

Eric R Gamazon

List of Publications by Citations

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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.

194
papers

21,450
citations

51
h-index

146
g-index

224
ext. papers

29,643
ext. citations

11.5
avg, IF

7.05
L-index

#	Paper	IF	Citations
194	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013 , 45, 580-5	36.3	4179
193	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , 2015 , 348, 648-60	33.3	3242
192	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017 , 550, 204-213	50.4	2086
191	Trait-associated SNPs are more likely to be eQTLs: annotation to enhance discovery from GWAS. <i>PLoS Genetics</i> , 2010 , 6, e1000888	6	941
190	A gene-based association method for mapping traits using reference transcriptome data. <i>Nature Genetics</i> , 2015 , 47, 1091-8	36.3	850
189	Obesity-associated variants within FTO form long-range functional connections with IRX3. <i>Nature</i> , 2014 , 507, 371-5	50.4	835
188	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
187	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020 , 369, 1318-1330	33.3	589
186	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , 2015 , 13, 311-9	2.1	432
185	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017 , 550, 244-248	50.4	417
184	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017 , 550, 249-254	50.4	286
183	Genome-wide association study of obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2013 , 18, 788-98	15.1	244
182	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018 , 50, 956-967	36.3	239
181	SCAN: SNP and copy number annotation. <i>Bioinformatics</i> , 2010 , 26, 259-62	7.2	203
180	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. <i>Lancet, The</i> , 2013 , 382, 790-6	40	191
179	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. <i>PLoS Genetics</i> , 2013 , 9, e1003864	6	189
178	Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. <i>PLoS Genetics</i> , 2011 , 7, e1002078	6	171

177	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015 , 348, 666-9	33.3	170
176	Gastric colonisation with a restricted commensal microbiota replicates the promotion of neoplastic lesions by diverse intestinal microbiota in the <i>Helicobacter pylori</i> INS-GAS mouse model of gastric carcinogenesis. <i>Gut</i> , 2014 , 63, 54-63	19.2	160
175	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017 , 3, 1654-1662	13.4	146
174	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017 , 550, 239-243	50.4	146
173	Genome-wide association study of Tourette's syndrome. <i>Molecular Psychiatry</i> , 2013 , 18, 721-8	15.1	138
172	Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. <i>Molecular Psychiatry</i> , 2013 , 18, 340-6	15.1	134
171	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015 , 5, 15145	4.9	128
170	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13127-32	11.5	121
169	Population differences in microRNA expression and biological implications. <i>RNA Biology</i> , 2011 , 8, 692-704.8	11.5	115
168	Evaluating phecodes, clinical classification software, and ICD-9-CM codes for phenome-wide association studies in the electronic health record. <i>PLoS ONE</i> , 2017 , 12, e0175508	3.7	111
167	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015 , 11, e1004220	5	104
166	Cross-disorder genome-wide analyses suggest a complex genetic relationship between Tourette's syndrome and OCD. <i>American Journal of Psychiatry</i> , 2015 , 172, 82-93	11.9	101
165	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	100
164	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019 , 51, 659-674	36.3	99
163	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017 , 27, 1843-1858	9.7	98
162	<i>Campylobacter jejuni</i> type VI secretion system: roles in adaptation to deoxycholic acid, host cell adherence, invasion, and in vivo colonization. <i>PLoS ONE</i> , 2012 , 7, e42842	3.7	96
161	Chemotherapeutic drug susceptibility associated SNPs are enriched in expression quantitative trait loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9287-92	11.5	96
160	The missing association: sequencing-based discovery of novel SNPs in VKORC1 and CYP2C9 that affect warfarin dose in African Americans. <i>Clinical Pharmacology and Therapeutics</i> , 2011 , 89, 408-15	6.1	94

