Eric R Gamazon

List of Publications by Year
in descending order

187	34,301	28274 55	5539 163
papers	citations	h-index	g-index

224	224	224	51188
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
3	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
4	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
5	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	21.4	1,473
6	Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS. PLoS Genetics, 2010, 6, e1000888.	3.5	1,161
7	Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 2014, 507, 371-375.	27.8	1,079
8	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
9	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
10	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. Biopreservation and Biobanking, 2015, 13, 311-319.	1.0	674
11	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495
12	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	21.4	389
13	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
14	Genome-wide association study of obsessive-compulsive disorder. Molecular Psychiatry, 2013, 18, 788-798.	7.9	312
15	Evaluating phecodes, clinical classification software, and ICD-9-CM codes for phenome-wide association studies in the electronic health record. PLoS ONE, 2017, 12, e0175508.	2.5	268
16	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
17	Gastric colonisation with a restricted commensal microbiota replicates the promotion of neoplastic lesions by diverse intestinal microbiota in theHelicobacter pyloriINS-GAS mouse model of gastric carcinogenesis. Gut, 2014, 63, 54-63.	12.1	246
18	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243

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19	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	3.5	241
20	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. Lancet, The, 2013, 382, 790-796.	13.7	237
21	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
22	SCAN: SNP and copy number annotation. Bioinformatics, 2010, 26, 259-262.	4.1	214
23	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. JAMA Oncology, 2017, 3, 1654.	7.1	208
24	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	12.6	192
25	Identification, Replication, and Functional Fine-Mapping of Expression Quantitative Trait Loci in Primary Human Liver Tissue. PLoS Genetics, 2011, 7, e1002078.	3.5	191
26	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	3.3	180
27	Genome-wide association study of Tourette's syndrome. Molecular Psychiatry, 2013, 18, 721-728.	7.9	161
28	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	3.2	158
29	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	21.4	154
30	Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. Molecular Psychiatry, 2013, 18, 340-346.	7.9	153
31	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	7.1	152
32	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
33	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
34	Population differences in microRNA expression and biological implications. RNA Biology, 2011, 8, 692-701.	3.1	138
35	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. Nature Genetics, 2020, 52, 1239-1246.	21.4	134
36	Campylobacter jejuni Type VI Secretion System: Roles in Adaptation to Deoxycholic Acid, Host Cell Adherence, Invasion, and In Vivo Colonization. PLoS ONE, 2012, 7, e42842.	2.5	132

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37	Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Tourette's Syndrome and OCD. American Journal of Psychiatry, 2015, 172, 82-93.	7.2	117
38	The impact of human copy number variation on gene expression: Figure 1. Briefings in Functional Genomics, 2015, 14, 352-357.	2.7	108
39	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. Diabetologia, 2011, 54, 2047-2055.	6.3	106
40	Chemotherapeutic drug susceptibility associated SNPs are enriched in expression quantitative trait loci. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9287-9292.	7.1	103
41	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	3.8	103
42	The Missing Association: Sequencing-Based Discovery of Novel SNPs in VKORC1 and CYP2C9 That Affect Warfarin Dose in African Americans. Clinical Pharmacology and Therapeutics, 2011, 89, 408-415.	4.7	100
43	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
44	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
45	Genetic Architecture of MicroRNA Expression: Implications for the Transcriptome and Complex Traits. American Journal of Human Genetics, 2012, 90, 1046-1063.	6.2	92
46	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
47	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
48	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells. Nature, 2021, 599, 136-140.	27.8	89
49	On Sharing Quantitative Trait GWAS Results in an Era of Multiple-omics Data and the Limits of Genomic Privacy. American Journal of Human Genetics, 2012, 90, 591-598.	6.2	87
50	Cross-Tissue and Tissue-Specific eQTLs: Partitioning the Heritability of a Complex Trait. American Journal of Human Genetics, 2014, 95, 521-534.	6.2	82
51	ExprTarget: An Integrative Approach to Predicting Human MicroRNA Targets. PLoS ONE, 2010, 5, e13534.	2.5	80
52	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. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	2.5	77
53	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. Nature Genetics, 2019, 51, 933-940.	21.4	77
54	A gene co-expression network-based analysis of multiple brain tissues reveals novel genes and molecular pathways underlying major depression. PLoS Genetics, 2019, 15, e1008245.	3.5	74

