	Estimating prevalence of human traits among populations from polygenic risk scores. Human Genomics, 2021, 15, 70.	1.4	5
1692	Integrated Pharmacogenetics Analysis of the Three Fangjis Decoctions for Treating Arrhythmias Based on Molecular Network Patterns. Frontiers in Cardiovascular Medicine, 2021, 8, 726694.	1.1	0
1693	Genome Chaos, Information Creation, and Cancer Emergence: Searching for New Frameworks on the 50th Anniversary of the â€œWar on Cancerâ€. Genes, 2022, 13, 101.	1.0	25
1695	Multiâ€Omic Approaches to Identify Genetic Factors in Metabolic Syndrome. , 2021, 12, 3045-3084.		4
1696	Periodontitis Risk Variants at <i>SIGLEC5</i> Impair ERG and MAFB Binding. Journal of Dental Research, 2022, 101, 551-558.	2.5	3
1697	Starring Role of Biomarkers and Anticancer Agents as a Major Driver in Precision Medicine of Cancer Therapy. Current Molecular Medicine, 2023, 23, 111-126.	0.6	1
1698	From DNA Copy Number Gains and Tumor Dependencies to Novel Therapeutic Targets for High-Risk Neuroblastoma. Journal of Personalized Medicine, 2021, 11, 1286.	1.1	2
1699	Identification and validation of a regulatory mutation upstream of the BMP2 gene associated with carcass length in pigs. Genetics Selection Evolution, 2021, 53, 94.	1.2	21
1701	Populations, Traits, and Their Spatial Structure in Humans. Genome Biology and Evolution, 2021, 13, .	1.1	3
1703	Physiology restores purpose to evolutionary biology. Biological Journal of the Linnean Society, 2023, 139, 357-369.	0.7	9
1705	Modeling common and rare genetic risk factors of neuropsychiatric disorders in human induced pluripotent stem cells. Schizophrenia Research, 2022, , .	1.1	6
1706	Causes of variability in estimates of mutational variance from mutation accumulation experiments. Genetics, 2022, 221, .	1.2	2
1707	Thermal biology of invasive Aedes mosquitoes in the context of climate change. Current Opinion in Insect Science, 2022, 51, 100920.	2.2	14
1708	Population differentiation of polygenic score predictions under stabilizing selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200416.	1.8	26
1709	Implications of the genomic revolution for education research and policy. British Educational Research Journal, 0, , .	1.4	1
1710	Development of a clinical polygenic risk score assay and reporting workflow. Nature Medicine, 2022, 28, 1006-1013.	15.2	74

#	ARTICLE	IF	CITATIONS
1711	Cerebral Polymorphisms for Lateralisation: Modelling the Genetic and Phenotypic Architectures of Multiple Functional Modules. Symmetry, 2022, 14, 814.	1.1	13
1713	Redefining the hypotheses driving Parkinsonâ€™s diseases research. Npj Parkinson's Disease, 2022, 8, 45.	2.5	7
1714	Predicting Archaic Hominin Phenotypes from Genomic Data. Annual Review of Genomics and Human Genetics, 2022, 23, 591-612.	2.5	12
1785	Genetic Bases of Complex Traits: From Quantitative Trait Loci to Prediction. Methods in Molecular Biology, 2022, 2467, 1-44.	0.4	0
1786	Polygenic risk score as a possible tool for identifying familial monogenic causes of complex diseases. Genetics in Medicine, 2022, 24, 1545-1555.	1.1	12
1787	Genome-Wide Causation Studies of Complex Diseases. Journal of Computational Biology, 2022, 29, 908-931.	0.8	2
1788	Higher-Order Interactions in Biology: The Curious Case of Epistasis. Understanding Complex Systems, 2022, , 417-433.	0.3	3
1789	PiER: web-based facilities tailored for genetic target prioritisation harnessing human disease genetics, functional genomics and protein interactions. Nucleic Acids Research, 2022, 50, W583-W592.	6.5	5
1791	A systems genomics approach to uncover patient-specific pathogenic pathways and proteins in ulcerative colitis. Nature Communications, 2022, 13, 2299.	5.8	9
1792	The Organ-Disease Annotations (ODiseA) Database of Hereditary Diseases and Inflicted Tissues. Journal of Molecular Biology, 2022, 434, 167619.	2.0	6
1793	Patterns of selection across gene regulatory networks. Seminars in Cell and Developmental Biology, 2023, 145, 60-67.	2.3	6
1795	Using Stem Cell Models to Explore the Genetics Underlying Psychiatric Disorders: Linking Risk Variants, Genes, and Biology in Brain Disease. American Journal of Psychiatry, 2022, 179, 322-328.	4.0	7
1798	Polygenic Scores for Plasticity: A New Tool for Studying Geneâ€“Environment Interplay. Demography, 2022, 59, 1045-1070.	1.2	7
1799	Polygenic score accuracy in ancient samples: Quantifying the effects of allelic turnover. PLoS Genetics, 2022, 18, e1010170.	1.5	4
1801	A dynamic single cell-based framework for digital twins to prioritize disease genes and drug targets. Genome Medicine, 2022, 14, 48.	3.6	16
1802	Building causal knowledge in behavior genetics. Behavioral and Brain Sciences, 2023, 46, 1-76.	0.4	12
1803	Expression of Beef- Versus Dairy-Type in Crossbred Beef Ã— Dairy Cattle Does Not Impact Shape, Eating Quality, or Color of Strip Loin Steaks. Meat and Muscle Biology, 2022, 6, .	0.7	3