159	Genome-wide association and meta-analysis in populations from Starr County, Texas, and Mexico City identify type 2 diabetes susceptibility loci and enrichment for expression quantitative trait loci in top signals. <i>Diabetologia</i> , 2011 , 54, 2047-55	10.3	90
158	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81
157	Genetic architecture of microRNA expression: implications for the transcriptome and complex traits. <i>American Journal of Human Genetics</i> , 2012 , 90, 1046-63	11	80
156	Identification of a genetic variant associated with treatment outcome in ovarian cancer: the potential role of cholesterol metabolism as a determinant of response to chemotherapy. <i>Hereditary Cancer in Clinical Practice</i> , 2012 , 10, A36	2.3	78
155	Response to Knoppers et al.. <i>American Journal of Human Genetics</i> , 2012 , 91, 579	11	78
154	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
153	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020 , 183, 269-283.e19	56.2	73
152	Genomics of alternative splicing: evolution, development and pathophysiology. <i>Human Genetics</i> , 2014 , 133, 679-87	6.3	71
151	The impact of human copy number variation on gene expression. <i>Briefings in Functional Genomics</i> , 2015 , 14, 352-7	4.9	69
150	ExpTarget: an integrative approach to predicting human microRNA targets. <i>PLoS ONE</i> , 2010 , 5, e13534	3.7	65
149	A genome-wide association study of early-onset breast cancer identifies PFKM as a novel breast cancer gene and supports a common genetic spectrum for breast cancer at any age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 658-69	4	63
148	Cross-tissue and tissue-specific eQTLs: partitioning the heritability of a complex trait. <i>American Journal of Human Genetics</i> , 2014 , 95, 521-34	11	61
147	On sharing quantitative trait GWAS results in an era of multiple-omics data and the limits of genomic privacy. <i>American Journal of Human Genetics</i> , 2012 , 90, 591-8	11	61
146	Platinum sensitivity-related germline polymorphism discovered via a cell-based approach and analysis of its association with outcome in ovarian cancer patients. <i>Clinical Cancer Research</i> , 2011 , 17, 5490-500	12.9	55
145	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. <i>Nature Genetics</i> , 2019 , 51, 933-940	36.3	51
144	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs. <i>Scientific Reports</i> , 2016 , 6, 19429	4.9	51
143	Ethnicity-specific pharmacogenetics: the case of warfarin in African Americans. <i>Pharmacogenomics Journal</i> , 2014 , 14, 223-8	3.5	50
142	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. <i>Blood</i> , 2014 , 124, 2298-305	2.2	49

141	Variants in and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. <i>Clinical Cancer Research</i> , 2017 , 23, 3325-3333	12.9	47
140	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
139	Functional genetic screen of human diversity reveals that a methionine salvage enzyme regulates inflammatory cell death. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2343-52	11.5	47
138	Variants affecting exon skipping contribute to complex traits. <i>PLoS Genetics</i> , 2012 , 8, e1002998	6	47
137	A study of CNVs as trait-associated polymorphisms and as expression quantitative trait loci. <i>PLoS Genetics</i> , 2011 , 7, e1001292	6	46
136	Integration of cell line and clinical trial genome-wide analyses supports a polygenic architecture of Paclitaxel-induced sensory peripheral neuropathy. <i>Clinical Cancer Research</i> , 2013 , 19, 491-9	12.9	45
135	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. <i>Pharmacogenomics Journal</i> , 2013 , 13, 35-43	3.5	45
134	Genetic factors affecting gene transcription and catalytic activity of UDP-glucuronosyltransferases in human liver. <i>Human Molecular Genetics</i> , 2014 , 23, 5558-69	5.6	44
133	Genetic association signal near NTN4 in Tourette syndrome. <i>Annals of Neurology</i> , 2014 , 76, 310-5	9.4	42
132	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 5757-5768	12.9	40
131	Identifying -mediators for -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017 , 27, 1859-1871	9.7	38
130	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021 , 22, 49	18.3	38
129	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. <i>Translational Research</i> , 2011 , 157, 265-72	11	37
128	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. <i>Nature Communications</i> , 2016 , 7, 10635	17.4	37
127	A gene co-expression network-based analysis of multiple brain tissues reveals novel genes and molecular pathways underlying major depression. <i>PLoS Genetics</i> , 2019 , 15, e1008245	6	36
126	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. <i>Blood</i> , 2013 , 121, 4366-76	2.2	36
125	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020 , 369,	33.3	36
124	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013 , 20, 619-29	8.6	35

