Hongyu Zhao

List of Publications by Year
in descending order

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254	15,461	22132	27389
papers	citations	59 h-index	106 g-index

290	290	290	24812
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Clustering High-Dimensional Data via Feature Selection. Biometrics, 2023, 79, 940-950.	0.8	5
2	Posttraumatic Stress Disorder Brain Transcriptomics: Convergent Genomic Signatures Across Biological Sex. Biological Psychiatry, 2022, 91, 6-13.	0.7	6
3	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. Biological Psychiatry, 2022, 91, 626-636.	0.7	21
4	A Manifold Proximal Linear Method for Sparse Spectral Clustering with Application to Single-Cell RNA Sequencing Data Analysis. INFORMS Journal on Optimization, 2022, 4, 200-214.	0.9	3
5	Deep Learning of the Retina Enables Phenome- and Genome-Wide Analyses of the Microvasculature. Circulation, 2022, 145, 134-150.	1.6	57
6	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. Nature Communications, 2022, 13, 440.	5.8	100
7	Characterizing Spatiotemporal Transcriptome of the Human Brain Via Low-Rank Tensor Decomposition. Statistics in Biosciences, 2022, 14, 485-513.	0.6	3
8	Photoreceptor Layer Thinning Is an Early Biomarker for Age-Related Macular Degeneration. Ophthalmology, 2022, 129, 694-707.	2.5	21
9	Low depression frequency is associated with decreased risk of cardiometabolic disease. , 2022, 1, 125-131.		8
10	Fibrillar Collagen Variants in Spontaneous Coronary Artery Dissection. JAMA Cardiology, 2022, 7, 396.	3.0	19
11	Non-linear archetypal analysis of single-cell RNA-seq data by deep autoencoders. PLoS Computational Biology, 2022, 18, e1010025.	1.5	7
12	Whole-exome sequencing reveals damaging gene variants associated with hypoalphalipoproteinemia. Journal of Lipid Research, 2022, 63, 100209.	2.0	2
13	Leveraging LD eigenvalue regression to improve the estimation of SNP heritability and confounding inflation. American Journal of Human Genetics, 2022, 109, 802-811.	2.6	12
14	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010113.	1.5	16
15	Incorporating local ancestry improves identification of ancestry-associated methylation signatures and meQTLs in African Americans. Communications Biology, 2022, 5, 401.	2.0	3
16	A Markov random field model-based approach for differentially expressed gene detection from single-cell RNA-seq data. Briefings in Bioinformatics, 2022, 23, .	3.2	3
17	Healthy lifestyle counteracts the risk effect of genetic factors on incident gout: a large population-based longitudinal study. BMC Medicine, 2022, 20, 138.	2.3	12
18	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	1.5	12

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19	SCADIE: simultaneous estimation of cell type proportions and cell type-specific gene expressions using SCAD-based iterative estimating procedure. Genome Biology, 2022, 23, .	3.8	4
20	Hemodynamic differences between women and men with elevated blood pressure in China: A non-invasive assessment of 45,082 adults using impedance cardiography. PLoS ONE, 2022, 17, e0269777.	1.1	4
21	Network assisted analysis of de novo variants using protein-protein interaction information identified 46 candidate genes for congenital heart disease. PLoS Genetics, 2022, 18, e1010252.	1.5	3
22	ResPAN: a powerful batch correction model for scRNA-seq data through residual adversarial networks. Bioinformatics, 2022, 38, 3942-3949.	1.8	4
23	Mendelian randomization for causal inference accounting for pleiotropy and sample structure using genome-wide summary statistics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	32
24	Integrating Multidimensional Data for Clustering Analysis With Applications to Cancer Patient Data. Journal of the American Statistical Association, 2021, 116, 14-26.	1.8	7
25	TLR9 Deficiency in B Cells Promotes Immune Tolerance via Interleukin-10 in a Type 1 Diabetes Mouse Model. Diabetes, 2021, 70, 504-515.	0.3	8
26	Overview of PAX gene family: analysis of human tissue-specific variant expression and involvement in human disease. Human Genetics, 2021, 140, 381-400.	1.8	25
27	A pooled genome-wide association study identifies pancreatic cancer susceptibility loci on chromosome 19p12 and 19p13.3 in the full-Jewish population. Human Genetics, 2021, 140, 309-319.	1.8	2
28	Elevated Blood Pressure Increases Pneumonia Risk: Epidemiological Association and Mendelian Randomization in the UK Biobank. Med, 2021, 2, 137-148.e4.	2.2	21
29	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. Schizophrenia Bulletin, 2021, 47, 517-529.	2.3	48
30	Transcriptomic organization of the human brain in post-traumatic stress disorder. Nature Neuroscience, 2021, 24, 24-33.	7.1	106
31	The role of the gut microbiome in cancer-related fatigue: pilot study on epigenetic mechanisms. Supportive Care in Cancer, 2021, 29, 3173-3182.	1.0	26
32	A comprehensive genetic and epidemiological association analysis of vitamin D with common diseases/traits in the UK Biobank. Genetic Epidemiology, 2021, 45, 24-35.	0.6	24
33	Cortical Transcriptomic Alterations in Association With Appetitive Neuropeptides and Body Mass Index in Posttraumatic Stress Disorder. International Journal of Neuropsychopharmacology, 2021, 24, 118-129.	1.0	7
34	A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. American Statistician, 2021, 75, 310-322.	0.9	15
35	Cytokine Profiles Before and After Immune Modulation in Hospitalized Patients with COVID-19. Journal of Clinical Immunology, 2021, 41, 738-747.	2.0	18
36	Toll-like receptor 7 deficiency suppresses type 1 diabetes development by modulating B-cell differentiation and function. Cellular and Molecular Immunology, 2021, 18, 328-338.	4.8	13