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55	Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
56	Genetic architecture of host proteins involved in SARS-CoV-2 infection. Nature Communications, 2020, 11, 6397.	12.8	71
57	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
58	Variants in WFS1 and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. Clinical Cancer Research, 2017, 23, 3325-3333.	7.0	65
59	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. Scientific Reports, 2016, 6, 19429.	3.3	63
60	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. Clinical Cancer Research, 2017, 23, 5757-5768.	7.0	63
61	Functional genetic screen of human diversity reveals that a methionine salvage enzyme regulates inflammatory cell death. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2343-52.	7.1	59
62	Ethnicity-specific pharmacogenetics: the case of warfarin in African Americans. Pharmacogenomics Journal, 2014, 14, 223-228.	2.0	59
63	Platinum Sensitivityâ€“Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	7.0	57
64	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. Blood, 2014, 124, 2298-2305.	1.4	57
65	Integration of Cell Line and Clinical Trial Genome-Wide Analyses Supports a Polygenic Architecture of Paclitaxel-Induced Sensory Peripheral Neuropathy. Clinical Cancer Research, 2013, 19, 491-499.	7.0	55
66	Variants Affecting Exon Skipping Contribute to Complex Traits. PLoS Genetics, 2012, 8, e1002998.	3.5	53
67	Genetic association signal near <scp>NTN</scp>4 in <scp>T</scp>ourette syndrome. Annals of Neurology, 2014, 76, 310-315.	5.3	53
68	Consistency in large pharmacogenomic studies. Nature, 2016, 540, E1-E2.	27.8	52
69	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
70	A Study of CNVs As Trait-Associated Polymorphisms and As Expression Quantitative Trait Loci. PLoS Genetics, 2011, 7, e1001292.	3.5	50
71	Genetic factors affecting gene transcription and catalytic activity of UDP-glucuronosyltransferases in human liver. Human Molecular Genetics, 2014, 23, 5558-5569.	2.9	50
72	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. Human Molecular Genetics, 2016, 25, ddw305.	2.9	50

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73	On Using Local Ancestry to Characterize the Genetic Architecture of Human Traits: Genetic Regulation of Gene Expression in Multiethnic or Admixed Populations. American Journal of Human Genetics, 2019, 104, 1097-1115.	6.2	50
74	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. Pharmacogenomics Journal, 2013, 13, 35-43.	2.0	49
75	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
76	Enrichment of inflammatory bowel disease and colorectal cancer risk variants in colon expression quantitative trait loci. BMC Genomics, 2015, 16, 138.	2.8	45
77	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. Nature Ecology and Evolution, 2019, 3, 1598-1606.	7.8	45
78	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. Nature Communications, 2016, 7, 10635.	12.8	44
79	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 619-629.	4.4	43
80	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. Translational Research, 2011, 157, 265-272.	5.0	42
81	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. Blood, 2013, 121, 4366-4376.	1.4	42
82	Poly-Omic Prediction of Complex Traits: OmicKriging. Genetic Epidemiology, 2014, 38, 402-415.	1.3	41
83	Regulation of Insulin Receptor Pathway and Glucose Metabolism by CD36 Signaling. Diabetes, 2018, 67, 1272-1284.	0.6	41
84	The impact of microRNA expression on cellular proliferation. Human Genetics, 2014, 133, 931-938.	3.8	40
85	PACdb: a database for cell-based pharmacogenomics. Pharmacogenetics and Genomics, 2010, 20, 269-273.	1.5	40
86	A genome-wide integrative study of microRNAs in human liver. BMC Genomics, 2013, 14, 395.	2.8	39
87	Cytotoxic and Pathogenic Properties of Klebsiella oxytoca Isolated from Laboratory Animals. PLoS ONE, 2014, 9, e100542.	2.5	39
88	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. Molecular Autism, 2012, 3, 3.	4.9	38
89	Novel genetic predictors of venous thromboembolism risk in African Americans. Blood, 2016, 127, 1923-1929.	1.4	38
90	Linking the genetic architecture of cytosine modifications with human complex traits. Human Molecular Genetics, 2014, 23, 5893-5905.	2.9	36