1804	Detecting signatures of selection on gene expression. Nature Ecology and Evolution, 2022, 6, 1035-1045.	3.4	37

#	Article	IF	Citations
1805	Different responses to risperidone treatment in Schizophrenia: a multicenter genome-wide association and whole exome sequencing joint study. Translational Psychiatry, 2022, 12, 173.	2.4	9
1806	Challenging the utility of polygenic scores for social science: Environmental confounding, downward causation, and unknown biology. Behavioral and Brain Sciences, 2023, 46, 1-36.	0.4	11
1807	Statistical methods for Mendelian randomization in genome-wide association studies: A review. Computational and Structural Biotechnology Journal, 2022, 20, 2338-2351.	1.9	56
1808	From Zero to Fifty: Considerations on Eric Lennebergâ€™s Biological Foundations of Language and Updates. Biolinguistics, 0, 11, 423-444.	0.6	2
1809	æ¸—å…¥æ•äºä¸Žå°°é•º¦æ•ç§§ä¼˜åŠ¿. Chinese Science Bulletin, 2022, , .	0.4	1
1810	Opportunities and challenges for the use of common controls in sequencing studies. Nature Reviews Genetics, 2022, 23, 665-679.	7.7	13
1811	Sleep and Late-Onset Alzheimerâ€™s Disease: Shared Genetic Risk Factors, Drug Targets, Molecular Mechanisms, and Causal Effects. Frontiers in Genetics, 2022, 13, .	1.1	5
1812	A polygenic architecture with habitatâ€dependent effects underlies ecological differentiation in <i>Silene</i>. New Phytologist, 2022, , .	3.5	2
1817	Host genetic basis of COVID-19: from methodologies to genes. European Journal of Human Genetics, 2022, 30, 899-907.	1.4	13
1819	Amplification is the Primary Mode of Gene-by-Sex Interaction in Complex Human Traits. SSRN Electronic Journal, 0, , .	0.4	0
1823	Five plants per RIL for phenotyping traits of high or moderate heritability ensure the power of QTL mapping in a rice MAGIC population. Molecular Breeding, 2022, 42, .	1.0	3
1825	A synthetic synthesis to explore animal evolution and development. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	1.8	5
1827	How does genetic architecture affect eco-evolutionary dynamics? A theoretical perspective. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	1.8	12
1828	A phenotypic spectrum of autism is attributable to the combined effects of rare variants, polygenic risk and sex. Nature Genetics, 2022, 54, 1284-1292.	9.4	66
1829	Integrated analysis of direct and proxy genome wide association studies highlights polygenicity of Alzheimerâ€™s disease outside of the APOE region. PLoS Genetics, 2022, 18, e1010208.	1.5	10
1832	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
1833	How Variation in Risk Allele Output and Gene Interactions Shape the Genetic Architecture of Schizophrenia. Genes, 2022, 13, 1040.	1.0	1
1834	Using population selection and sequencing to characterize natural variation of starvation resistance in Caenorhabditis elegans. ELife, 0, 11, .	2.8	4

#	ARTICLE	IF	CITATIONS
1835	Spina Bifida: A Review of the Genetics, Pathophysiology and Emerging Cellular Therapies. Journal of Developmental Biology, 2022, 10, 22.	0.9	13
1836	Open problems in human trait genetics. Genome Biology, 2022, 23, .	3.8	33
1837	An eco-evo-devo genetic network model of stress response. Horticulture Research, 2022, 9, .	2.9	3
1838	Acute thermal stress elicits interactions between gene expression and alternative splicing in a fish of conservation concern. Journal of Experimental Biology, 2022, 225, .	0.8	6
1841	One step closer to linking GWAS SNPs with the right genes. Nature Genetics, 2022, 54, 748-749.	9.4	4
1842	Circadian-period variation underlies the local adaptation of photoperiodism in the short-day plant Lemna aequinoctialis. IScience, 2022, 25, 104634.	1.9	4
1844	Discovery of eQTL Alleles Associated with Autism Spectrum Disorder: A Caseâ€"Control Study. Journal of Autism and Developmental Disorders, 0, , .	1.7	2
1845	Biology: Motion is Function. Function, 2022, 3, .	1.1	2
1846	The Awesome Power of Human Genetics of Infectious Disease. Annual Review of Genetics, 2022, 56, 41-62.	3.2	5
1847	Enhancer-promoter interaction maps provide insights into skeletal muscle-related traits in pig genome. BMC Biology, 2022, 20, .	1.7	13
1848	Graph pangenome captures missing heritability and empowers tomato breeding. Nature, 2022, 606, 527-534.	13.7	131
1849	<i>In Vitro</i>Insertional Mutagenesis Screen Identifies Novel Genes Driving Breast Cancer Metastasis. Molecular Cancer Research, 2022, 20, 1502-1515.	1.5	3
1851	3DFAACTS-SNP: using regulatory T cell-specific epigenomics data to uncover candidate mechanisms of type 1 diabetes (T1D) risk. Epigenetics and Chromatin, 2022, 15, .	1.8	2
1852	Single-cell Transcriptomics Reveals Dynamic Role of Smooth Muscle Cells and Enrichment of Immune Cell Subsets in Human Abdominal Aortic Aneurysms. Annals of Surgery, 2022, 276, 511-521.	2.1	11
