Hongyu Zhao

List of Publications by Citations

250	8,597	48	87
papers	citations	h-index	g-index
290	12,513	8.4	6.18
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
250	Rare independent mutations in renal salt handling genes contribute to blood pressure variation. *Nature Genetics*, **2008**, 40, 592-599	36.3	639
249	Light control of Arabidopsis development entails coordinated regulation of genome expression and cellular pathways. *Plant Cell*, **2001**, 13, 2589-607	11.6	453
248	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. *Nature Genetics*, **2017**, 49, 1593-1601	36.3	348
247	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
246	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nature Neuroscience*, **2018**, 21, 1656-1669	25.5	257
245	Metabolic Regulation of Gene Expression by Histone Lysine ꞵHydroxybutyrylation. *Molecular Cell*, **2016**, 62, 194-206	17.6	240
244	A global survey of haplotype frequencies and linkage disequilibrium at the DRD2 locus. *Human Genetics*, **1998**, 103, 211-27	6.3	188
243	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. *Nature Communications*, **2019**, 10, 1499	17.4	164
242	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. *Nature Communications*, **2019**, 10, 4558	17.4	151
241	Genome-wide association study of opioid dependence: multiple associations mapped to calcium and potassium pathways. *Biological Psychiatry*, **2014**, 76, 66-74	7.9	143
240	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	36.3	140
239	Next-generation sequencing in liquid biopsy: cancer screening and early detection. *Human Genomics*, **2019**, 13, 34	6.8	139
238	GPA: a statistical approach to prioritizing GWAS results by integrating pleiotropy and annotation. *PLoS Genetics*, **2014**, 10, e1004787	6	137
237	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, 827-32	11.5	132
236	Genome-wide association study identifies new susceptibility loci for posttraumatic stress disorder. *Biological Psychiatry*, **2013**, 74, 656-63	7.9	129
235	Elevated serum interleukin-8 is associated with enhanced intratumor neutrophils and reduced clinical benefit of immune-checkpoint inhibitors. *Nature Medicine*, **2020**, 26, 688-692	50.5	128
234	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127

233	Spatiotemporal transcriptomic divergence across human and macaque brain development. *Science*, **2018**, 362,	33.3	127
232	Haplotype analysis in population genetics and association studies. *Pharmacogenomics*, **2003**, 4, 171-8	2.6	116
231	Two locus inheritance of non-syndromic midline craniosynostosis via rare and common alleles. *ELife* , **2016**, 5,	8.9	115
230	Strong association of the alcohol dehydrogenase 1B gene (ADH1B) with alcohol dependence and alcohol-induced medical diseases. *Biological Psychiatry*, **2011**, 70, 504-12	7.9	113
229	Genome-wide Association Study of Cannabis Dependence Severity, Novel Risk Variants, and Shared Genetic Risks. *JAMA Psychiatry*, **2016**, 73, 472-80	14.5	113
228	A statistical framework for cross-tissue transcriptome-wide association analysis. *Nature Genetics*, **2019**, 51, 568-576	36.3	108
227	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, 725-37	6.3	105
226	Genomewide linkage scan for opioid dependence and related traits. *American Journal of Human Genetics*, **2006**, 78, 759-769	11	98
225	T cell-intrinsic role of IL-6 signaling in primary and memory responses. *ELife*, **2014**, 3, e01949	8.9	93
224	Spatially Resolved and Quantitative Analysis of VISTA/PD-1H as a Novel Immunotherapy Target in Human Non-Small Cell Lung Cancer. *Clinical Cancer Research*, **2018**, 24, 1562-1573	12.9	93
223	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. *Nature Neuroscience*, **2019**, 22, 1394-1401	25.5	92
222	A statistical framework to predict functional non-coding regions in the human genome through integrated analysis of annotation data. *Scientific Reports*, **2015**, 5, 10576	4.9	88
221	CCLasso: correlation inference for compositional data through Lasso. *Bioinformatics*, **2015**, 31, 3172-80	7.2	87
220	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	18	85
219	Haplotypic variants in DRD2, ANKK1, TTC12, and NCAM1 are associated with comorbid alcohol and drug dependence. *Alcoholism: Clinical and Experimental Research*, **2008**, 32, 2117-27	3.7	79
218	Signaling through the adaptor molecule MyD88 in CD4+ T cells is required to overcome suppression by regulatory T cells. *Immunity*, **2014**, 40, 78-90	32.3	77
217	Association of gamma-aminobutyric acid A receptor α2 gene (GABRA2) with alcohol use disorder. *Neuropsychopharmacology*, **2014**, 39, 907-18	8.7	76
216	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	4.9	75