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37	Comparison of methods for estimating genetic correlation between complex traits using GWAS summary statistics. Briefings in Bioinformatics, 2021, 22, .	3.2	24
38	Interactions Between Enhanced Polygenic Risk Scores and Lifestyle for Cardiovascular Disease, Diabetes, and Lipid Levels. Circulation Genomic and Precision Medicine, 2021, 14, e003128.	1.6	61
39	RePhine: An Integrative Method for Identification of Drug Response-related Transcriptional Regulators. Genomics, Proteomics and Bioinformatics, 2021, 19, 534-548.	3.0	5
40	Polygenic risk score, healthy lifestyles, and risk of incident depression. Translational Psychiatry, 2021, 11, 189.	2.4	22
41	Identifying modules of cooperating cancer drivers. Molecular Systems Biology, 2021, 17, e9810.	3.2	13
42	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits. American Journal of Human Genetics, 2021, 108, 632-655.	2.6	73
43	Epigenetic age acceleration, fatigue, and inflammation in patients undergoing radiation therapy for head and neck cancer: A longitudinal study. Cancer, 2021, 127, 3361-3371.	2.0	28
44	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. Nature Communications, 2021, 12, 2878.	5.8	25
45	The impact of removing former drinkers from genomeâ€wide association studies of AUDITâ€€. Addiction, 2021, 116, 3044-3054.	1.7	11
46	Genomics of Gulf War Illness in U.S. Veterans Who Served during the 1990â€“1991 Persian Gulf War: Methods and Rationale for Veterans Affairs Cooperative Study #2006. Brain Sciences, 2021, 11, 845.	1.1	7
47	Correlating genomic copy number alterations with clinicopathologic findings in 75 cases of hepatocellular carcinoma. BMC Medical Genomics, 2021, 14, 150.	0.7	5
48	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
49	A fast and robust Bayesian nonparametric method for prediction of complex traits using summary statistics. PLoS Genetics, 2021, 17, e1009697.	1.5	34
50	DIAPH1 Variants in Nonâ€“East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993.	4.5	33
51	Association of Epigenetic Age Acceleration With Risk Factors, Survival, and Quality of Life in Patients With Head and Neck Cancer. International Journal of Radiation Oncology Biology Physics, 2021, 111, 157-167.	0.4	18
52	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. Genome Biology, 2021, 22, 262.	3.8	56
53	Calculating Orthologous Protein-Coding Sequence Set Probability Using the Poisson Process. Journal of Computational Biology, 2021, 28, 961-974.	0.8	0
54	A reservoir of stem-like CD8 ⁺ T cells in the tumor-draining lymph node preserves the ongoing antitumor immune response. Science Immunology, 2021, 6, eabg7836.	5.6	123