1855	IGF1R and LOX Modules Are Related to Antler Growth Rate Revealed by Integrated Analyses of Genomics and Transcriptomics. Animals, 2022, 12, 1522.	1.0	0
1856	NRN1 Gene as a Potential Marker of Early-Onset Schizophrenia: Evidence from Genetic and Neuroimaging Approaches. International Journal of Molecular Sciences, 2022, 23, 7456.	1.8	2
1857	chromMAGMA: regulatory element-centric interrogation of risk variants. Life Science Alliance, 2022, 5, e202201446.	1.3	1
1859	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. Genes, 2022, 13, 1220.	1.0	0

#	Article	IF	Citations
1860	Translational impact of omics studies in alopecia areata: recent advances and future perspectives. Expert Review of Clinical Immunology, 2022, 18, 845-857.	1.3	2
1861	Pan-cancer proteomic map of 949 human cell lines. Cancer Cell, 2022, 40, 835-849.e8.	7.7	52
1862	Genetics of adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	37
1863	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. Nature Genetics, 2022, 54, 1133-1144.	9.4	31
1864	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. Cell Genomics, 2022, 2, 100145.	3.0	19
1865	Three laws of teleonometrics. Biological Journal of the Linnean Society, 2022, 137, 112-124.	0.7	1
1867	The â€œNew Synthesisâ€. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	27
1868	Challenges and potential solutions for studying the genetic and phenotypic architecture of adaptation in microbes. Current Opinion in Genetics and Development, 2022, 75, 101951.	1.5	7
1869	A polygenic score indexing a DRD2-related co-expression network is associated with striatal dopamine function. Scientific Reports, 2022, 12, .	1.6	4
1871	Aggregative trans-eQTL analysis detects trait-specific target gene sets in whole blood. Nature Communications, 2022, 13, .	5.8	7
1872	Complexity, Evolvability, and the Process of Adaptation. Annual Review of Ecology, Evolution, and Systematics, 2022, 53, 137-159.	3.8	6
1873	Genomic divergence of <i>Stellera chamaejasme</i> through local selection across the Qinghaiâ€"Tibet plateau and northern China. Molecular Ecology, 2022, 31, 4782-4796.	2.0	15
1874	The False Dawn of Polygenic Risk Scores for Human Disease Prediction. Journal of Personalized Medicine, 2022, 12, 1266.	1.1	6
1876	Toward Precision Medicine in ADHD. Frontiers in Behavioral Neuroscience, 0, 16, .	1.0	16
1877	Differentially Active and Conserved Neural Enhancers Define Two Forms of Adaptive Noncoding Evolution in Humans. Genome Biology and Evolution, 2022, 14, .	1.1	2
1878	Restlessness and an Increased Urge to Move (Drive for Activity) in Anorexia Nervosa May Strengthen Personal Motivation to Maintain Caloric Restriction and May Augment Body Awareness and Proprioception: A Lesson From Leptin Administration in Anorexia Nervosa. Frontiers in Psychology, 0, 13, .	1.1	4
1879	Genetic and environmental variation impact transferability of polygenic risk scores. Cell Reports Medicine, 2022, 3, 100687.	3.3	5
1880	Incomplete Penetrance and Variable Expressivity: From Clinical Studies to Population Cohorts. Frontiers in Genetics, 0, 13, .	1.1	67

#	Article	IF	Citations
1881	A Novel Penalized Inverse-Variance Weighted Estimator for Mendelian Randomization with Applications to COVID-19 Outcomes. Biometrics, 2023, 79, 2184-2195.	0.8	11
1882	Genetic identification of tissues and cell types underlying attention-deficit/hyperactivity disorder. Frontiers in Psychiatry, 0, 13, .	1.3	1
1883	Exploring Links Between Psychosis and Frontotemporal Dementia Using Multimodal Machine Learning. JAMA Psychiatry, 2022, 79, 907.	6.0	15
1884	Polygenic adaptation contributes to the invasive success of the Colorado potato beetle. Molecular Ecology, 0, , .	2.0	5
1885	Peripheral gene interactions define interpretable clusters of core ASD genes in a network-based investigation of the omnigenic theory. Npj Systems Biology and Applications, 2022, 8, .	1.4	1
1886	Caseâ€only design identifies interactions of genetic risk variants at <scp> <i>SIGLEC5</i> </scp> and <scp> <i>PLG</i> </scp> with the <scp>lncRNA CTDâ€2353F22</scp> .1 implying the importance of periodontal wound healing for disease aetiology. Journal of Clinical Periodontology, 0, , .	2.3	2
1888	Host association, environment, and geography underlie genomic differentiation in a major forest pest. Evolutionary Applications, 2022, 15, 1749-1765.	1.5	6
1889	Novel functional genomics approaches bridging neuroscience and psychiatry. Biological Psychiatry Global Open Science, 2022, , .	1.0	1
1890	eQTLs as causal instruments for the reconstruction of hormone linked gene networks. Frontiers in Endocrinology, 0, 13, .	1.5	1
1891	Linkage mapping reveals loci that underlie differences in <i>Caenorhabditis elegans</i> growth. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	3