215	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	35.1	72
214	Leveraging functional annotations in genetic risk prediction for human complex diseases. *PLoS Computational Biology*, **2017**, 13, e1005589	5	71
213	A Branched-Chain Amino Acid-Related Metabolic Signature Characterizes Obese Adolescents with Non-Alcoholic Fatty Liver Disease. *Nutrients*, **2017**, 9,	6.7	65
212	A Powerful Approach to Estimating Annotation-Stratified Genetic Covariance via GWAS Summary Statistics. *American Journal of Human Genetics*, **2017**, 101, 939-964	11	61
211	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	35.1	59
210	Improving genetic risk prediction by leveraging pleiotropy. *Human Genetics*, **2014**, 133, 639-50	6.3	58
209	Pervasive pleiotropy between psychiatric disorders and immune disorders revealed by integrative analysis of multiple GWAS. *Human Genetics*, **2015**, 134, 1195-209	6.3	57
208	DNA co-methylation modules in postmortem prefrontal cortex tissues of European Australians with alcohol use disorders. *Scientific Reports*, **2016**, 6, 19430	4.9	57
207	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	6	57
206	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimerß disease. *PLoS Genetics*, **2017**, 13, e1006933	6	56
205	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. *Scientific Reports*, **2017**, 7, 16954	4.9	56
204	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	7.9	56
203	Epigenome-wide differential DNA methylation between HIV-infected and uninfected individuals. *Epigenetics*, **2016**, 11, 750-760	5.7	49
202	Genetic Risk Variants Associated With Comorbid Alcohol Dependence and Major Depression. *JAMA Psychiatry*, **2017**, 74, 1234-1241	14.5	47
201	Genomewide Association Study for Maximum Number of Alcoholic Drinks in European Americans and African Americans. *Alcoholism: Clinical and Experimental Research*, **2015**, 39, 1137-47	3.7	46
200	Assessing reliability of gene clusters from gene expression data. *Functional and Integrative Genomics*, **2000**, 1, 156-73	3.8	44
199	Transcriptomic organization of the human brain in post-traumatic stress disorder. *Nature Neuroscience*, **2021**, 24, 24-33	25.5	44
198	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, Aedes aegypti. *G3: Genes, Genomes, Genetics*, **2015**, 5, 711-8	3.2	43

