

Hongyu Zhao

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

250
papers

8,597
citations

48
h-index

87
g-index

290
ext. papers

12,513
ext. citations

8.4
avg, IF

6.18
L-index

#	Paper	IF	Citations
250	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19.. <i>Nature Communications</i> , 2022 , 13, 440	17.4	13
249	Photoreceptor layer thinning is an early biomarker for age-related macular degeneration: Epidemiological and genetic evidence from UK Biobank optical coherence tomography data.. <i>Ophthalmology</i> , 2022 ,	7.3	3
248	Posttraumatic Stress Disorder Brain Transcriptomics: Convergent Genomic Signatures Across Biological Sex. <i>Biological Psychiatry</i> , 2022 , 91, 6-13	7.9	2
247	Low depression frequency is associated with decreased risk of cardiometabolic disease 2022 , 1, 125-131		1
246	Non-linear archetypal analysis of single-cell RNA-seq data by deep autoencoders.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010025	5	0
245	Whole Exome Sequencing Reveals Damaging Gene Variants Associated with Hypoalphalipoproteinemia.. <i>Journal of Lipid Research</i> , 2022 , 100209	6.3	
244	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program.. <i>PLoS Genetics</i> , 2022 , 18, e1010113	6	0
243	Incorporating local ancestry improves identification of ancestry-associated methylation signatures and meQTLs in African Americans.. <i>Communications Biology</i> , 2022 , 5, 401	6.7	0
242	Healthy lifestyle counteracts the risk effect of genetic factors on incident gout: a large population-based longitudinal study.. <i>BMC Medicine</i> , 2022 , 20, 138	11.4	0
241	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. <i>PLoS Genetics</i> , 2022 , 18, e1010193	6	0
240	M-DATA: A statistical approach to jointly analyzing de novo mutations for multiple traits. <i>PLoS Genetics</i> , 2021 , 17, e1009849	6	0
239	Deep Learning of the Retina Enables Phenome- and Genome-wide Analyses of the Microvasculature. <i>Circulation</i> , 2021 ,	16.7	7
238	Neoantigen-driven B cell and CD4 ⁺ follicular helper cell collaboration promotes anti-tumor CD8 T _H cell responses. <i>Cell</i> , 2021 , 184, 6101-6118.e13	56.2	29
237	Circadian Rhythm Analysis Using Wearable Device Data: Novel Penalized Machine Learning Approach. <i>Journal of Medical Internet Research</i> , 2021 , 23, e18403	7.6	0
236	A Markov random field model for network-based differential expression analysis of single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2021 , 22, 524	3.6	0
235	CD4 ⁺ follicular regulatory T cells optimize the influenza virus-specific B cell response. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	13
234	Polygenic risk score, healthy lifestyles, and risk of incident depression. <i>Translational Psychiatry</i> , 2021 , 11, 189	8.6	1