1893	Information Theory as an Experimental Tool for Integrating Disparate Biophysical Signaling Modules. International Journal of Molecular Sciences, 2022, 23, 9580.	1.8	2
1894	Joint Consideration of Means and Variances Might Change the Understanding of Etiology. Perspectives on Psychological Science, 2023, 18, 416-427.	5.2	2
1895	Genetic heterogeneity: Challenges, impacts, and methods through an associative lens. Genetic Epidemiology, 2022, 46, 555-571.	0.6	12
1897	Functional regulatory variants implicate distinct transcriptional networks in dementia. Science, 2022, 377, .	6.0	49
1898	Polygenic autoimmune disease risk alleles impacting B cell tolerance act in concert across shared molecular networks in mouse and in humans. Frontiers in Immunology, 0, 13, .	2.2	5
1899	Genomic basis and phenotypic manifestation of (nonâ€)parallel serpentine adaptation in <i>Arabidopsis arenosa</i>. Evolution; International Journal of Organic Evolution, 2022, 76, 2315-2331.	1.1	2
1901	Genetic determinants of chromatin reveal prostate cancer risk mediated by context-dependent gene regulation. Nature Genetics, 2022, 54, 1364-1375.	9.4	19
1902	â€œltâ€™s completely erasureâ€: A Qualitative Exploration of Experiences of Transgender, Nonbinary, Gender Nonconforming, and Questioning Students in Biology Courses. CBE Life Sciences Education, 2022, 21, .	1.1	11

#	Article	IF	Citations
1903	Characterization of sequence determinants of enhancer function using natural genetic variation. ELife, 0, 11, .	2.8	7
1905	Accumulation and maintenance of information in evolution. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
1906	Using Polygenic Risk Scores Related to Complex Traits to Predict Production Performance in Cross-Breeding of Yeast. Journal of Fungi (Basel, Switzerland), 2022, 8, 914.	1.5	2
1908	Genome scanning of behavioral selection in a canine olfactory detection breeding cohort. Scientific Reports, 2022, 12, .	1.6	4
1909	Conditional GWAS of non-CG transposon methylation in Arabidopsis thaliana reveals major polymorphisms in five genes. PLoS Genetics, 2022, 18, e1010345.	1.5	14
1912	Polygenic adaptation after a sudden change in environment. ELife, 0, 11, .	2.8	30
1913	A quantile integral linear model to quantify genetic effects on phenotypic variability. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	7
1914	How dysregulation of the immune system promotes diabetes mellitus and cardiovascular risk complications. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	11
1915	Evolution and dysfunction of human cognitive and social traits: a transcriptional regulation perspective. Evolutionary Human Sciences, 0, , 1-47.	0.9	1
1916	Detecting associated genes for complex traits shared across East Asian and European populations under the framework of composite null hypothesis testing. Journal of Translational Medicine, 2022, 20, .	1.8	5
1917	How broad is the selfing syndrome? Insights from convergent evolution of gene expression across species and tissues in the <i>Capsella</i> genus. New Phytologist, 2022, 236, 2344-2357.	3.5	5
1918	Estimation of predictive performance in high-dimensional data settings using learning curves. Computational Statistics and Data Analysis, 2022, , 107622.	0.7	0
1922	A Patientâ€toâ€Modelâ€toâ€Patient (PMP) Cancer Drug Discovery Protocol for Identifying and Validating Therapeutic Agents Targeting Tumor Regulatory Architecture. Current Protocols, 2022, 2, .	1.3	0
1923	Differences and commonalities in the genetic architecture of protein quantitative trait loci in European and Arab populations. Human Molecular Genetics, 2023, 32, 907-916.	1.4	9
1924	MATS: a novel multi-ancestry transcriptome-wide association study to account for heterogeneity in the effects of cis-regulated gene expression on complex traits. Human Molecular Genetics, 2023, 32, 1237-1251.	1.4	3
1926	Incorporating kernelized multi-omics data improves the accuracy of genomic prediction. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	0
1929	Haplotype-specific chromatin looping reveals genetic interactions of regulatory regions modulating gene expression in 8p23.1. Frontiers in Genetics, 0, 13, .	1.1	3
1930	A guidance of model selection for genomic prediction based on linear mixed models for complex traits. Frontiers in Genetics, 0, 13, .	1.1	0

#	Article	IF	Citations
1931	Correlation scan: identifying genomic regions that affect genetic correlations applied to fertility traits. BMC Genomics, 2022, 23, .	1.2	1
1932	Low-coverage sequencing in a deep intercross of the Virginia body weight lines provides insight to the polygenic genetic architecture of growth: novel loci revealed by increased power and improved genome-coverage. Poultry Science, 2023, 102, 102203.	1.5	0
1933	Selection-driven adaptation to the extreme Antarctic environment in the Emperor penguin. Heredity, 2022, 129, 317-326.	1.2	5