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91	Genetic Variation That Predicts Platinum Sensitivity Reveals the Role of miR-193b* in Chemotherapeutic Susceptibility. Molecular Cancer Therapeutics, 2012, 11, 2054-2061.	4.1	35
92	An Exponential Combination Procedure for Set-Based Association Tests in Sequencing Studies. American Journal of Human Genetics, 2012, 91, 977-986.	6.2	34
93	E-MAGMA: an eQTL-informed method to identify risk genes using genome-wide association study summary statistics. Bioinformatics, 2021, 37, 2245-2249.	4.1	34
94	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. Nature Metabolism, 2020, 2, 487-498.	11.9	32
95	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. Nature Medicine, 2020, 26, 98-109.	30.7	32
96	Genetic Risk Factors for Type 2 Diabetes: A Trans-Regulatory Genetic Architecture?. American Journal of Human Genetics, 2012, 91, 466-477.	6.2	31
97	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
98	Population differences in platinum toxicity as a means to identify novel genetic susceptibility variants. Pharmacogenetics and Genomics, 2010, 20, 327-337.	1.5	30
99	Trans-population Analysis of Genetic Mechanisms of Ethnic Disparities in Neuroblastoma Survival. Journal of the National Cancer Institute, 2012, 105, 302-309.	6.3	30
100	The limits of genome-wide methods for pharmacogenomic testing. Pharmacogenetics and Genomics, 2012, 22, 261-272.	1.5	29
101	Identification of a Variant in KDR Associated with Serum VEGFR2 and Pharmacodynamics of Pazopanib. Clinical Cancer Research, 2015, 21, 365-372.	7.0	29
102	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. Pharmacogenetics and Genomics, 2012, 22, 498-507.	1.5	28
103	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. Cancer Research, 2020, 80, 4346-4354.	0.9	28
104	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. Clinical Cancer Research, 2019, 25, 4104-4116.	7.0	27
105	Mixed Effects Modeling of Proliferation Rates in Cell-Based Models: Consequence for Pharmacogenomics and Cancer. PLoS Genetics, 2012, 8, e1002525.	3.5	26
106	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. Carcinogenesis, 2013, 34, 1520-1528.	2.8	26
107	Copy number polymorphisms and anticancer pharmacogenomics. Genome Biology, 2011, 12, R46.	9.6	25
108	Identification of novel germline polymorphisms governing capecitabine sensitivity. Cancer, 2012, 118, 4063-4073.	4.1	25

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109	A transcriptome-wide association study of Alzheimerâ€™s disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. Genome Medicine, 2021, 13, 141.	8.2	25
110	Genome-Wide Local Ancestry Approach Identifies Genes and Variants Associated with Chemotherapeutic Susceptibility in African Americans. PLoS ONE, 2011, 6, e21920.	2.5	25
111	Clinical Translation of Cell-Based Pharmacogenomic Discovery. Clinical Pharmacology and Therapeutics, 2012, 92, 425-427.	4.7	24
112	Structural Architecture of SNP Effects on Complex Traits. American Journal of Human Genetics, 2014, 95, 477-489.	6.2	24
113	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. Pharmacogenomics Journal, 2017, 17, 137-145.	2.0	24
114	The regulatory effect of miRNAs is a heritable genetic trait in humans. BMC Genomics, 2012, 13, 383.	2.8	23
115	Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. BMC Genomics, 2014, 15, 292.	2.8	23
116	Differential expression of systemic inflammatory mediators in amputees with chronic residual limb pain. Pain, 2017, 158, 68-74.	4.2	22
117	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. American Journal of Human Genetics, 2019, 104, 503-519.	6.2	21
118	An analysis of genetically regulated gene expression across multiple tissues implicates novel gene candidates in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2020, 12, 43.	6.2	20
119	SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav025-bav025.	3.0	19
120	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. Pain, 2019, 160, 2328-2337.	4.2	19
121	Post-GWAS analysis of six substance use traits improves the identification and functional interpretation of genetic risk loci. Drug and Alcohol Dependence, 2020, 206, 107703.	3.2	19
122	Bid maintains mitochondrial cristae structure and function and protects against cardiac disease in an integrative genomics study. ELife, 2018, 7, .	6.0	19
123	A pharmacogene database enhanced by the 1000 Genomes Project. Pharmacogenetics and Genomics, 2009, 19, 829-832.	1.5	18
124	Comprehensive Survey of SNPs in the Affymetrix Exon Array Using the 1000 Genomes Dataset. PLoS ONE, 2010, 5, e9366.	2.5	18
125	Genetic variation associated with euphorigenic effects of d -amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5968-5973.	7.1	18
126	MicroRNA biogenesis and cellular proliferation. Translational Research, 2015, 166, 145-151.	5.0	18