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197	Transcriptional Profiles from Paired Normal Samples Offer Complementary Information on Cancer Patient Survival--Evidence from TCGA Pan-Cancer Data. *Scientific Reports*, **2016**, 6, 20567	4.9	43
196	Spectral clustering based on learning similarity matrix. *Bioinformatics*, **2018**, 34, 2069-2076	7.2	42
195	Guilt by rewiring: gene prioritization through network rewiring in genome wide association studies. *Human Molecular Genetics*, **2014**, 23, 2780-90	5.6	42
194	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. *American Journal of Human Genetics*, **2019**, 105, 763-772	11	41
193	Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. *PLoS Genetics*, **2017**, 13, e1006836	6	40
192	Genome-wide association analyses of post-traumatic stress disorder and its symptom subdomains in the Million Veteran Program. *Nature Genetics*, **2021**, 53, 174-184	36.3	40
191	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. *Nature Genetics*, **2020**, 52, 1046-1056	36.3	38
190	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	7.9	37
189	Genetic Architecture of a Rice Nested Association Mapping Population. *G3: Genes, Genomes, Genetics*, **2017**, 7, 1913-1926	3.2	36
188	A novel mechanism of LIN-28 regulation of let-7 microRNA expression revealed by in vivo HITS-CLIP in C. elegans. *Rna*, **2015**, 21, 985-96	5.8	36
187	Imputing Genotypes in Biallelic Populations from Low-Coverage Sequence Data. *Genetics*, **2016**, 202, 487-95	4	34
186	Extensive sequence variation in the 3′untranslated region of the KRAS gene in lung and ovarian cancer cases. *Cell Cycle*, **2014**, 13, 1030-40	4.7	34
185	GenoWAP: GWAS signal prioritization through integrated analysis of genomic functional annotation. *Bioinformatics*, **2016**, 32, 542-8	7.2	33
184	Expression of the type 3 InsP receptor is a final common event in the development of hepatocellular carcinoma. *Gut*, **2019**, 68, 1676-1687	19.2	32
183	Catalase deletion promotes prediabetic phenotype in mice. *Free Radical Biology and Medicine*, **2017**, 103, 48-56	7.8	31
182	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanol-Response Behaviors in Model Organisms. *Alcoholism: Clinical and Experimental Research*, **2017**, 41, 911-928	3.7	30
181	Genome-wide association study of copy number variations (CNVs) with opioid dependence. *Neuropsychopharmacology*, **2015**, 40, 1016-26	8.7	30
180	Neoantigen-driven B cell and CD4 T follicular helper cell collaboration promotes anti-tumor CD8 T cell responses. *Cell*, **2021**, 184, 6101-6118.e13	56.2	29

179	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	8.7	28
178	gCoda: Conditional Dependence Network Inference for Compositional Data. *Journal of Computational Biology*, **2017**, 24, 699-708	1.7	27
177	Phosphorylation of GATA-6 is required for vascular smooth muscle cell differentiation after mTORC1 inhibition. *Science Signaling*, **2015**, 8, ra44	8.8	27
176	Asymptotically Normal and Efficient Estimation of Covariate-Adjusted Gaussian Graphical Model. *Journal of the American Statistical Association*, **2016**, 111, 394-406	2.8	26
175	Statistical analysis of half-tetrads. *Genetics*, **1998**, 150, 473-85	4	26
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	11.5	24
173	A putative causal relationship between genetically determined female body shape and posttraumatic stress disorder. *Genome Medicine*, **2017**, 9, 99	14.4	23
172	Interactions Between Enhanced Polygenic Risk Scores and Lifestyle for Cardiovascular Disease, Diabetes, and Lipid Levels. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003128	5.2	23
171	On joint estimation of Gaussian graphical models for spatial and temporal data. *Biometrics*, **2017**, 73, 769-779	1.8	22
170	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	10.2	22
169	Test of association for quantitative traits in general pedigrees: the quantitative pedigree disequilibrium test. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S370-5	2.6	22
168	Genotyping Array Design and Data Quality Control in the Million Veteran Program. *American Journal of Human Genetics*, **2020**, 106, 535-548	11	22
167	Genomic influences on self-reported childhood maltreatment. *Translational Psychiatry*, **2020**, 10, 38	8.6	20
166	Dissecting ancestry genomic background in substance dependence genome-wide association studies. *Pharmacogenomics*, **2015**, 16, 1487-98	2.6	20
165	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. *Nature Communications*, **2017**, 8, 2243	17.4	19
164	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. *Genetics in Medicine*, **2019**, 21, 896-903	8.1	19
163	Genome-wide association study of body mass index in subjects with alcohol dependence. *Addiction Biology*, **2017**, 22, 535-549	4.6	18
162	Genomic Comparison Among Global Isolates of Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. *Frontiers in Cellular and Infection Microbiology*, **2018**, 8, 193	5.9	18