123	PACdb: a database for cell-based pharmacogenomics. <i>Pharmacogenetics and Genomics</i> , 2010 , 20, 269-73	1.9	35
122	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. <i>Nature Genetics</i> , 2020 , 52, 1239-1246	36.3	35
121	Consistency in large pharmacogenomic studies. <i>Nature</i> , 2016 , 540, E1-E2	50.4	35
120	Poly-omic prediction of complex traits: OmicKriging. <i>Genetic Epidemiology</i> , 2014 , 38, 402-15	2.6	34
119	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. <i>Human Molecular Genetics</i> , 2016 , 25, 4835-4846	5.6	34
118	Cytotoxic and pathogenic properties of <i>Klebsiella oxytoca</i> isolated from laboratory animals. <i>PLoS ONE</i> , 2014 , 9, e100542	3.7	33
117	Genetic variation that predicts platinum sensitivity reveals the role of miR-193b* in chemotherapeutic susceptibility. <i>Molecular Cancer Therapeutics</i> , 2012 , 11, 2054-61	6.1	33
116	A genome-wide integrative study of microRNAs in human liver. <i>BMC Genomics</i> , 2013 , 14, 395	4.5	31
115	Linking the genetic architecture of cytosine modifications with human complex traits. <i>Human Molecular Genetics</i> , 2014 , 23, 5893-905	5.6	30
114	An exponential combination procedure for set-based association tests in sequencing studies. <i>American Journal of Human Genetics</i> , 2012 , 91, 977-86	11	30
113	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
112	Enrichment of inflammatory bowel disease and colorectal cancer risk variants in colon expression quantitative trait loci. <i>BMC Genomics</i> , 2015 , 16, 138	4.5	29
111	The impact of microRNA expression on cellular proliferation. <i>Human Genetics</i> , 2014 , 133, 931-8	6.3	29
110	Genetic risk factors for type 2 diabetes: a trans-regulatory genetic architecture?. <i>American Journal of Human Genetics</i> , 2012 , 91, 466-77	11	28
109	Novel genetic predictors of venous thromboembolism risk in African Americans. <i>Blood</i> , 2016 , 127, 1923-9.2	9.2	28
108	Loci nominally associated with autism from genome-wide analysis show enrichment of brain expression quantitative trait loci but not lymphoblastoid cell line expression quantitative trait loci. <i>Molecular Autism</i> , 2012 , 3, 3	6.5	27
107	Regulation of Insulin Receptor Pathway and Glucose Metabolism by CD36 Signaling. <i>Diabetes</i> , 2018 , 67, 1272-1284	0.9	26
106	Trans-population analysis of genetic mechanisms of ethnic disparities in neuroblastoma survival. <i>Journal of the National Cancer Institute</i> , 2013 , 105, 302-9	9.7	25

105	Population differences in platinum toxicity as a means to identify novel genetic susceptibility variants. <i>Pharmacogenetics and Genomics</i> , 2010 , 20, 327-37	1.9	25
104	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. <i>American Journal of Human Genetics</i> , 2016 , 98, 697-708	11	25
103	Identification of a variant in KDR associated with serum VEGFR2 and pharmacodynamics of Pazopanib. <i>Clinical Cancer Research</i> , 2015 , 21, 365-72	12.9	24
102	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. <i>Carcinogenesis</i> , 2013 , 34, 1520-8	4.6	24
101	Mixed effects modeling of proliferation rates in cell-based models: consequence for pharmacogenomics and cancer. <i>PLoS Genetics</i> , 2012 , 8, e1002525	6	24
100	On Using Local Ancestry to Characterize the Genetic Architecture of Human Traits: Genetic Regulation of Gene Expression in Multiethnic or Admixed Populations. <i>American Journal of Human Genetics</i> , 2019 , 104, 1097-1115	11	23
99	Identification of novel germline polymorphisms governing capecitabine sensitivity. <i>Cancer</i> , 2012 , 118, 4063-73	6.4	23
98	Copy number polymorphisms and anticancer pharmacogenomics. <i>Genome Biology</i> , 2011 , 12, R46	18.3	23
97	The limits of genome-wide methods for pharmacogenomic testing. <i>Pharmacogenetics and Genomics</i> , 2012 , 22, 261-72	1.9	23
96	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1598-1606	12.3	22
95	Genetic architecture of host proteins involved in SARS-CoV-2 infection. <i>Nature Communications</i> , 2020 , 11, 6397	17.4	22
94	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
93	Local genetic effects on gene expression across 44 human tissues		22
92	The regulatory effect of miRNAs is a heritable genetic trait in humans. <i>BMC Genomics</i> , 2012 , 13, 383	4.5	21
91	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. <i>Pharmacogenetics and Genomics</i> , 2012 , 22, 498-507	1.9	21
90	Genome-wide local ancestry approach identifies genes and variants associated with chemotherapeutic susceptibility in African Americans. <i>PLoS ONE</i> , 2011 , 6, e21920	3.7	21
89	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci		21
88	Structural architecture of SNP effects on complex traits. <i>American Journal of Human Genetics</i> , 2014 , 95, 477-89	11	20