233	Identifying modules of cooperating cancer drivers. <i>Molecular Systems Biology</i> , 2021 , 17, e9810	12.2	2
232	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits. <i>American Journal of Human Genetics</i> , 2021 , 108, 632-655	11	11
231	Epigenetic age acceleration, fatigue, and inflammation in patients undergoing radiation therapy for head and neck cancer: A longitudinal study. <i>Cancer</i> , 2021 , 127, 3361-3371	6.4	3
230	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. <i>Nature Communications</i> , 2021 , 12, 2878	17.4	2
229	The impact of removing former drinkers from genome-wide association studies of AUDIT-C. <i>Addiction</i> , 2021 , 116, 3044-3054	4.6	1
228	Genomics of Gulf War Illness in U.S. Veterans Who Served during the 1990-1991 Persian Gulf War: Methods and Rationale for Veterans Affairs Cooperative Study #2006. <i>Brain Sciences</i> , 2021 , 11,	3.4	2
227	Correlating genomic copy number alterations with clinicopathologic findings in 75 cases of hepatocellular carcinoma. <i>BMC Medical Genomics</i> , 2021 , 14, 150	3.7	1
226	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021 , 27, 1012-1024	50.5	16
225	Integrating Multidimensional Data for Clustering Analysis With Applications to Cancer Patient Data. <i>Journal of the American Statistical Association</i> , 2021 , 116, 14-26	2.8	3
224	TLR9 Deficiency in B Cells Promotes Immune Tolerance via Interleukin-10 in a Type 1 Diabetes Mouse Model. <i>Diabetes</i> , 2021 , 70, 504-515	0.9	1
223	Overview of PAX gene family: analysis of human tissue-specific variant expression and involvement in human disease. <i>Human Genetics</i> , 2021 , 140, 381-400	6.3	8
222	A pooled genome-wide association study identifies pancreatic cancer susceptibility loci on chromosome 19p12 and 19p13.3 in the full-Jewish population. <i>Human Genetics</i> , 2021 , 140, 309-319	6.3	2
221	Elevated Blood Pressure Increases Pneumonia Risk: Epidemiological Association and Mendelian Randomization in the UK Biobank. <i>Med</i> , 2021 , 2, 137-148.e4	31.7	9
220	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. <i>Schizophrenia Bulletin</i> , 2021 , 47, 517-529	1.3	7
219	Transcriptomic organization of the human brain in post-traumatic stress disorder. <i>Nature Neuroscience</i> , 2021 , 24, 24-33	25.5	44
218	The role of the gut microbiome in cancer-related fatigue: pilot study on epigenetic mechanisms. <i>Supportive Care in Cancer</i> , 2021 , 29, 3173-3182	3.9	12
217	A comprehensive genetic and epidemiological association analysis of vitamin D with common diseases/traits in the UK Biobank. <i>Genetic Epidemiology</i> , 2021 , 45, 24-35	2.6	6
216	Cortical Transcriptomic Alterations in Association With Appetitive Neuropeptides and Body Mass Index in Posttraumatic Stress Disorder. <i>International Journal of Neuropsychopharmacology</i> , 2021 , 24, 118-129	5.8	3

215	A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. <i>American Statistician</i> , 2021 , 75, 310-322	5	4
214	Cytokine Profiles Before and After Immune Modulation in Hospitalized Patients with COVID-19. <i>Journal of Clinical Immunology</i> , 2021 , 41, 738-747	5.7	7
213	Toll-like receptor 7 deficiency suppresses type 1 diabetes development by modulating B-cell differentiation and function. <i>Cellular and Molecular Immunology</i> , 2021 , 18, 328-338	15.4	2
212	Interactions Between Enhanced Polygenic Risk Scores and Lifestyle for Cardiovascular Disease, Diabetes, and Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003128	5.2	23
211	RePhine: An Integrative Method for Identification of Drug Response-related Transcriptional Regulators. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	4
210	A fast and robust Bayesian nonparametric method for prediction of complex traits using summary statistics. <i>PLoS Genetics</i> , 2021 , 17, e1009697	6	5
209	DIAPH1 Variants in Non-East Asian Patients With Sporadic Moyamoya Disease. <i>JAMA Neurology</i> , 2021 , 78, 993-1003	17.2	7
208	Association of Epigenetic Age Acceleration With Risk Factors, Survival, and Quality of Life in Patients With Head and Neck Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2021 , 111, 157-167	4	2
207	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. <i>Genome Biology</i> , 2021 , 22, 262	18.3	7
206	Calculating Orthologous Protein-Coding Sequence Set Probability Using the Poisson Process. <i>Journal of Computational Biology</i> , 2021 , 28, 961-974	1.7	
205	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. <i>Biological Psychiatry</i> , 2021 ,	7.9	3
204	A reservoir of stem-like CD8 T cells in the tumor-draining lymph node preserves the ongoing antitumor immune response. <i>Science Immunology</i> , 2021 , 6, eabg7836	28	12
203	Integrative modeling of transmitted and variants identifies novel risk genes for congenital heart disease.. <i>Quantitative Biology</i> , 2021 , 9, 216-227	3.9	0
202	Genome-wide association analyses of post-traumatic stress disorder and its symptom subdomains in the Million Veteran Program. <i>Nature Genetics</i> , 2021 , 53, 174-184	36.3	40
201	Differential Protein Expression in Striatal D1- and D2-Dopamine Receptor-Expressing Medium Spiny Neurons. <i>Proteomes</i> , 2020 , 8,	4.6	5
200	Elevated serum interleukin-8 is associated with enhanced intratumor neutrophils and reduced clinical benefit of immune-checkpoint inhibitors. <i>Nature Medicine</i> , 2020 , 26, 688-692	50.5	128
199	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. <i>Nature Communications</i> , 2020 , 11, 2438	17.4	17
198	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. <i>Nature Genetics</i> , 2020 , 52, 680-691	36.3	140