1935	Anthropometric characteristics according to the role performed by World Tour road cyclists for their team. European Journal of Sport Science, 2023, 23, 1821-1828.	1.4	0
1937	Genetic susceptibility to autoimmunityâ€"Current status and challenges. Advances in Immunology, 2022, , 25-54.	1.1	2
1938	A transcriptome-wide association study provides new insights into the etiology of osteoarthritis. Annals of Translational Medicine, 2022, 10, 1116-1116.	0.7	3
1940	â€œMendelian Codeâ€•in the Genetic Structure of Common Multifactorial Diseases. Russian Journal of Genetics, 2022, 58, 1159-1168.	0.2	2
1941	Evolutionary Origins of Metabolic Reprogramming in Cancer. International Journal of Molecular Sciences, 2022, 23, 12063.	1.8	0
1942	Lessons Learned From Parsing Genetic Risk for Schizophrenia Into Biological Pathways. Biological Psychiatry, 2023, 94, 121-130.	0.7	8
1943	Redundancy analysis, genomeâ€wide association studies and the pigmentation of brown trout (<i>Salmo) Tj ETQq1 1 0.784314 rgBT /	0.7	5
1945	Open problems in mathematical biology. Mathematical Biosciences, 2022, 354, 108926.	0.9	9
1946	Defining the extent of gene function using ROC curvature. Bioinformatics, 0, , .	1.8	1
1948	Mapping the genetic architecture of cortical morphology through neuroimaging: progress and perspectives. Translational Psychiatry, 2022, 12, .	2.4	10
1949	Common microgeographical selection patterns revealed in four European conifers. Molecular Ecology, 2023, 32, 393-411.	2.0	9
1950	<i>Gattaca</i> as a lens on contemporary genetics: marking 25 years into the filmâ€™s â€œnot-too-distantâ€• future. Genetics, 2022, 222, .	1.2	3
1952	A possible genomic footprint of polygenic adaptation on population divergence in seed beetles?. Ecology and Evolution, 2022, 12, .	0.8	3
1953	SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification. Nature Communications, 2022, 13, .	5.8	6
1954	Constructing an atlas of associations between polygenic scores from across the human phenome and circulating metabolic biomarkers. ELife, 0, 11, .	2.8	10

#	Article	IF	Citations
1956	GIFT: new method for the genetic analysis of small gene effects involving small sample sizes. Physical Biology, 2023, 20, 016001.	0.8	0
1957	Socioeconomic resources are associated with distributed alterations of the brainâ€™s intrinsic functional architecture in youth. Developmental Cognitive Neuroscience, 2022, 58, 101164.	1.9	6
1958	Chicken chromatin accessibility atlas accelerates epigenetic annotation of birds and gene fine-mapping associated with growth traits. Zoological Research, 2023, 44, 53-62.	0.9	5
1959	Measurement and meaning in gene expression evolution. , 2023, , 111-129.		2
1960	Mosaic patterns of selection in genomic regions associated with diverse human traits. PLoS Genetics, 2022, 18, e1010494.	1.5	1
1961	Genetic architecture of natural variation of cardiac performance from flies to humans. ELife, 0, 11, .	2.8	5
1962	Polyunsaturated Fatty Acids Mend Macrophage Transcriptome, Glycome, and Phenotype in the Patients with Neurodegenerative Diseases, Including Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2023, 91, 245-261.	1.2	1
1963	Dissecting the loci underlying maturation timing in Atlantic salmon using haplotype and multi-SNP based association methods. Heredity, 2022, 129, 356-365.	1.2	4
1966	Preliminary studies on apparent mendelian psychotic disorders in consanguineous families. BMC Psychiatry, 2022, 22, .	1.1	1
1967	Identification of genetic loci that overlap between schizophrenia and metabolic syndrome. Psychiatry Research, 2022, 318, 114947.	1.7	1
1968	Biomedical knowledge graph embeddings for personalized medicine: Predicting diseaseâ€gene associations. Expert Systems, 2023, 40, .	2.9	5
1969	Identifying Genetic Loci Associated with Complex Trait Variability. Springer Handbooks of Computational Statistics, 2022, , 257-270.	0.2	0
1970	Investigating the morphology and genetics of scalp and facial hair characteristics for phenotype prediction. Science and Justice - Journal of the Forensic Science Society, 2023, 63, 135-148.	1.3	4
1971	Causal analysis of plasma IL-8 on carotid intima media thickness, a measure of subclinical atherosclerosis. Current Research in Translational Medicine, 2023, 71, 103374.	1.2	0
1972	Moving beyond the adaptationist paradigm for human evolution, and why it matters. Journal of Human Evolution, 2023, 174, 103296.	1.3	5
1973	Association of polymorphisms in the catalase gene with the susceptibility to noise-induced hearing loss: A meta-analysis. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 2023, 44, 103699.	0.6	2
1975	Lineage and hybridization effects on size potential in the Largemouth Bass complex. Transactions of the American Fisheries Society, 2023, 152, 145-168.	0.6	2
1977	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, .	1.6	3