161	Androgen Regulates SARS-CoV-2 Receptor Levels and Is Associated with Severe COVID-19 Symptoms in Men **2020**,		18
160	Machine learning selected smoking-associated DNA methylation signatures that predict HIV prognosis and mortality. *Clinical Epigenetics*, **2018**, 10, 155	7.7	18
159	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. *Nature Communications*, **2020**, 11, 2438	17.4	17
158	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	2.5	17
157	Mapping the Interactome of a Major Mammalian Endoplasmic Reticulum Heat Shock Protein 90. *PLoS ONE*, **2017**, 12, e0169260	3.7	17
156	Normalized modularity optimization method for community identification with degree adjustment. *Physical Review E*, **2013**, 88, 052802	2.4	16
155	Gut Microbiome Associated with the Psychoneurological Symptom Cluster in Patients with Head and Neck Cancers. *Cancers*, **2020**, 12,	6.6	16
154	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. *Nature Medicine*, **2021**, 27, 1012-1024	50.5	16
153	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	9.4	15
152	Loneliness 5 years ante-mortem is associated with disease-related differential gene expression in postmortem dorsolateral prefrontal cortex. *Translational Psychiatry*, **2018**, 8, 2	8.6	15
151	Data-Independent Acquisition and Parallel Reaction Monitoring Mass Spectrometry Identification of Serum Biomarkers for Ovarian Cancer. *Biomarker Insights*, **2017**, 12, 1177271917710948	3.5	15
150	Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. *Nature Communications*, **2020**, 11, 5302	17.4	15
149	Mutations in the Histone Modifier PRDM6 Are Associated with Isolated Nonsyndromic Patent Ductus Arteriosus. *American Journal of Human Genetics*, **2016**, 98, 1082-1091	11	15
148	Ancestry-specific and sex-specific risk alleles identified in a genome-wide gene-by-alcohol dependence interaction study of risky sexual behaviors. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 846-853	3.5	14
147	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. *Molecular Psychiatry*, **2018**, 23, 2277-2286	15.1	14
146	A STATISTICAL FRAMEWORK FOR DATA INTEGRATION THROUGH GRAPHICAL MODELS WITH APPLICATION TO CANCER GENOMICS. *Annals of Applied Statistics*, **2017**, 11, 161-184	2.1	13
145	Reducing False-Positive Results in Newborn Screening Using Machine Learning. *International Journal of Neonatal Screening*, **2020**, 6,	2.6	13
144	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. *PLoS Computational Biology*, **2020**, 16, e1007565	5	13

143	AUDIT-C and ICD codes as phenotypes for harmful alcohol use: association with ADH1B polymorphisms in two US populations. *Addiction*, **2018**, 113, 2214-2224	4.6	13
142	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	10.3	13
141	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	4.9	13
140	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19.. *Nature Communications*, **2022**, 13, 440	17.4	13
139	CD4+ follicular regulatory T cells optimize the influenza virus-specific B cell response. *Journal of Experimental Medicine*, **2021**, 218,	16.6	13
138	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	2.4	13
137	Validating Harmful Alcohol Use as a Phenotype for Genetic Discovery Using Phosphatidylethanol and a Polymorphism in ADH1B. *Alcoholism: Clinical and Experimental Research*, **2017**, 41, 998-1003	3.7	12
136	International variations in trust in health care systems. *International Journal of Health Planning and Management*, **2019**, 34, 130-139	2.2	12
135	Exploring the genetic architecture of alcohol dependence in African-Americans via analysis of a genomewide set of common variants. *Human Genetics*, **2014**, 133, 617-24	6.3	12
134	Strategies to identify genes for complex diseases. *Annals of Medicine*, **1997**, 29, 493-8	1.5	12
133	The role of the gut microbiome in cancer-related fatigue: pilot study on epigenetic mechanisms. *Supportive Care in Cancer*, **2021**, 29, 3173-3182	3.9	12
132	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	28	12
131	Validation of an Electronic Medical Record-Based Algorithm for Identifying Posttraumatic Stress Disorder in U.S. Veterans. *Journal of Traumatic Stress*, **2019**, 32, 226-237	3.8	11
130	A novel machine learning unsupervised algorithm for sleep/wake identification using actigraphy. *Chronobiology International*, **2020**, 37, 1002-1015	3.6	11
129	Ethnic variability in newborn metabolic screening markers associated with false-positive outcomes. *Journal of Inherited Metabolic Disease*, **2020**, 43, 934-943	5.4	11
128	Genomic analyses of African Trypanozoon strains to assess evolutionary relationships and identify markers for strain identification. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005949	4.8	11
127	On an additive partial correlation operator and nonparametric estimation of graphical models. *Biometrika*, **2016**, 103, 513-530	2	11
126	Rare deleterious mutations of the gene EFR3A in autism spectrum disorders. *Molecular Autism*, **2014**, 5, 31	6.5	11