197	Reducing False-Positive Results in Newborn Screening Using Machine Learning. <i>International Journal of Neonatal Screening</i> , 2020 , 6,	2.6	13
196	Relationship of Age With the Hemodynamic Parameters in Individuals With Elevated Blood Pressure. <i>Journal of the American Geriatrics Society</i> , 2020 , 68, 1520-1528	5.6	0
195	Genomic influences on self-reported childhood maltreatment. <i>Translational Psychiatry</i> , 2020 , 10, 38	8.6	20
194	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. <i>PLoS Computational Biology</i> , 2020 , 16, e1007565	5	13
193	Statistical Methods in Genome-Wide Association Studies. <i>Annual Review of Biomedical Data Science</i> , 2020 , 3, 265-288	5.6	1
192	A novel machine learning unsupervised algorithm for sleep/wake identification using actigraphy. <i>Chronobiology International</i> , 2020 , 37, 1002-1015	3.6	11
191	Ethnic variability in newborn metabolic screening markers associated with false-positive outcomes. <i>Journal of Inherited Metabolic Disease</i> , 2020 , 43, 934-943	5.4	11
190	Pilot study of combined aerobic and resistance exercise on fatigue for patients with head and neck cancer: Inflammatory and epigenetic changes. <i>Brain, Behavior, and Immunity</i> , 2020 , 88, 184-192	16.6	4
189	Hematopoietic mosaic chromosomal alterations and risk for infection among 767,891 individuals without blood cancer 2020 ,		2
188	Leveraging functional annotation to identify genes associated with complex diseases. <i>PLoS Computational Biology</i> , 2020 , 16, e1008315	5	3
187	Androgen Regulates SARS-CoV-2 Receptor Levels and Is Associated with Severe COVID-19 Symptoms in Men 2020 ,		18
186	Hematopoietic mosaic chromosomal alterations and risk for infection among 767,891 individuals without blood cancer 2020 ,		5
185	Genome-wide association study of cognitive performance in U.S. veterans with schizophrenia or bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020 , 183, 181-194	3.5	9
184	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. <i>Sleep</i> , 2020 , 43,	1.1	9
183	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. <i>Nature Genetics</i> , 2020 , 52, 1046-1056	10.56	38
182	Automated feature extraction from population wearable device data identified novel loci associated with sleep and circadian rhythms. <i>PLoS Genetics</i> , 2020 , 16, e1009089	6	1
181	Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. <i>Nature Communications</i> , 2020 , 11, 5302	17.4	15
180	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127

179	Androgen Signaling Regulates SARS-CoV-2 Receptor Levels and Is Associated with Severe COVID-19 Symptoms in Men. <i>Cell Stem Cell</i> , 2020 , 27, 876-889.e12	18	85
178	An enhanced machine learning tool for cis-eQTL mapping with regularization and confounder adjustments. <i>Genetic Epidemiology</i> , 2020 , 44, 798-810	2.6	
177	Gut Microbiome Associated with the Psychoneurological Symptom Cluster in Patients with Head and Neck Cancers. <i>Cancers</i> , 2020 , 12,	6.6	16
176	Hemodynamic Phenotypes of Hypertension Based on Cardiac Output and Systemic Vascular Resistance. <i>American Journal of Medicine</i> , 2020 , 133, e127-e139	2.4	4
175	NITUMID: Nonnegative matrix factorization-based Immune-Tumor Microenvironment Deconvolution. <i>Bioinformatics</i> , 2020 , 36, 1344-1350	7.2	4
174	Genotyping Array Design and Data Quality Control in the Million Veteran Program. <i>American Journal of Human Genetics</i> , 2020 , 106, 535-548	11	22
173	Timing of Newborn Blood Collection Alters Metabolic Disease Screening Performance. <i>Frontiers in Pediatrics</i> , 2020 , 8, 623184	3.4	5
172	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
171	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
170	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
169	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
168	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
167	Leveraging functional annotation to identify genes associated with complex diseases 2020 , 16, e1008315		
166	Benchmarking variant identification tools for plant diversity discovery. <i>BMC Genomics</i> , 2019 , 20, 701	4.5	8
165	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2019 , 105, 763-772	11	41
164	An evaluation of noncoding genome annotation tools through enrichment analysis of 15 genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2019 , 20, 995-1003	13.4	3
163	Genetic Link Between Arterial Stiffness and Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002453	5.2	6
162	Genetic Association of Finger Photoplethysmography-Derived Arterial Stiffness Index With Blood Pressure and Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019 , 39, 1253-1261	9.4	15