#	ARTICLE	IF	CITATIONS
1978	SNRMPACDC: computational model focused on Siamese network and random matrix projection for anticancer synergistic drug combination prediction. Briefings in Bioinformatics, 2023, 24, .	3.2	18
1979	GhostKnockoff inference empowers identification of putative causal variants in genome-wide association studies. Nature Communications, 2022, 13, .	5.8	1
1980	The Power and Perils of De Novo Domestication Using Genome Editing. Annual Review of Plant Biology, 2023, 74, 727-750.	8.6	10
1981	Multi-omics peripheral and core regions of cancer. Npj Systems Biology and Applications, 2022, 8, .	1.4	1
1982	Humanising and dehumanising pigs in genomic and transplantation research. History and Philosophy of the Life Sciences, 2022, 44, .	0.6	7
1983	Increasing plant group productivity through latent genetic variation for cooperation. PLoS Biology, 2022, 20, e3001842.	2.6	12
1985	Unravelling the genetics of non-random fertilization associated with gametic incompatibility. Scientific Reports, 2022, 12, .	1.6	1
1987	Protein-to-protein interaction of genes responsible for the economic trait of Madura Cattle: an in silico analysis. IOP Conference Series: Earth and Environmental Science, 2022, 1114, 012084.	0.2	0
1989	NetMix2: A Principled Network Propagation Algorithm for Identifying Altered Subnetworks. Journal of Computational Biology, 2022, 29, 1305-1323.	0.8	0
1990	Pleiotropic fitness effects of a <i>Drosophila</i> odorant-binding protein. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	0
1991	Taking quantitative genomics into the wild. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	1.2	5
1992	Plant Transcriptomics: Data-driven Global Approach to Understand Cellular Processes and Their Regulation in Model and Non-Model Plants. , 2022, , 10-29.		0
1993	Genomic correlates for migratory direction in a free-ranging cervid. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	1.2	0
1994	The collective effects of genetic variants and complex traits. Journal of Human Genetics, 2023, 68, 255-262.	1.1	2
1995	A multidimensional approach to understanding the emergence of sex differences in internalizing symptoms in adolescence. Developmental Cognitive Neuroscience, 2022, 58, 101182.	1.9	2
1996	Towards evolutionary predictions: Current promises and challenges. Evolutionary Applications, 2023, 16, 3-21.	1.5	19
1997	Long-range regulatory effects of Neandertal DNA in modern humans. Genetics, 0, , .	1.2	0
1998	Common protein-coding variants influence the racing phenotype in galloping racehorse breeds. Communications Biology, 2022, 5, .	2.0	4

#	ARTICLE	IF	CITATIONS
1999	The evolutionary tuning of hearing. Trends in Neurosciences, 2023, 46, 110-123.	4.2	2
2000	Genome-wide association studies of cardiovascular disease. Physiological Reviews, 2023, 103, 2039-2055.	13.1	13
2001	Probabilistic integration of transcriptome-wide association studies and colocalization analysis identifies key molecular pathways of complex traits. American Journal of Human Genetics, 2023, 110, 44-57.	2.6	5
2002	Multi-omic association study identifies DNA methylation-mediated genotype and smoking exposure effects on lung function in children living in urban settings. PLoS Genetics, 2023, 19, e1010594.	1.5	2
2007	Shifting Paradigm from Gene Expressions to Pathways Reveals Physiological Mechanisms in Blood Pressure Control in Causation. International Journal of Molecular Sciences, 2023, 24, 1262.	1.8	0
2008	Constrained neuro fuzzy inference methodology for explainable personalised modelling with applications on gene expression data. Scientific Reports, 2023, 13, .	1.6	1
2010	A Unified Mediation Analysis Framework for Integrative Cancer Proteogenomics with Clinical Outcomes. Bioinformatics, 0, , .	1.8	0
2011	Genetic architecture of terpene chemistry and growth traits and the impact of inbreeding on these traits in western redcedar (<i>Thuja plicata</i>). Evolutionary Applications, 2023, 16, 673-687.	1.5	2
2012	Cellular Competency during Development Alters Evolutionary Dynamics in an Artificial Embryogeny Model. Entropy, 2023, 25, 131.	1.1	5
2014	Single-cell omics: A new direction for functional genetic research in human diseases and animal models. Frontiers in Genetics, 0, 13, .	1.1	9
2015	Genome-wide imputed differential expression enrichment analysis identifies trait-relevant tissues. Frontiers in Genetics, 0, 13, .	1.1	1
2016	Micro and macroevolution of sea anemone venom phenotype. Nature Communications, 2023, 14, .	5.8	10
2017	Natural selection of immune and metabolic genes associated with health in two lowland Bolivian populations. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	8
2019	Sparse canonical correlation to identify breast cancer related genes regulated by copy number aberrations. PLoS ONE, 2022, 17, e0276886.	1.1	1