87	Clinical translation of cell-based pharmacogenomic discovery. <i>Clinical Pharmacology and Therapeutics</i> , 2012 , 92, 425-7	6.1	20
86	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021 , 184, 2633-2648.e19	56.2	20
85	Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. <i>BMC Genomics</i> , 2014 , 15, 292	4.5	19
84	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020 , 21, 234	18.3	18
83	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. <i>Pharmacogenomics Journal</i> , 2017 , 17, 137-145	3.5	17
82	SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	17
81	MicroRNA biogenesis and cellular proliferation. <i>Translational Research</i> , 2015 , 166, 145-51	11	16
80	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. <i>Nature Medicine</i> , 2020 , 26, 98-109	50.5	16
79	Comprehensive survey of SNPs in the Affymetrix exon array using the 1000 Genomes dataset. <i>PLoS ONE</i> , 2010 , 5, e9366	3.7	16
78	A pharmacogene database enhanced by the 1000 Genomes Project. <i>Pharmacogenetics and Genomics</i> , 2009 , 19, 829-32	1.9	16
77	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. <i>Clinical Cancer Research</i> , 2019 , 25, 4104-4116	12.9	15
76	Genetic variation associated with euphorogenic effects of d-amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5968-73	11.5	15
75	Genome-wide interrogation of longitudinal FEV1 in children with asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014 , 190, 619-27	10.2	14
74	Integrative genomics: quantifying significance of phenotype-genotype relationships from multiple sources of high-throughput data. <i>Frontiers in Genetics</i> , 2012 , 3, 202	4.5	13
73	Gene and MicroRNA Perturbations of Cellular Response to Pemetrexed Implicate Biological Networks and Enable Imputation of Response in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2018 , 8, 733	4.9	12
72	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. <i>Human Molecular Genetics</i> , 2012 , 21, 1470-80	5.6	12
71	STAMS: STRING-assisted module search for genome wide association studies and application to autism. <i>Bioinformatics</i> , 2016 , 32, 3815-3822	7.2	11
70	Discovery and functional assessment of gene variants in the vascular endothelial growth factor pathway. <i>Human Mutation</i> , 2014 , 35, 227-35	4.7	11

69	Differential expression of systemic inflammatory mediators in amputees with chronic residual limb pain. <i>Pain</i> , 2017 , 158, 68-74	8	11
68	Mapping the proteo-genomic convergence of human diseases. <i>Science</i> , 2021 , 374, eabj1541	33.3	11
67	An analysis of genetically regulated gene expression across multiple tissues implicates novel gene candidates in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2020 , 12, 43	9	11
66	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018 , 42, 49-63	2.6	11
65	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. <i>Nature Metabolism</i> , 2020 , 2, 487-498	14.6	10
64	Genetic susceptibility to type 2 diabetes and breast cancer risk in women of European and African ancestry. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 552-6	4	10
63	Bid maintains mitochondrial cristae structure and function and protects against cardiac disease in an integrative genomics study. <i>ELife</i> , 2018 , 7,	8.9	10
62	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. <i>American Journal of Human Genetics</i> , 2019 , 104, 503-519	11	10
61	A pharmacogenetic study of aldehyde oxidase I in patients treated with XK469. <i>Pharmacogenetics and Genomics</i> , 2014 , 24, 129-32	1.9	9
60	Genome-wide discovery of genetic variants affecting tamoxifen sensitivity and their clinical and functional validation. <i>Annals of Oncology</i> , 2013 , 24, 1867-1873	10.3	9
59	Transcriptomic Imputation of Bipolar Disorder and Bipolar subtypes reveals 29 novel associated genes		9
58	E-MAGMA: an eQTL-informed method to identify risk genes using genome-wide association study summary statistics. <i>Bioinformatics</i> , 2021 ,	7.2	9
57	SCAN: a systems biology approach to pharmacogenomic discovery. <i>Methods in Molecular Biology</i> , 2013 , 1015, 213-24	1.4	8
56	Post-GWAS analysis of six substance use traits improves the identification and functional interpretation of genetic risk loci. <i>Drug and Alcohol Dependence</i> , 2020 , 206, 107703	4.9	8
55	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. <i>Pain</i> , 2019 , 160, 2328-2337	8	8
54	Integrating cell-based and clinical genome-wide studies to identify genetic variants contributing to treatment failure in neuroblastoma patients. <i>Clinical Pharmacology and Therapeutics</i> , 2014 , 95, 644-52	6.1	7
53	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. <i>Scientific Reports</i> , 2017 , 7, 5980	4.9	7
52	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. <i>BMC Genomics</i> , 2015 , 16, 1109	4.5	7