161	Validation of an Electronic Medical Record-Based Algorithm for Identifying Posttraumatic Stress Disorder in U.S. Veterans. <i>Journal of Traumatic Stress</i> , 2019 , 32, 226-237	3.8	11
160	Genome-wide Association Study of Maximum Habitual Alcohol Intake in >140,000 U.S. European and African American Veterans Yields Novel Risk Loci. <i>Biological Psychiatry</i> , 2019 , 86, 365-376	7.9	37
159	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 497-508	35.1	72
158	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. <i>Nature Communications</i> , 2019 , 10, 1499	17.4	164
157	A statistical framework for cross-tissue transcriptome-wide association analysis. <i>Nature Genetics</i> , 2019 , 51, 568-576	36.3	108
156	Genomics of posttraumatic stress disorder in veterans: Methods and rationale for Veterans Affairs Cooperative Study #575B. <i>International Journal of Methods in Psychiatric Research</i> , 2019 , 28, e1767	4.3	5
155	International variations in trust in health care systems. <i>International Journal of Health Planning and Management</i> , 2019 , 34, 130-139	2.2	12
154	Next-generation sequencing in liquid biopsy: cancer screening and early detection. <i>Human Genomics</i> , 2019 , 13, 34	6.8	139
153	Expression of the type 3 InsP receptor is a final common event in the development of hepatocellular carcinoma. <i>Gut</i> , 2019 , 68, 1676-1687	19.2	32
152	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. <i>Nature Neuroscience</i> , 2019 , 22, 1394-1401	25.5	92
151	Joint Models for Time-to-Event Data and Longitudinal Biomarkers of High Dimension. <i>Statistics in Biosciences</i> , 2019 , 11, 614-629	1.5	1
150	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. <i>Nature Communications</i> , 2019 , 10, 4558	17.4	151
149	Retrospective Association Analysis of Longitudinal Binary Traits Identifies Important Loci and Pathways in Cocaine Use. <i>Genetics</i> , 2019 , 213, 1225-1236	4	3
148	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. <i>BMC Medical Genetics</i> , 2019 , 20, 204	2.1	2
147	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. <i>Genetics in Medicine</i> , 2019 , 21, 896-903	8.1	19
146	Understanding the determinants of public trust in the health care system in China: an analysis of a cross-sectional survey. <i>Journal of Health Services Research and Policy</i> , 2019 , 24, 37-43	2.4	13
145	Regularized Latent Class Model for Joint Analysis of High-Dimensional Longitudinal Biomarkers and a Time-to-Event Outcome. <i>Biometrics</i> , 2019 , 75, 69-77	1.8	4
144	Elevated methylmalonic acidemia (MMA) screening markers in Hispanic and preterm newborns. <i>Molecular Genetics and Metabolism</i> , 2019 , 126, 39-42	3.7	3