2020	An Alzheimerâ€™s disease gene prediction method based on ensemble of genome-wide association study summary statistics. , 2022, , .		1
2022	Systems Biology Approaches to the Genetic Complexity of Epilepsy. , 2022, , 5-18.		0
2023	Leveraging pleiotropy to discover and interpret GWAS results for sleep-associated traits. PLoS Genetics, 2022, 18, e1010557.	1.5	4
2024	Paving the way towards futureâ€proofing our crops. Food and Energy Security, 2023, 12, .	2.0	4

#	Article	IF	Citations
2025	351. Quantitative trait simulation using MeSCoT software. , 2022, , .		0
2027	Epigenomic charting and functional annotation of risk loci in renal cell carcinoma. Nature Communications, 2023, 14, .	5.8	10
2029	A Single Nucleotide Variant in the PPARÎ³-homolog <i>Eip75B</i> Affects Fecundity in <i>Drosophila</i>. Molecular Biology and Evolution, 2023, 40, .	3.5	5
2031	Using epigenomics to understand cellular responses to environmental influences in diseases. PLoS Genetics, 2023, 19, e1010567.	1.5	3
2033	Mechanism of Tao Hong Decoction in the treatment of atherosclerosis based on network pharmacology and experimental validation. Frontiers in Cardiovascular Medicine, 0, 10, .	1.1	0
2034	Celebrating a Century of Research in Behavioral Genetics. Behavior Genetics, 2023, 53, 75-84.	1.4	2
2037	LAVAA: a lightweight association viewer across ailments. Bioinformatics Advances, 2023, 3, .	0.9	0
2038	Polygenic adaptation from standing genetic variation allows rapid ecotype formation. ELife, 0, 12, .	2.8	4
2039	Genome-wide association study identifies 12 new genetic loci associated with growth traits in pigs. Journal of Integrative Agriculture, 2024, 23, 217-227.	1.7	1
2040	Host genetic traits underlying the composition/assembly of the citrus microbiome. Phytobiomes Journal, 0, , .	1.4	0
2041	Genetic outline of the hermeneutics of the diseases connection phenomenon in human. Vavilovskii Zhurnal Genetiki I Selektsii, 2023, 27, 7-17.	0.4	0
2043	The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits. Cell Metabolism, 2023, 35, 695-710.e6.	7.2	29
2044	Nutrigenomics in the context of evolution. Redox Biology, 2023, 62, 102656.	3.9	3
2045	Digenic genotypes: The interface of inbreeding, linkage, and linkage disequilibrium. Theoretical Population Biology, 2023, 151, 1-18.	0.5	1
2046	Future prospects for human genetics and genomics in drug discovery. Current Opinion in Structural Biology, 2023, 80, 102568.	2.6	3
2047	Moving beyond heritability in the search for coral adaptive potential. Global Change Biology, 2023, 29, 3869-3882.	4.2	0
2049	Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity. IScience, 2023, 26, 106024.	1.9	6
2050	NSPA: characterizing the disease association of multiple genetic interactions at single-subject resolution. Bioinformatics Advances, 2023, 3, .	0.9	0

#	Article	IF	Citations
2052	Polygenic architecture of rare coding variation across 394,783 exomes. Nature, 2023, 614, 492-499.	13.7	46
2053	Plant water use theory should incorporate hypotheses about extreme environments, population ecology, and community ecology. New Phytologist, 2023, 238, 2271-2283.	3.5	9
2055	596. Chicken quantitative traits follow the omnigenic model. , 2022, , .		0
2056	Predicting the prevalence of complex genetic diseases from individual genotype profiles using capsule networks. Nature Machine Intelligence, 2023, 5, 114-125.	8.3	3
2057	Nonparallel genome changes within subpopulations over time contributed to genetic diversity within the US Holstein population. Journal of Dairy Science, 2023, 106, 2551-2572.	1.4	2
2060	Pathogenesis of systemic lupus erythematosus: risks, mechanisms and therapeutic targets. Annals of the Rheumatic Diseases, 2023, 82, 999-1014.	0.5	37
2062	Mendelian inheritance revisited: dominance and recessiveness in medical genetics. Nature Reviews Genetics, 2023, 24, 442-463.	7.7	16
2064	Network expansion of genetic associations defines a pleiotropy map of human cell biology. Nature Genetics, 2023, 55, 389-398.	9.4	19
2067	Unified views on variant impact across many diseases. Trends in Genetics, 2023, 39, 442-450.	2.9	3
2068	An autoimmune pleiotropic SNP modulates IRF5 alternative promoter usage through ZBTB3-mediated chromatin looping. Nature Communications, 2023, 14, .	5.8	6
2069	The genetic architecture of behavioral canalization. Trends in Genetics, 2023, 39, 602-608.	2.9	0
2072	Thereâ€™s Plenty of Room Right Here: Biological Systems as Evolved, Overloaded, Multi-Scale Machines. Biomimetics, 2023, 8, 110.	1.5	10
2073	Editorial: Harnessing genebanks: High-throughput phenotyping and genotyping of crop wild relatives and landraces. Frontiers in Plant Science, 0, 14, .	1.7	4
2074	Abnormal features of human selfâ€domestication in bipolar disorder. European Journal of Neuroscience, 2023, 57, 1406-1431.	1.2	0