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127	Multi-omic analysis elucidates the genetic basis of hydrocephalus. Cell Reports, 2021, 35, 109085.	6.4	18
128	Genome-wide Interrogation of Longitudinal FEV₁ in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 619-627.	5.6	17
129	STAMS: STRING-assisted module search for genome wide association studies and application to autism. Bioinformatics, 2016, 32, 3815-3822.	4.1	17
130	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
131	Integrative Network-Based Analysis Reveals Gene Networks and Novel Drug Repositioning Candidates for Alzheimer Disease. Neurology: Genetics, 2021, 7, e622.	1.9	17
132	Genetically regulated expression in late-onset Alzheimerâ€™s disease implicates risk genes within known and novel loci. Translational Psychiatry, 2021, 11, 618.	4.8	17
133	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. Human Molecular Genetics, 2012, 21, 1470-1480.	2.9	16
134	The impact of sex on gene expression across human tissues. Yearbook of Paediatric Endocrinology, 0, , .	0.0	16
135	Integrative Genomics: Quantifying Significance of Phenotype-Genotype Relationships from Multiple Sources of High-Throughput Data. Frontiers in Genetics, 2012, 3, 202.	2.3	14
136	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. Frontiers in Genetics, 2021, 12, 624128.	2.3	14
137	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. BMC Genomics, 2015, 16, 1109.	2.8	13
138	Discovery and Functional Assessment of Gene Variants in the Vascular Endothelial Growth Factor Pathway. Human Mutation, 2014, 35, 227-235.	2.5	12
139	Gene and MicroRNA Perturbations of Cellular Response to Pemetrexed Implicate Biological Networks and Enable Imputation of Response in Lung Adenocarcinoma. Scientific Reports, 2018, 8, 733.	3.3	12
140	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
141	Genome-wide approaches in pharmacogenomics: heritability estimation and pharmacoethnicity as primary challenges. Pharmacogenomics, 2012, 13, 1101-1104.	1.3	11
142	Contextualizing genetic risk score for disease screening and rare variant discovery. Nature Communications, 2021, 12, 4418.	12.8	11
143	Transcriptional regulation of PNPLA3 and its impact on susceptibility to nonalcoholic fatty liver Disease (NAFLD) in humans. Aging, 2016, 9, 26-40.	3.1	11
144	Genetic Susceptibility to Type 2 Diabetes and Breast Cancer Risk in Women of European and African Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 552-556.	2.5	10

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145	Genome-wide discovery of genetic variants affecting tamoxifen sensitivity and their clinical and functional validation. Annals of Oncology, 2013, 24, 1867-1873.	1.2	10
146	A pharmacogenetic study of aldehyde oxidase I in patients treated with XK469. Pharmacogenetics and Genomics, 2014, 24, 129-132.	1.5	10
147	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. Scientific Reports, 2017, 7, 5980.	3.3	10
148	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. Drug and Alcohol Dependence, 2018, 188, 94-101.	3.2	10
149	Integrative genetic analysis suggests that skin color modifies the genetic architecture of melanoma. PLoS ONE, 2017, 12, e0185730.	2.5	10
150	A transcriptomeâ€wide association study identifies novel candidate susceptibility genes for prostate cancer risk. International Journal of Cancer, 2022, 150, 80-90.	5.1	9
151	SCAN: A Systems Biology Approach to Pharmacogenomic Discovery. Methods in Molecular Biology, 2013, 1015, 213-224.	0.9	8
152	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. Npj Genomic Medicine, 2019, 4, 29.	3.8	8
153	CD36 maintains the gastric mucosa and associates with gastric disease. Communications Biology, 2021, 4, 1247.	4.4	8
154	Integrating Cell-Based and Clinical Genome-Wide Studies to Identify Genetic Variants Contributing to Treatment Failure in Neuroblastoma Patients. Clinical Pharmacology and Therapeutics, 2014, 95, 644-652.	4.7	7
155	A genomeâ€wide sibâ€pair scan for quantitative language traits reveals linkage to chromosomes 10 and 13. Genes, Brain and Behavior, 2015, 14, 387-397.	2.2	7
156	The Relation Between Inflation in Type-I and Type-II Error Rate and Population Divergence in Genome-Wide Association Analysis of Multi-Ethnic Populations. Behavior Genetics, 2017, 47, 360-368.	2.1	7
157	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. Pharmacogenomics Journal, 2018, 18, 106-112.	2.0	7
158	Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. Npj Systems Biology and Applications, 2021, 7, 24.	3.0	7
159	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimerâ€™s disease risk. Human Molecular Genetics, 2021, 31, 289-299.	2.9	7
160	Translating pharmacogenomics discoveries into the clinic: an implementation framework. Genome Medicine, 2013, 5, 94.	8.2	6
161	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. Genetics in Medicine, 2020, 22, 1191-1200.	2.4	6
162	A Local Genetic Correlation Analysis Provides Biological Insights Into the Shared Genetic Architecture of Psychiatric and Substance Use Phenotypes. Biological Psychiatry, 2022, 92, 583-591.	1.3	6