125	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	6.3	11
124	Statistical analysis of ordered tetrads. *Genetics*, **1998**, 150, 459-72	4	11
123	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	11	11
122	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	5	10
121	Transcriptional profiling of ectoderm specification to keratinocyte fate in human embryonic stem cells. *PLoS ONE*, **2015**, 10, e0122493	3.7	10
120	The power of transmission disequilibrium tests for quantitative traits. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S632-7	2.6	10
119	Novel genetic variants modify the effect of smoking on carotid plaque burden in Hispanics. *Journal of the Neurological Sciences*, **2014**, 344, 27-31	3.2	9
118	Genome-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	3.5	9
117	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. *Sleep*, **2020**, 43,	1.1	9
116	Elevated Blood Pressure Increases Pneumonia Risk: Epidemiological Association and Mendelian Randomization in the UK Biobank. *Med*, **2021**, 2, 137-148.e4	31.7	9
115	Benchmarking variant identification tools for plant diversity discovery. *BMC Genomics*, **2019**, 20, 701	4.5	8
114	graph-GPA: A graphical model for prioritizing GWAS results and investigating pleiotropic architecture. *PLoS Computational Biology*, **2017**, 13, e1005388	5	8
113	Cytogenomic mapping and bioinformatic mining reveal interacting brain expressed genes for intellectual disability. *Molecular Cytogenetics*, **2014**, 7, 4	2	8
112	Admixture mapping analysis in the context of GWAS with GAW18 data. *BMC Proceedings*, **2014**, 8, S3	2.3	8
111	Collapsing-based and kernel-based single-gene analyses applied to Genetic Analysis Workshop 17 mini-exome data. *BMC Proceedings*, **2011**, 5 Suppl 9, S117	2.3	8
110	Evidence of Polygenic Adaptation in the Systems Genetics of Anthropometric Traits. *PLoS ONE*, **2016**, 11, e0160654	3.7	8
109	Local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits		8
108	Overview of PAX gene family: analysis of human tissue-specific variant expression and involvement in human disease. *Human Genetics*, **2021**, 140, 381-400	6.3	8