2076	Unlocking the genome of perch â€“ From genes to ecology and back again. Ecology of Freshwater Fish, 2023, 32, 677-702.	0.7	3
2078	Models based on best-available information support a low inbreeding load and potential for recovery in the vaquita. Heredity, 2023, 130, 183-187.	1.2	2
2079	Complexities of recapitulating polygenic effects in natural populations: replication of genetic effects on wing shape in artificially selected and wild-caught populations of <i>Drosophila melanogaster</i>. Genetics, 2023, 224, .	1.2	2
2080	Gene-environment interaction explains a part of missing heritability in human body mass index. Communications Biology, 2023, 6, .	2.0	2

#	Article	IF	Citations
2082	The Creativity of Natural Selection and the Creativity of Organisms: Their Roles in Traditional Evolutionary Theory and Some Proposed Extensions. Evolutionary Biology, 2023, , 65-107.	0.6	0
2083	Population Genomics of Eucalypts. Population Genomics, 2023, , .	0.2	0
2084	Epigenetics as a mediator of genetic risk in osteoarthritis: role during development, homeostasis, aging, and disease progression. American Journal of Physiology - Cell Physiology, 2023, 324, C1078-C1088.	2.1	5
2085	Characterization of grain carotenoids in global sorghum germplasm to guide genomics-assisted breeding strategies. BMC Plant Biology, 2023, 23, .	1.6	1
2086	Gradualism, natural selection, and the randomness of mutationâ€"fisher, Kimura, and Orr, connecting the dots. Biology and Philosophy, 2023, 38, .	0.7	1
2088	The potential of integrating human and mouse discovery platforms to advance our understanding of cardiometabolic diseases. ELife, 0, 12, .	2.8	3
2089	Predicting ExWAS findings from GWAS data: a shorter path to causal genes. Human Genetics, 2023, 142, 749-758.	1.8	3
2090	FHL5 Controls Vascular Diseaseâ€"Associated Gene Programs in Smooth Muscle Cells. Circulation Research, 2023, 132, 1144-1161.	2.0	5
2091	Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. Nature Genetics, 2023, 55, 841-851.	9.4	23
2092	Amplification is the primary mode of gene-by-sex interaction in complex human traits. Cell Genomics, 2023, 3, 100297.	3.0	14
2093	Amyotrophic lateral sclerosis: translating genetic discoveries into therapies. Nature Reviews Genetics, 2023, 24, 642-658.	7.7	30
2094	Crossing the Threshold: An Epigenetic Alternative to Dimensional Accounts of Mental Disorders. British Journal for the Philosophy of Science, 0, , .	1.4	1
2095	Esearch3D: propagating gene expression in chromatin networks to illuminate active enhancers. Nucleic Acids Research, 0, , .	6.5	1
2096	Developing the genotypeâ€toâ€phenotype relationship in evolutionary theory: A primer of developmental features. Evolution & Development, 2023, 25, 393-409.	1.1	3
2097	Whole-exome sequencing study of hypospadias. IScience, 2023, 26, 106663.	1.9	2
2098	Consensus molecular environment of schizophrenia risk genes in coexpression networks shifting across age and brain regions. Science Advances, 2023, 9, .	4.7	5
2099	Genome-wide CRISPR screening of chondrocyte maturation newly implicates genes in skeletal growth and height-associated GWAS loci. Cell Genomics, 2023, 3, 100299.	3.0	3
2100	Single-cell genomics meets human genetics. Nature Reviews Genetics, 2023, 24, 535-549.	7.7	18

#	ARTICLE	IF	CITATIONS
2101	Genes, environments, and epigenetics. , 2023, , 181-200.		0
2116	Darwinâ€™s agential materials: evolutionary implications of multiscale competency in developmental biology. Cellular and Molecular Life Sciences, 2023, 80, .	2.4	9
2123	Genes, environments, and epigenetics. , 2023, , 207-223.		0
2169	Experimental precision medicine: Mouse models to test precision medicine. , 2024, , 382-399.		0
2197	Genetic modification can improve crop yields â€" but stop overselling it. Nature, 2023, 621, 470-473.	13.7	10
2216	Predicting Gene Regulatory Interactions Using Natural Genetic Variation. Methods in Molecular Biology, 2023, , 301-322.	0.4	0
2238	The power paradox of detecting disease-associated and gene-expression-associated variants. Nature Genetics, 0, , .	9.4	0
2263	Gene Regulatory Networks in Coronary Artery Disease. Current Atherosclerosis Reports, 0, , .	2.0	0
2268	A Historical Perspective on the Development of Models of Rhythm in the Heart. , 2023, , 27-42.		0
2284	Beyond the factor indeterminacy problem using genome-wide association data. Nature Human Behaviour, 2024, 8, 205-218.	6.2	0
2303	Genetic architecture and biology of youth-onset type 2 diabetes. Nature Metabolism, 2024, 6, 226-237.	5.1	1
2315	Translational bioinformatics approach to combat cardiovascular disease and cancers. Advances in Protein Chemistry and Structural Biology, 2024, , 221-261.	1.0	1
2320	Predicting Cell Line-Specific Synergistic Drug Combinations Through Siamese Network with Attention Mechanism. Communications in Computer and Information Science, 2024, , 87-95.	0.4	0