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163	Comprehensive Evaluation of the Contribution of X Chromosome Genes to Platinum Sensitivity. Molecular Cancer Therapeutics, 2011, 10, 472-480.	4.1	5
164	An integrative systemsâ€based analysis of substance use: <scp>eQTL</scp>â€informed geneâ€based tests, gene networks, and biological mechanisms. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 162-172.	1.7	5
165	Transcriptomeâ€wide association analysis offers novel opportunities for clinical translation of genetic discoveries on mental disorders. World Psychiatry, 2020, 19, 113-114.	10.4	4
166	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes. Human Molecular Genetics, 2022, 31, 3191-3205.	2.9	4
167	Integrated analysis of genetic variation and gene expression reveals novel variant for increased warfarin dose requirement in African Americans. Journal of Thrombosis and Haemostasis, 2017, 15, 735-743.	3.8	3
168	Genomic Variants of Cytarabine Sensitivity Associated with Treatment-Related Mortality in Pediatric AML: A Report from the Children's Oncology Group. Clinical Cancer Research, 2020, 26, 2891-2897.	7.0	3
169	An analysis of genetically regulated gene expression and the role of co-expression networks across 16 psychiatric and substance use phenotypes. European Journal of Human Genetics, 2022, 30, 560-566.	2.8	3
170	Integrative transcriptomic, evolutionary, and causal inference framework for region-level analysis: Application to COVID-19. Npj Genomic Medicine, 2022, 7, 24.	3.8	3
171	Modeling mutational effects on biochemical phenotypes using convolutional neural networks: application to SARS-CoV-2. IScience, 2022, 25, 104500.	4.1	2
172	Shared Genetic Control of Brain Activity During Sleep and Insulin Secretion: A Laboratory-Based Family Study. Diabetes, 2018, 67, 155-164.	0.6	1
173	Revisiting Some Useful Statistical Guidelines in Circulation Research in Response to a Changing Landscape. Circulation Research, 2021, 128, 1724-1727.	4.5	1
174	Detecting context-dependent gene regulation. Nature Computational Science, 2021, 1, 393-394.	8.0	1
175	Variation in protein-coding sequence and the genetic basis of cisplatin-induced toxicities among testicular cancer survivors (TCS) in the Platinum Study.. Journal of Clinical Oncology, 2016, 34, 1537-1537.	1.6	1
176	Two polymorphic gene loci associated with treprostinil dose in pulmonary arterial hypertension. Pharmacogenetics and Genomics, 2022, Publish Ahead of Print, .	1.5	1
177	Small Science: High Stakes. Science, 2012, 338, 883-883.	12.6	0
178	Response to Knoppers etÂal.. American Journal of Human Genetics, 2012, 91, 579.	6.2	0
179	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. Hereditary Cancer in Clinical Practice, 2012, 10, A36.	1.5	0
180	EXPLORING THE ROLE OF GENETIC REGULATION OF GENE EXPRESSION IN SUBSTANCE USE AND DEPENDENCE. European Neuropsychopharmacology, 2019, 29, S803-S804.	0.7	0

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181	M52 EMAGMA: A NOVEL METHOD TO INTEGRATE GENETIC AND TRANSCRIPTOMIC INFORMATION. European Neuropsychopharmacology, 2019, 29, S193-S194.	0.7	0
182	Optimizing Genetic Analyses of Serum Lipids in Longitudinal Data. Circulation Research, 2020, 127, 1337-1339.	4.5	0
183	Tissueâ€specific genetically regulated expression in lateâ€onset Alzheimerâ€™s disease implicates risk genes within known and 30 novel loci. Alzheimer's and Dementia, 2020, 16, e039475.	0.8	0
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