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55	Integrative modeling of transmitted and de novo variants identifies novel risk genes for congenital heart disease. Quantitative Biology, 2021, 9, 216-227.	0.3	4
56	Genome-wide association analyses of post-traumatic stress disorder and its symptom subdomains in the Million Veteran Program. Nature Genetics, 2021, 53, 174-184.	9.4	121
57	CD4+ follicular regulatory T cells optimize the influenza virusâ€“specific B cell response. Journal of Experimental Medicine, 2021, 218, .	4.2	30
58	Circadian Rhythm Analysis Using Wearable Device Data: Novel Penalized Machine Learning Approach. Journal of Medical Internet Research, 2021, 23, e18403.	2.1	5
59	A Markov random field model for network-based differential expression analysis of single-cell RNA-seq data. BMC Bioinformatics, 2021, 22, 524.	1.2	5
60	M-DATA: A statistical approach to jointly analyzing de novo mutations for multiple traits. PLoS Genetics, 2021, 17, e1009849.	1.5	4
61	Neoantigen-driven B cell and CD4ÂT follicular helper cell collaboration promotes anti-tumor CD8 TÂcell responses. Cell, 2021, 184, 6101-6118.e13.	13.5	192
62	Hemodynamic Phenotypes of Hypertension Based on Cardiac Output and Systemic Vascular Resistance. American Journal of Medicine, 2020, 133, e127-e139.	0.6	14
63	NITUMID: Nonnegative matrix factorization-based Immune-TUmor MIcroenvironment Deconvolution. Bioinformatics, 2020, 36, 1344-1350.	1.8	19
64	Genomeâ€wide association study of cognitive performance in U.S. veterans with schizophrenia or bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 181-194.	1.1	17
65	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. Sleep, 2020, 43, .	0.6	32
66	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nature Genetics, 2020, 52, 1046-1056.	9.4	96
67	Automated feature extraction from population wearable device data identified novel loci associated with sleep and circadian rhythms. PLoS Genetics, 2020, 16, e1009089.	1.5	13
68	Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. Nature Communications, 2020, 11, 5302.	5.8	59
69	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
70	Androgen Signaling Regulates SARS-CoV-2 Receptor Levels and Is Associated with Severe COVID-19 Symptoms in Men. Cell Stem Cell, 2020, 27, 876-889.e12.	5.2	167
71	An enhanced machine learning tool for cis â€eQTL mapping with regularization and confounder adjustments. Genetic Epidemiology, 2020, 44, 798-810.	0.6	0
72	Gut Microbiome Associated with the Psychoneurological Symptom Cluster in Patients with Head and Neck Cancers. Cancers, 2020, 12, 2531.	1.7	27

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73	Differential Protein Expression in Striatal D1- and D2-Dopamine Receptor-Expressing Medium Spiny Neurons. Proteomes, 2020, 8, 27.	1.7	6
74	Elevated serum interleukin-8 is associated with enhanced intratumor neutrophils and reduced clinical benefit of immune-checkpoint inhibitors. Nature Medicine, 2020, 26, 688-692.	15.2	296
75	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. Nature Communications, 2020, 11, 2438.	5.8	52
76	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. Nature Genetics, 2020, 52, 680-691.	9.4	445
77	Reducing False-Positive Results in Newborn Screening Using Machine Learning. International Journal of Neonatal Screening, 2020, 6, 16.	1.2	33
78	Relationship of Age With the Hemodynamic Parameters in Individuals With Elevated Blood Pressure. Journal of the American Geriatrics Society, 2020, 68, 1520-1528.	1.3	7
79	Genomic influences on self-reported childhood maltreatment. Translational Psychiatry, 2020, 10, 38.	2.4	47
80	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. PLoS Computational Biology, 2020, 16, e1007565.	1.5	32
81	Statistical Methods in Genome-Wide Association Studies. Annual Review of Biomedical Data Science, 2020, 3, 265-288.	2.8	6
82	A novel machine learning unsupervised algorithm for sleep/wake identification using actigraphy. Chronobiology International, 2020, 37, 1002-1015.	0.9	34
83	Ethnic variability in newborn metabolic screening markers associated with falseâ€positive outcomes. Journal of Inherited Metabolic Disease, 2020, 43, 934-943.	1.7	23
84	Pilot study of combined aerobic and resistance exercise on fatigue for patients with head and neck cancer: Inflammatory and epigenetic changes. Brain, Behavior, and Immunity, 2020, 88, 184-192.	2.0	11
85	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	2.6	118
86	Timing of Newborn Blood Collection Alters Metabolic Disease Screening Performance. Frontiers in Pediatrics, 2020, 8, 623184.	0.9	14
87	Leveraging functional annotation to identify genes associated with complex diseases. PLoS Computational Biology, 2020, 16, e1008315.	1.5	16
88	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0
89	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0
90	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0

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91	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0
92	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0
93	Leveraging functional annotation to identify genes associated with complex diseases. , 2020, 16, e1008315.		0
94	International variations in trust in health care systems. International Journal of Health Planning and Management, 2019, 34, 130-139.	0.7	25
95	Next-generation sequencing in liquid biopsy: cancer screening and early detection. Human Genomics, 2019, 13, 34.	1.4	302
96	Expression of the type 3 InsP₃receptor is a final common event in the development of hepatocellular carcinoma. Gut, 2019, 68, 1676-1687.	6.1	56
97	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401.	7.1	145
98	Joint Models for Time-to-Event Data and Longitudinal Biomarkers of High Dimension. Statistics in Biosciences, 2019, 11, 614-629.	0.6	3
99	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	5.8	363
100	Benchmarking variant identification tools for plant diversity discovery. BMC Genomics, 2019, 20, 701.	1.2	20
101	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. American Journal of Human Genetics, 2019, 105, 763-772.	2.6	169
102	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
103	Genetic Link Between Arterial Stiffness and Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2019, 12, e002453.	1.6	11
104	Genetic Association of Finger Photoplethysmography-Derived Arterial Stiffness Index With Blood Pressure and Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1253-1261.	1.1	35
105	Validation of an Electronic Medical Recordâ€"Based Algorithm for Identifying Posttraumatic Stress Disorder in U.S. Veterans. Journal of Traumatic Stress, 2019, 32, 226-237.	1.0	30
106	Genome-wide Association Study of Maximum Habitual Alcohol Intake in >140,000 U.S. European and African American Veterans Yields Novel Risk Loci. Biological Psychiatry, 2019, 86, 365-376.	0.7	82
107	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. Lancet Respiratory Medicine,the, 2019, 7, 497-508.	5.2	168
108	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. Nature Communications, 2019, 10, 1499.	5.8	346