107	Risk Locus Identification Ties Alcohol Withdrawal Symptoms to SORCS2. *Alcoholism: Clinical and Experimental Research*, **2018**, 42, 2337-2348	3.7	8
106	Random Effects Model for Multiple Pathway Analysis with Applications to Type II Diabetes Microarray Data. *Statistics in Biosciences*, **2015**, 7, 167-186	1.5	7
105	Adaptive clinical trial designs to detect interaction between treatment and a dichotomous biomarker. *Canadian Journal of Statistics*, **2013**, 41, 525-539	0.4	7
104	Deep Learning of the Retina Enables Phenome- and Genome-wide Analyses of the Microvasculature. *Circulation*, **2021**,	16.7	7
103	Trans-ancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders		7
102	Genomic Characterization of Posttraumatic Stress Disorder in a Large US Military Veteran Sample		7
101	Using DNA methylation to validate an electronic medical record phenotype for smoking. *Addiction Biology*, **2019**, 24, 1056-1065	4.6	7
100	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. *Schizophrenia Bulletin*, **2021**, 47, 517-529	1.3	7
99	Cytokine Profiles Before and After Immune Modulation in Hospitalized Patients with COVID-19. *Journal of Clinical Immunology*, **2021**, 41, 738-747	5.7	7
98	DIAPH1 Variants in Non-East Asian Patients With Sporadic Moyamoya Disease. *JAMA Neurology*, **2021**, 78, 993-1003	17.2	7
97	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. *Genome Biology*, **2021**, 22, 262	18.3	7
96	Genetic Link Between Arterial Stiffness and Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002453	5.2	6
95	Leveraging protein quaternary structure to identify oncogenic driver mutations. *BMC Bioinformatics*, **2016**, 17, 137	3.6	6
94	Linkage disequilibrium mapping in populations of variable size using the decay of haplotype sharing and a stepwise-mutation model. *Genetic Epidemiology*, **2000**, 19 Suppl 1, S99-105	2.6	6
93	A comprehensive genetic and epidemiological association analysis of vitamin D with common diseases/traits in the UK Biobank. *Genetic Epidemiology*, **2021**, 45, 24-35	2.6	6
92	Genomics of posttraumatic stress disorder in veterans: Methods and rationale for Veterans Affairs Cooperative Study #575B. *International Journal of Methods in Psychiatric Research*, **2019**, 28, e1767	4.3	5
91	Sparse Regression by Projection and Sparse Discriminant Analysis. *Journal of Computational and Graphical Statistics*, **2015**, 24, 416-438	1.4	5
90	Differential Protein Expression in Striatal D1- and D2-Dopamine Receptor-Expressing Medium Spiny Neurons. *Proteomes*, **2020**, 8,	4.6	5

89	identified in a genome-wide gene ꞏcannabis dependence interaction analysis of risky sexual behaviours. *Journal of Psychiatry and Neuroscience*, **2017**, 42, 252-261	4.5	5
88	Uncovering Genomic Regions Associated with Infections in Wild Populations of the Tsetse Fly. *G3: Genes, Genomes, Genetics*, **2018**, 8, 887-897	3.2	5
87	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. *Statistics in Biosciences*, **2018**, 10, 86-106	1.5	5
86	Impact of Sixteen Established Pancreatic Cancer Susceptibility Loci in American Jews. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1540-1548	4	5
85	Ovarian Cancer Classification Based on Mass Spectrometry Analysis of Sera. *Cancer Informatics*, **2006**, 2, 117693510600200	2.4	5
84	Gene-based and pathway-based genome-wide association study of alcohol dependence. *Shanghai Archives of Psychiatry*, **2015**, 27, 111-8		5
83	Noninvasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma. *Annals of the American Thoracic Society*, **2016**, 13 Suppl 1, S104-5	4.7	5
82	Variable importance-weighted Random Forests. *Quantitative Biology*, **2017**, 5, 338-351	3.9	5
81	Hematopoietic mosaic chromosomal alterations and risk for infection among 767,891 individuals without blood cancer **2020**,		5
80	Timing of Newborn Blood Collection Alters Metabolic Disease Screening Performance. *Frontiers in Pediatrics*, **2020**, 8, 623184	3.4	5
79	A fast and robust Bayesian nonparametric method for prediction of complex traits using summary statistics. *PLoS Genetics*, **2021**, 17, e1009697	6	5
78	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	16.6	4
77	CHANGE POINT ANALYSIS OF HISTONE MODIFICATIONS REVEALS EPIGENETIC BLOCKS LINKING TO PHYSICAL DOMAINS. *Annals of Applied Statistics*, **2016**, 10, 506-526	2.1	4
76	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	2.2	4
75	Measuring genetic variation in the multi-ethnic Million Veteran Program (MVP)		4
74	Regularized Latent Class Model for Joint Analysis of High-Dimensional Longitudinal Biomarkers and a Time-to-Event Outcome. *Biometrics*, **2019**, 75, 69-77	1.8	4
73	Hemodynamic Phenotypes of Hypertension Based on Cardiac Output and Systemic Vascular Resistance. *American Journal of Medicine*, **2020**, 133, e127-e139	2.4	4
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