51	Integrative genetic analysis suggests that skin color modifies the genetic architecture of melanoma. <i>PLoS ONE</i> , 2017 , 12, e0185730	3.7	7
50	Transcriptional regulation of PNPLA3 and its impact on susceptibility to nonalcoholic fatty liver Disease (NAFLD) in humans. <i>Aging</i> , 2016 , 9, 26-40	5.6	7
49	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells. <i>Nature</i> , 2021 , 599, 136-140	3.4	7
48	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. <i>Cancer Research</i> , 2020 , 80, 4346-4354	10.1	7
47	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. <i>Drug and Alcohol Dependence</i> , 2018 , 188, 94-101	4.9	7
46	Translating pharmacogenomics discoveries into the clinic: an implementation framework. <i>Genome Medicine</i> , 2013 , 5, 94	14.4	6
45	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
44	Distant regulatory effects of genetic variation in multiple human tissues		6
43	Gene expression imputation across multiple brain regions reveals schizophrenia risk throughout development		6
42	The Relation Between Inflation in Type-I and Type-II Error Rate and Population Divergence in Genome-Wide Association Analysis of Multi-Ethnic Populations. <i>Behavior Genetics</i> , 2017 , 47, 360-368	3.2	5
41	A genome-wide sib-pair scan for quantitative language traits reveals linkage to chromosomes 10 and 13. <i>Genes, Brain and Behavior</i> , 2015 , 14, 387-97	3.6	5
40	SNP-based heritability estimation: measurement noise, population stratification, and stability		5
39	Genetic architecture of host proteins interacting with SARS-CoV-2 2020 ,		5
38	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019 , 28, 1212-1224	5.6	5
37	Alternative Splicing and Genome Evolution 2016 , 1-6		4
36	Comprehensive evaluation of the contribution of X chromosome genes to platinum sensitivity. <i>Molecular Cancer Therapeutics</i> , 2011 , 10, 472-80	6.1	4
35	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. <i>Pharmacogenomics Journal</i> , 2018 , 18, 106-112	3.5	3
34	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3

33	Multi-omic analysis elucidates the genetic basis of hydrocephalus. <i>Cell Reports</i> , 2021 , 35, 109085	10.6	3
32	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. <i>Npj Genomic Medicine</i> , 2019 , 4, 29	6.2	3
31	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. <i>Genetics in Medicine</i> , 2020 , 22, 1191-1200	8.1	3
30	Integrated analysis of genetic variation and gene expression reveals novel variant for increased warfarin dose requirement in African Americans. <i>Journal of Thrombosis and Haemostasis</i> , 2017 , 15, 735-743	15.4	2
29	Genomic Variants of Cytarabine Sensitivity Associated with Treatment-Related Mortality in Pediatric AML: A Report from the Children's Oncology Group. <i>Clinical Cancer Research</i> , 2020 , 26, 2891-2897	12.9	2
28	Uncovering the role of admixture in disease and drug response: Association of hepatocyte gene expression and DNA methylation with African Ancestry in African Americans		2
27	Modeling mutational effects on biochemical phenotypes using convolutional neural networks: application to SARS-CoV-2 2021 ,		2
26	Contextualizing genetic risk score for disease screening and rare variant discovery. <i>Nature Communications</i> , 2021 , 12, 4418	17.4	2
25	Integrative Network-Based Analysis Reveals Gene Networks and Novel Drug Repositioning Candidates for Alzheimer Disease. <i>Neurology: Genetics</i> , 2021 , 7, e622	3.8	2
24	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. <i>International Journal of Cancer</i> , 2022 , 150, 80-90	7.5	2
23	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. <i>Translational Psychiatry</i> , 2021 , 11, 618	8.6	2
22	Shared Genetic Control of Brain Activity During Sleep and Insulin Secretion: A Laboratory-Based Family Study. <i>Diabetes</i> , 2018 , 67, 155-164	0.9	1
21	Variation in protein-coding sequence and the genetic basis of cisplatin-induced toxicities among testicular cancer survivors (TCS) in the Platinum Study.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 1537-1537	2.2	1
20	CD36 maintains the gastric mucosa and associates with gastric disease. <i>Communications Biology</i> , 2021 , 4, 1247	6.7	1
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