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109	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	9.4	262
110	LCox: a tool for selecting genes related to survival outcomes using longitudinal gene expression data. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.2	0
111	Genomics of posttraumatic stress disorder in veterans: Methods and rationale for <scp>V</scp>eterans <scp>A</scp>ffairs <scp>C</scp>ooperative <scp>S</scp>tudy #575B. International Journal of Methods in Psychiatric Research, 2019, 28, e1767.	1.1	5
112	Retrospective Association Analysis of Longitudinal Binary Traits Identifies Important Loci and Pathways in Cocaine Use. Genetics, 2019, 213, 1225-1236.	1.2	13
113	Genomic analysis of a spinal muscular atrophy (SMA) discordant family identifies a novel mutation in TLL2, an activator of growth differentiation factor 8 (myostatin): a case report. BMC Medical Genetics, 2019, 20, 204.	2.1	8
114	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	1.1	31
115	Understanding the determinants of public trust in the health care system in China: an analysis of a cross-sectional survey. Journal of Health Services Research and Policy, 2019, 24, 37-43.	0.8	22
116	Regularized Latent Class Model for Joint Analysis of High-Dimensional Longitudinal Biomarkers and a Time-to-Event Outcome. Biometrics, 2019, 75, 69-77.	0.8	7
117	Elevated methylmalonic acidemia (MMA) screening markers in Hispanic and preterm newborns. Molecular Genetics and Metabolism, 2019, 126, 39-42.	0.5	6
118	ProteomicsBrowser: MS/proteomics data visualization and investigation. Bioinformatics, 2019, 35, 2313-2314.	1.8	2
119	Using DNA methylation to validate an electronic medical record phenotype for smoking. Addiction Biology, 2019, 24, 1056-1065.	1.4	11
120	Trends in the Prevalence of Overweight and Obesity among Chinese School-Age Children and Adolescents from 2010 to 2015. Childhood Obesity, 2018, 14, 182-188.	0.8	21
121	Distance-correlation based gene set analysis in longitudinal studies. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.2	0
122	Spectral clustering based on learning similarity matrix. Bioinformatics, 2018, 34, 2069-2076.	1.8	96
123	Loneliness 5 years ante-mortem is associated with disease-related differential gene expression in postmortem dorsolateral prefrontal cortex. Translational Psychiatry, 2018, 8, 2.	2.4	25
124	Improving SNP prioritization and pleiotropic architecture estimation by incorporating prior knowledge using graph-GPA. Bioinformatics, 2018, 34, 2139-2141.	1.8	6
125	Uncovering Genomic Regions Associated withTrypanosomaInfections in Wild Populations of the Tsetse FlyGlossina fuscipes. G3: Genes, Genomes, Genetics, 2018, 8, 887-897.	0.8	8
126	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. Statistics in Biosciences, 2018, 10, 86-106.	0.6	9