143	ProteomicsBrowser: MS/proteomics data visualization and investigation. <i>Bioinformatics</i> , 2019 , 35, 2313-2314	2	
142	Using DNA methylation to validate an electronic medical record phenotype for smoking. <i>Addiction Biology</i> , 2019 , 24, 1056-1065	4.6	7
141	Trends in the Prevalence of Overweight and Obesity among Chinese School-Age Children and Adolescents from 2010 to 2015. <i>Childhood Obesity</i> , 2018 , 14, 182-188	2.5	17
140	Spectral clustering based on learning similarity matrix. <i>Bioinformatics</i> , 2018 , 34, 2069-2076	7.2	42
139	Loneliness 5 years ante-mortem is associated with disease-related differential gene expression in postmortem dorsolateral prefrontal cortex. <i>Translational Psychiatry</i> , 2018 , 8, 2	8.6	15
138	Improving SNP prioritization and pleiotropic architecture estimation by incorporating prior knowledge using graph-GPA. <i>Bioinformatics</i> , 2018 , 34, 2139-2141	7.2	3
137	Uncovering Genomic Regions Associated with Infections in Wild Populations of the Tsetse Fly. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 887-897	3.2	5
136	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. <i>Statistics in Biosciences</i> , 2018 , 10, 86-106	1.5	5
135	Genomic Comparison Among Global Isolates of Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 193	5.9	18
134	AUDIT-C and ICD codes as phenotypes for harmful alcohol use: association with ADH1B polymorphisms in two US populations. <i>Addiction</i> , 2018 , 113, 2214-2224	4.6	13
133	Toll-like receptor 9 negatively regulates pancreatic islet beta cell growth and function in a mouse model of type 1 diabetes. <i>Diabetologia</i> , 2018 , 61, 2333-2343	10.3	13
132	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. <i>Molecular Psychiatry</i> , 2018 , 23, 2277-2286	15.1	14
131	Spatially Resolved and Quantitative Analysis of VISTA/PD-1H as a Novel Immunotherapy Target in Human Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 1562-1573	12.9	93
130	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018 , 21, 1656-1669	25.5	257
129	Machine learning selected smoking-associated DNA methylation signatures that predict HIV prognosis and mortality. <i>Clinical Epigenetics</i> , 2018 , 10, 155	7.7	18
128	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277
127	Spatiotemporal transcriptomic divergence across human and macaque brain development. <i>Science</i> , 2018 , 362,	33.3	127
126	Risk Locus Identification Ties Alcohol Withdrawal Symptoms to SORCS2. <i>Alcoholism: Clinical and Experimental Research</i> , 2018 , 42, 2337-2348	3.7	8

125	Genome-wide association study of body mass index in subjects with alcohol dependence. <i>Addiction Biology</i> , 2017 , 22, 535-549	4.6	18
124	On joint estimation of Gaussian graphical models for spatial and temporal data. <i>Biometrics</i> , 2017 , 73, 769-779	1.8	22
123	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanol-Response Behaviors in Model Organisms. <i>Alcoholism: Clinical and Experimental Research</i> , 2017 , 41, 911-928	3.7	30
122	Transcriptomic analysis and plasma metabolomics in Aldh16a1-null mice reveals a potential role of ALDH16A1 in renal function. <i>Chemico-Biological Interactions</i> , 2017 , 276, 15-22	5	10
121	Use of a Targeted Urine Proteome Assay (TUPA) to identify protein biomarkers of delayed recovery after kidney transplant. <i>Proteomics - Clinical Applications</i> , 2017 , 11, 1600132	3.1	3
120	A STATISTICAL FRAMEWORK FOR DATA INTEGRATION THROUGH GRAPHICAL MODELS WITH APPLICATION TO CANCER GENOMICS. <i>Annals of Applied Statistics</i> , 2017 , 11, 161-184	2.1	13
119	gCoda: Conditional Dependence Network Inference for Compositional Data. <i>Journal of Computational Biology</i> , 2017 , 24, 699-708	1.7	27
118	Genetic Architecture of a Rice Nested Association Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1913-1926	3.2	36
117	Validating Harmful Alcohol Use as a Phenotype for Genetic Discovery Using Phosphatidylethanol and a Polymorphism in ADH1B. <i>Alcoholism: Clinical and Experimental Research</i> , 2017 , 41, 998-1003	3.7	12
116	Catalase deletion promotes prediabetic phenotype in mice. <i>Free Radical Biology and Medicine</i> , 2017 , 103, 48-56	7.8	31
115	Genetic Risk Variants Associated With Comorbid Alcohol Dependence and Major Depression. <i>JAMA Psychiatry</i> , 2017 , 74, 1234-1241	14.5	47
114	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. <i>Nature Genetics</i> , 2017 , 49, 1593-1601	36.3	348
113	Ancestry-specific and sex-specific risk alleles identified in a genome-wide gene-by-alcohol dependence interaction study of risky sexual behaviors. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017 , 174, 846-853	3.5	14
112	Genomic analyses of African Trypanozoon strains to assess evolutionary relationships and identify markers for strain identification. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005949	4.8	11
111	graph-GPA: A graphical model for prioritizing GWAS results and investigating pleiotropic architecture. <i>PLoS Computational Biology</i> , 2017 , 13, e1005388	5	8
110	Leveraging functional annotations in genetic risk prediction for human complex diseases. <i>PLoS Computational Biology</i> , 2017 , 13, e1005589	5	71
109	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease. <i>PLoS Genetics</i> , 2017 , 13, e1006933	6	56
108	A putative causal relationship between genetically determined female body shape and posttraumatic stress disorder. <i>Genome Medicine</i> , 2017 , 9, 99	14.4	23