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127	Spatially Resolved and Quantitative Analysis of VISTA/PD-1H as a Novel Immunotherapy Target in Human Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2018, 24, 1562-1573.	3.2	150
128	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	7.1	490
129	Machine learning selected smoking-associated DNA methylation signatures that predict HIV prognosis and mortality. Clinical Epigenetics, 2018, 10, 155.	1.8	37
130	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
131	Spatiotemporal transcriptomic divergence across human and macaque brain development. Science, 2018, 362, .	6.0	279
132	Risk Locus Identification Ties Alcohol Withdrawal Symptoms to <scp>SORCS</scp>2. Alcoholism: Clinical and Experimental Research, 2018, 42, 2337-2348.	1.4	14
133	Genomic Comparison Among Global Isolates of L. interrogans Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. Frontiers in Cellular and Infection Microbiology, 2018, 8, 193.	1.8	39
134	AUDITâ€€ and ICD codes as phenotypes for harmful alcohol use: association with ADH1B polymorphisms in two US populations. Addiction, 2018, 113, 2214-2224.	1.7	24
135	Toll-like receptor 9 negatively regulates pancreatic islet beta cell growth and function in a mouse model of type 1 diabetes. Diabetologia, 2018, 61, 2333-2343.	2.9	24
136	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. Molecular Psychiatry, 2018, 23, 2277-2286.	4.1	20
137	Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. Statistics in Biosciences, 2017, 9, 605-621.	0.6	2
138	Genomeâ€wide association study of body mass index in subjects with alcohol dependence. Addiction Biology, 2017, 22, 535-549.	1.4	21
139	On Joint Estimation of Gaussian Graphical Models for Spatial and Temporal Data. Biometrics, 2017, 73, 769-779.	0.8	30
140	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanolâ€Response Behaviors in Model Organisms. Alcoholism: Clinical and Experimental Research, 2017, 41, 911-928.	1.4	43
141	Transcriptomic analysis and plasma metabolomics in Aldh16a1 -null mice reveals a potential role of ALDH16A1 in renal function. Chemico-Biological Interactions, 2017, 276, 15-22.	1.7	17
142	Use of a Targeted Urine Proteome Assay (TUPA) to identify protein biomarkers of delayed recovery after kidney transplant. Proteomics - Clinical Applications, 2017, 11, 1600132.	0.8	8
143	A statistical framework for data integration through graphical models with application to cancer genomics. Annals of Applied Statistics, 2017, 11, 161-184.	0.5	19
144	gCoda: Conditional Dependence Network Inference for Compositional Data. Journal of Computational Biology, 2017, 24, 699-708.	0.8	40

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145	Genetic Architecture of a Rice Nested Association Mapping Population. G3: Genes, Genomes, Genetics, 2017, 7, 1913-1926.	0.8	71
146	Validating Harmful Alcohol Use as a Phenotype for Genetic Discovery Using Phosphatidylethanol and a Polymorphism in <scp>ADH</scp>1B. Alcoholism: Clinical and Experimental Research, 2017, 41, 998-1003.	1.4	15
147	Catalase deletion promotes prediabetic phenotype in mice. Free Radical Biology and Medicine, 2017, 103, 48-56.	1.3	50
148	Genetic Risk Variants Associated With Comorbid Alcohol Dependence and Major Depression. JAMA Psychiatry, 2017, 74, 1234.	6.0	74
149	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. Nature Genetics, 2017, 49, 1593-1601.	9.4	624
150	Ancestryâ€specific and sexâ€specific risk alleles identified in a genomeâ€wide geneâ€byâ€alcohol dependence interaction study of risky sexual behaviors. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 846-853.	1.1	17
151	Validation of a 52-gene risk profile for outcome prediction in patients with idiopathic pulmonary fibrosis: an international, multicentre, cohort study. Lancet Respiratory Medicine,the, 2017, 5, 857-868.	5.2	115
152	Impact of Sixteen Established Pancreatic Cancer Susceptibility Loci in American Jews. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1540-1548.	1.1	6
153	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. American Journal of Human Genetics, 2017, 101, 939-964.	2.6	141
154	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	1.6	79
155	Daily Time-Use Patterns and Obesity and Mental Health among Primary School Students in Shanghai: A Population-Based Cross-Sectional Study. Scientific Reports, 2017, 7, 16200.	1.6	17
156	Data-Independent Acquisition and Parallel Reaction Monitoring Mass Spectrometry Identification of Serum Biomarkers for Ovarian Cancer. Biomarker Insights, 2017, 12, 117727191771094.	1.0	21
157	Genetic factor common to schizophrenia and HIV infection is associated with risky sexual behavior: antagonistic vs. synergistic pleiotropic SNPs enriched for distinctly different biological functions. Human Genetics, 2017, 136, 75-83.	1.8	17
158	A novel pathway-based distance score enhances assessment of disease heterogeneity in gene expression. BMC Bioinformatics, 2017, 18, 309.	1.2	2
159	A Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms for Acute Kidney Injury. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 482-490.	2.5	31
160	The Interplay Between Risky Sexual Behaviors and Alcohol Dependence: Genome-Wide Association and Neuroimaging Support for LHPP as a Risk Gene. Neuropsychopharmacology, 2017, 42, 598-605.	2.8	40
161	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. Nature Communications, 2017, 8, 2243.	5.8	32
162	A Branched-Chain Amino Acid-Related Metabolic Signature Characterizes Obese Adolescents with Non-Alcoholic Fatty Liver Disease. Nutrients, 2017, 9, 642.	1.7	92

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163	Genomic analyses of African Trypanozoon strains to assess evolutionary relationships and identify markers for strain identification. PLoS Neglected Tropical Diseases, 2017, 11, e0005949.	1.3	13
164	graph-GPA: A graphical model for prioritizing GWAS results and investigating pleiotropic architecture. PLoS Computational Biology, 2017, 13, e1005388.	1.5	12
165	Leveraging functional annotations in genetic risk prediction for human complex diseases. PLoS Computational Biology, 2017, 13, e1005589.	1.5	134
166	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimerâ€™s disease. PLoS Genetics, 2017, 13, e1006933.	1.5	96
167	A putative causal relationship between genetically determined female body shape and posttraumatic stress disorder. Genome Medicine, 2017, 9, 99.	3.6	31
168	S100A10 identified in a genome-wide gene Ã— cannabis dependence interaction analysis of risky sexual behaviours. Journal of Psychiatry and Neuroscience, 2017, 42, 252-261.	1.4	9
169	Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. PLoS Genetics, 2017, 13, e1006836.	1.5	70
170	Mapping the Interactome of a Major Mammalian Endoplasmic Reticulum Heat Shock Protein 90. PLoS ONE, 2017, 12, e0169260.	1.1	20
171	Variable importance-weighted Random Forests. Quantitative Biology, 2017, 5, 338-351.	0.3	5
172	Integrative Tissue-Specific Functional Annotations in the Human Genome Provide Novel Insights on Many Complex Traits and Improve Signal Prioritization in Genome Wide Association Studies. PLoS Genetics, 2016, 12, e1005947.	1.5	94
173	Transcriptional Profiles from Paired Normal Samples Offer Complementary Information on Cancer Patient Survival â€“ Evidence from TCGA Pan-Cancer Data. Scientific Reports, 2016, 6, 20567.	1.6	59
174	Simultaneous dimension reduction and adjustment for confounding variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14662-14667.	3.3	42
175	Genome-wide Association Study of Cannabis Dependence Severity, Novel Risk Variants, and Shared Genetic Risks. JAMA Psychiatry, 2016, 73, 472.	6.0	148
176	Metabolic Regulation of Gene Expression by Histone Lysine Î²-Hydroxybutyrylation. Molecular Cell, 2016, 62, 194-206.	4.5	406
177	Mutations in the Histone Modifier PRDM6 Are Associated with Isolated Nonsyndromic Patent Ductus Arteriosus. American Journal of Human Genetics, 2016, 98, 1082-1091.	2.6	29
178	Epigenome-wide differential DNA methylation between HIV-infected and uninfected individuals. Epigenetics, 2016, 11, 750-760.	1.3	78
179	On an additive partial correlation operator and nonparametric estimation of graphical models. Biometrika, 2016, 103, 513-530.	1.3	14
180	Change point analysis of histone modifications reveals epigenetic blocks linking to physical domains. Annals of Applied Statistics, 2016, 10, 506-526.	0.5	4

#	Article	IF	Citations
181	DNA co-methylation modules in postmortem prefrontal cortex tissues of European Australians with alcohol use disorders. Scientific Reports, 2016, 6, 19430.	1.6	68
182	Leveraging protein quaternary structure to identify oncogenic driver mutations. BMC Bioinformatics, 2016, 17, 137.	1.2	8
183	CCor: A Whole Genome Network-Based Similarity Measure Between Two Genes. Biometrics, 2016, 72, 1216-1225.	0.8	3
184	Imputing Genotypes in Biallelic Populations from Low-Coverage Sequence Data. Genetics, 2016, 202, 487-495.	1.2	59
185	GenoWAP: GWAS signal prioritization through integrated analysis of genomic functional annotation. Bioinformatics, 2016, 32, 542-548.	1.8	47
186	Asymptotically Normal and Efficient Estimation of Covariate-Adjusted Gaussian Graphical Model. Journal of the American Statistical Association, 2016, 111, 394-406.	1.8	29
187	Objective measurement and significance of PD-L1, B7-H3, B7-H4 and TILs in small cell lung cancer (SCLC).. Journal of Clinical Oncology, 2016, 34, 8566-8566.	0.8	5
188	Evidence of Polygenic Adaptation in the Systems Genetics of Anthropometric Traits. PLoS ONE, 2016, 11, e0160654.	1.1	11
189	Two locus inheritance of non-syndromic midline craniosynostosis via rare SMAD6 and common BMP2 alleles. ELife, 2016, 5, .	2.8	168
190	Noninvasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma. Annals of the American Thoracic Society, 2016, 13 Suppl 1, S104-5.	1.5	5
191	A Statistical Framework to Predict Functional Non-Coding Regions in the Human Genome Through Integrated Analysis of Annotation Data. Scientific Reports, 2015, 5, 10576.	1.6	144
192	Dissecting ancestry genomic background in substance dependence genome-wide association studies. Pharmacogenomics, 2015, 16, 1487-1498.	0.6	22
193	M3-S: a genotype calling method incorporating information from samples with known genotypes. BMC Bioinformatics, 2015, 16, 403.	1.2	0
194	Genomewide Association Study for Maximum Number of Alcoholic Drinks in European Americans and African Americans. Alcoholism: Clinical and Experimental Research, 2015, 39, 1137-1147.	1.4	58
195	Transcriptional Profiling of Ectoderm Specification to Keratinocyte Fate in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0122493.	1.1	13
196	CCLasso: correlation inference for compositional data through Lasso. Bioinformatics, 2015, 31, 3172-3180.	1.8	133
197	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, Aedes aegypti. G3: Genes, Genomes, Genetics, 2015, 5, 711-718.	0.8	56
198	DATA INTEGRATION METHODS IN GENOME WIDE ASSOCIATION STUDIES. , 2015, , 961-976.		0