107	identified in a genome-wide gene \times cannabis dependence interaction analysis of risky sexual behaviours. <i>Journal of Psychiatry and Neuroscience</i> , 2017 , 42, 252-261	4.5	5
106	Validation of a 52-gene risk profile for outcome prediction in patients with idiopathic pulmonary fibrosis: an international, multicentre, cohort study. <i>Lancet Respiratory Medicine</i> , 2017 , 5, 857-868	35.1	59
105	Impact of Sixteen Established Pancreatic Cancer Susceptibility Loci in American Jews. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1540-1548	4	5
104	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. <i>American Journal of Human Genetics</i> , 2017 , 101, 939-964	11	61
103	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. <i>Scientific Reports</i> , 2017 , 7, 16954	4.9	56
102	Daily Time-Use Patterns and Obesity and Mental Health among Primary School Students in Shanghai: A Population-Based Cross-Sectional Study. <i>Scientific Reports</i> , 2017 , 7, 16200	4.9	13
101	Data-Independent Acquisition and Parallel Reaction Monitoring Mass Spectrometry Identification of Serum Biomarkers for Ovarian Cancer. <i>Biomarker Insights</i> , 2017 , 12, 1177271917710948	3.5	15
100	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. <i>Human Genetics</i> , 2017 , 136, 75-83	6.3	11
99	A novel pathway-based distance score enhances assessment of disease heterogeneity in gene expression. <i>BMC Bioinformatics</i> , 2017 , 18, 309	3.6	1
98	A Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms for Acute Kidney Injury. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017 , 195, 482-490	10.2	22
97	The Interplay Between Risky Sexual Behaviors and Alcohol Dependence: Genome-Wide Association and Neuroimaging Support for LHPP as a Risk Gene. <i>Neuropsychopharmacology</i> , 2017 , 42, 598-605	8.7	28
96	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. <i>Nature Communications</i> , 2017 , 8, 2243	17.4	19
95	A Branched-Chain Amino Acid-Related Metabolic Signature Characterizes Obese Adolescents with Non-Alcoholic Fatty Liver Disease. <i>Nutrients</i> , 2017 , 9,	6.7	65
94	Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. <i>PLoS Genetics</i> , 2017 , 13, e1006836	6	40
93	Mapping the Interactome of a Major Mammalian Endoplasmic Reticulum Heat Shock Protein 90. <i>PLoS ONE</i> , 2017 , 12, e0169260	3.7	17
92	Variable importance-weighted Random Forests. <i>Quantitative Biology</i> , 2017 , 5, 338-351	3.9	5
91	Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. <i>Statistics in Biosciences</i> , 2016 , 2016, 1-17	1.5	2
90	On an additive partial correlation operator and nonparametric estimation of graphical models. <i>Biometrika</i> , 2016 , 103, 513-530	2	11

89	CHANGE POINT ANALYSIS OF HISTONE MODIFICATIONS REVEALS EPIGENETIC BLOCKS LINKING TO PHYSICAL DOMAINS. <i>Annals of Applied Statistics</i> , 2016 , 10, 506-526	2.1	4
88	DNA co-methylation modules in postmortem prefrontal cortex tissues of European Australians with alcohol use disorders. <i>Scientific Reports</i> , 2016 , 6, 19430	4.9	57
87	Leveraging protein quaternary structure to identify oncogenic driver mutations. <i>BMC Bioinformatics</i> , 2016 , 17, 137	3.6	6
86	CCor: A whole genome network-based similarity measure between two genes. <i>Biometrics</i> , 2016 , 72, 1216-1225	1	
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4	Local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits		8
3	Trans-ancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders		7
2	Genomic Characterization of Posttraumatic Stress Disorder in a Large US Military Veteran Sample		7
1	TP53-mediated clonal hematopoiesis confers increased risk for incident peripheral artery disease		3