#	Article	IF	Citations
199	A novel mechanism of LIN-28 regulation oflet-7microRNA expression revealed by in vivo HITS-CLIP inC. elegans. Rna, 2015, 21, 985-996.	1.6	39
200	Temperature-dependent innate defense against the common cold virus limits viral replication at warm temperature in mouse airway cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 827-832.	3.3	199
201	Genome-Wide Association Study of Nicotine Dependence in American Populations: Identification of Novel Risk Loci in Both African-Americans and European-Americans. Biological Psychiatry, 2015, 77, 493-503.	0.7	78
202	PHY906(KD018), an adjuvant based on a 1800-year-old Chinese medicine, enhanced the anti-tumor activity of Sorafenib by changing the tumor microenvironment. Scientific Reports, 2015, 5, 9384.	1.6	116
203	Phosphorylation of GATA-6 is required for vascular smooth muscle cell differentiation after mTORC1 inhibition. Science Signaling, 2015, 8, ra44.	1.6	39
204	Sparse Regression by Projection and Sparse Discriminant Analysis. Journal of Computational and Graphical Statistics, 2015, 24, 416-438.	0.9	6
205	Pervasive pleiotropy between psychiatric disorders and immune disorders revealed by integrative analysis of multiple GWAS. Human Genetics, 2015, 134, 1195-1209.	1.8	72
206	Random Effects Model for Multiple Pathway Analysis with Applications to Type II Diabetes Microarray Data. Statistics in Biosciences, 2015, 7, 167-186.	0.6	8
207	Genome-Wide Association Study of Copy Number Variations (CNVs) with Opioid Dependence. Neuropsychopharmacology, 2015, 40, 1016-1026.	2.8	39
208	Gene-based and pathway-based genome-wide association study of alcohol dependence. Shanghai Archives of Psychiatry, 2015, 27, 111-8.	0.7	5
209	Data Pre-Processing for Label-Free Multiple Reaction Monitoring (MRM) Experiments. Biology, 2014, 3, 383-402.	1.3	2
210	Stratified Pathway Analysis to Identify Gene Sets Associated with Oral Contraceptive Use and Breast Cancer. Cancer Informatics, 2014, 13s4, CIN.S13973.	0.9	3
211	T cell-intrinsic role of IL-6 signaling in primary and memory responses. ELife, 2014, 3, e01949.	2.8	135
212	Extensive sequence variation in the 3â€² untranslated region of theKRASgene in lung and ovarian cancer cases. Cell Cycle, 2014, 13, 1030-1040.	1.3	39
213	GPA: A Statistical Approach to Prioritizing GWAS Results by Integrating Pleiotropy and Annotation. PLoS Genetics, 2014, 10, e1004787.	1.5	189
214	Putting things in order. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16236-16237.	3.3	7
215	Improving genetic risk prediction by leveraging pleiotropy. Human Genetics, 2014, 133, 639-650.	1.8	71
216	Exploring the genetic architecture of alcohol dependence in African-Americans via analysis of a genomewide set of common variants. Human Genetics, 2014, 133, 617-624.	1.8	15

#	Article	IF	Citations
217	Cytogenomic mapping and bioinformatic mining reveal interacting brain expressed genes for intellectual disability. Molecular Cytogenetics, 2014, 7, 4.	0.4	19
218	Guilt by rewiring: gene prioritization through network rewiring in Genome Wide Association Studies. Human Molecular Genetics, 2014, 23, 2780-2790.	1.4	54
219	Novel genetic variants modify the effect of smoking on carotid plaque burden in Hispanics. Journal of the Neurological Sciences, 2014, 344, 27-31.	0.3	13
220	Admixture mapping analysis in the context of GWAS with GAW18 data. BMC Proceedings, 2014, 8, S3.	1.8	12
221	Adjustment of familial relatedness in association test for rare variants. BMC Proceedings, 2014, 8, S39.	1.8	1
222	A penalized linear mixed model for genomic prediction using pedigree structures. BMC Proceedings, 2014, 8, S67.	1.8	2
223	Rare deleterious mutations of the gene EFR3A in autism spectrum disorders. Molecular Autism, 2014, 5, 31.	2.6	27
224	Association of Gamma-Aminobutyric Acid A Receptor Î±2 Gene (GABRA2) with Alcohol Use Disorder. Neuropsychopharmacology, 2014, 39, 907-918.	2.8	93
225	Genome-Wide Association Study of Opioid Dependence: Multiple Associations Mapped to Calcium and Potassium Pathways. Biological Psychiatry, 2014, 76, 66-74.	0.7	192
226	Signaling through the Adaptor Molecule MyD88 in CD4+ T Cells Is Required to Overcome Suppression by Regulatory T Cells. Immunity, 2014, 40, 78-90.	6.6	100
227	Genome-wide Association Study Identifies New Susceptibility Loci for Posttraumatic Stress Disorder. Biological Psychiatry, 2013, 74, 656-663.	0.7	150
228	Adaptive clinical trial designs to detect interaction between treatment and a dichotomous biomarker. Canadian Journal of Statistics, 2013, 41, 525-539.	0.6	11
229	Normalized modularity optimization method for community identification with degree adjustment. Physical Review E, 2013, 88, 052802.	0.8	17
230	Time Course RNA-seq: A Potential Avenue with Somewhat Different Approach in Tandem of Differential Analysis. , 2012, , .		0
231	Strong protective effect of the aldehyde dehydrogenase gene (ALDH2) 504lys (*2) allele against alcoholism and alcohol-induced medical diseases in Asians. Human Genetics, 2012, 131, 725-737.	1.8	132
232	Strong Association of the Alcohol Dehydrogenase 1B Gene (ADH1B) with Alcohol Dependence and Alcohol-Induced Medical Diseases. Biological Psychiatry, 2011, 70, 504-512.	0.7	150
233	Collapsing-based and kernel-based single-gene analyses applied to Genetic Analysis Workshop 17 mini-exome data. BMC Proceedings, 2011, 5, S117.	1.8	8
234	A permutation test approach to the choice of sizekfor the nearest neighbors classifier. Journal of Applied Statistics, 2011, 38, 2289-2302.	0.6	0

#	Article	IF	Citations
235	Protein Interaction Predictions from Diverse Sources. Frontiers of Statistics, 2009, , 159-178.	0.2	0
236	Rare independent mutations in renal salt handling genes contribute to blood pressure variation. Nature Genetics, 2008, 40, 592-599.	9.4	728
237	Haplotypic Variants in DRD2, ANKK1, TTC12, and NCAM1 are Associated With Comorbid Alcohol and Drug Dependence. Alcoholism: Clinical and Experimental Research, 2008, 32, 2117-2127.	1.4	93
238	Genomewide Linkage Scan for Opioid Dependence and Related Traits. American Journal of Human Genetics, 2006, 78, 759-769.	2.6	125
239	Ovarian Cancer Classification Based on Mass Spectrometry Analysis of Sera. Cancer Informatics, 2006, 2, 117693510600200.	0.9	5
240	Haplotype analysis in population genetics and association studies. Pharmacogenomics, 2003, 4, 171-178.	0.6	131
241	Light Control of Arabidopsis Development Entails Coordinated Regulation of Genome Expression and Cellular Pathways. Plant Cell, 2001, 13, 2589-2607.	3.1	498
242	The Power of Transmission Disequilibrium Tests for Quantitative Traits. Genetic Epidemiology, 2001, 21, S632-7.	0.6	11
243	Test of Association for Quantitative Traits in General Pedigrees: The Quantitative Pedigree Disequilibrium Test. Genetic Epidemiology, 2001, 21, S370-5.	0.6	23
244	Linkage disequilibrium mapping in populations of variable size using the decay of haplotype sharing and a stepwise-mutation model. Genetic Epidemiology, 2000, 19, S99-S105.	0.6	10
245	Assessing reliability of gene clusters from gene expression data. Functional and Integrative Genomics, 2000, 1, 156-173.	1.4	50
246	A more powerful method to evaluate p-values in GENEHUNTER. Genetic Epidemiology, 1999, 17, S415-S420.	0.6	2
247	A global survey of haplotype frequencies and linkage disequilibrium at the DRD2 locus. Human Genetics, 1998, 103, 211-227.	1.8	197
248	Stochastic modeling of the crossover process during meiosis. Communications in Statistics - Theory and Methods, 1998, 27, 1557-1580.	0.6	3
249	Statistical Analysis of Ordered Tetrads. Genetics, 1998, 150, 459-472.	1.2	14
250	Statistical Analysis of Half-Tetrads. Genetics, 1998, 150, 473-485.	1.2	29
251	Strategies to Identify Genes for Complex Diseases. Annals of Medicine, 1997, 29, 493-498.	1.5	12
252	Insightful Data Science. , 0, , .		0

#	Article	IF	Citations
253	Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, .	2.8	3
254	Comparison of Methods Utilizing Sex-Specific PRSs Derived From GWAS Summary Statistics. Frontiers in Genetics, 0, 13, .	1.1	4