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	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
2	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
3	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
4	Integrative transcriptomic, evolutionary, and causal inference framework for region-level analysis: Application to COVID-19. Npj Genomic Medicine, 2022, 7, 24.	3.8	3
5	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
6	Two polymorphic gene loci associated with treprostinil dose in pulmonary arterial hypertension. Pharmacogenetics and Genomics, 2022, Publish Ahead of Print, .	1.5	1
7	Modeling mutational effects on biochemical phenotypes using convolutional neural networks: application to SARS-CoV-2. IScience, 2022, 25, 104500.	4.1	2
8	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
9	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
10	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. Frontiers in Genetics, 2021, 12, 624128.	2.3	14
11	Multi-omic analysis elucidates the genetic basis of hydrocephalus. Cell Reports, 2021, 35, 109085.	6.4	18
12	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
13	Revisiting Some Useful Statistical Guidelines in Circulation Research in Response to a Changing Landscape. Circulation Research, 2021, 128, 1724-1727.	4.5	1
14	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
15	Detecting context-dependent gene regulation. Nature Computational Science, 2021, 1, 393-394.	8.0	1
16	Contextualizing genetic risk score for disease screening and rare variant discovery. Nature Communications, 2021, 12, 4418.	12.8	11
17	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
18	Integrative Network-Based Analysis Reveals Gene Networks and Novel Drug Repositioning Candidates for Alzheimer Disease. Neurology: Genetics, 2021, 7, e622.	1.9	17

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19	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
20	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
21	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells. Nature, 2021, 599, 136-140.	27.8	89
22	CD36 maintains the gastric mucosa and associates with gastric disease. Communications Biology, 2021, 4, 1247.	4.4	8
23	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	12.6	192
24	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
25	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
26	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
27	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. Nature Genetics, 2020, 52, 1239-1246.	21.4	134
28	Optimizing Genetic Analyses of Serum Lipids in Longitudinal Data. Circulation Research, 2020, 127, 1337-1339.	4.5	0
29	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
30	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
31	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
32	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
33	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. Cancer Research, 2020, 80, 4346-4354.	0.9	28
34	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
35	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
36	Genetic architecture of host proteins involved in SARS-CoV-2 infection. Nature Communications, 2020, 11, 6397.	12.8	71

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37	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. Nature Metabolism, 2020, 2, 487-498.	11.9	32
38	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
39	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
40	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
41	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
42	Evaluation of ICD codes and phecodes for the identification of pancreatic cancer in a large genomic database.. Journal of Clinical Oncology, 2020, 38, 642-642.	1.6	0
43	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
44	EXPLORING THE ROLE OF GENETIC REGULATION OF GENE EXPRESSION IN SUBSTANCE USE AND DEPENDENCE. European Neuropsychopharmacology, 2019, 29, S803-S804.	0.7	0
45	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. Nature Ecology and Evolution, 2019, 3, 1598-1606.	7.8	45
46	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. Nature Genetics, 2019, 51, 933-940.	21.4	77
47	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
48	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
49	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	21.4	154
50	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. Clinical Cancer Research, 2019, 25, 4104-4116.	7.0	27
51	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
52	M52 EMAGMA: A NOVEL METHOD TO INTEGRATE GENETIC AND TRANSCRIPTOMIC INFORMATION. European Neuropsychopharmacology, 2019, 29, S193-S194.	0.7	0
53	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. Npj Genomic Medicine, 2019, 4, 29.	3.8	8
54	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. Pain, 2019, 160, 2328-2337.	4.2	19

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55	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
56	243-LB: Characterization and Genetic Validation of Gene Expression Changes across Diabetes Development. Diabetes, 2019, 68, .	0.6	0
57	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
58	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
59	Shared Genetic Control of Brain Activity During Sleep and Insulin Secretion: A Laboratory-Based Family Study. Diabetes, 2018, 67, 155-164.	0.6	1
60	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
61	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
62	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
63	Regulation of Insulin Receptor Pathway and Glucose Metabolism by CD36 Signaling. Diabetes, 2018, 67, 1272-1284.	0.6	41
64	Bid maintains mitochondrial cristae structure and function and protects against cardiac disease in an integrative genomics study. ELife, 2018, 7, .	6.0	19
65	Pharmacokinetic (PK) modeling of serum platinum to reveal extent of long-term exposure and associated comorbidities after cisplatin treatment.. Journal of Clinical Oncology, 2018, 36, 10058-10058.	1.6	0
66	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. Pharmacogenomics Journal, 2017, 17, 137-145.	2.0	24
67	Variants in WFS1 and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. Clinical Cancer Research, 2017, 23, 3325-3333.	7.0	65
68	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
69	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
70	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
71	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
72	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495

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73	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
74	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
75	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
76	Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
77	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
78	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. Scientific Reports, 2017, 7, 5980.	3.3	10
79	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
80	Differential expression of systemic inflammatory mediators in amputees with chronic residual limb pain. Pain, 2017, 158, 68-74.	4.2	22
81	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
82	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
83	Integrative genetic analysis suggests that skin color modifies the genetic architecture of melanoma. PLoS ONE, 2017, 12, e0185730.	2.5	10
84	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
85	Consistency in large pharmacogenomic studies. Nature, 2016, 540, E1-E2.	27.8	52
86	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
87	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
88	Novel genetic predictors of venous thromboembolism risk in African Americans. Blood, 2016, 127, 1923-1929.	1.4	38
89	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
90	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

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91	STAMS: STRING-assisted module search for genome wide association studies and application to autism. Bioinformatics, 2016, 32, 3815-3822.	4.1	17
92	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
93	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
94	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
95	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
96	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
97	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
98	Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Touretteâ€™s Syndrome and OCD. American Journal of Psychiatry, 2015, 172, 82-93.	7.2	117
99	MicroRNA biogenesis and cellular proliferation. Translational Research, 2015, 166, 145-151.	5.0	18
100	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	3.2	158
101	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
102	The impact of human copy number variation on gene expression: Figure 1. Briefings in Functional Genomics, 2015, 14, 352-357.	2.7	108
103	Enrichment of inflammatory bowel disease and colorectal cancer risk variants in colon expression quantitative trait loci. BMC Genomics, 2015, 16, 138.	2.8	45
104	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
105	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
106	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. Biopreservation and Biobanking, 2015, 13, 311-319.	1.0	674
107	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	21.4	1,473
108	Identification of a Variant in KDR Associated with Serum VEGFR2 and Pharmacodynamics of Pazopanib. Clinical Cancer Research, 2015, 21, 365-372.	7.0	29

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109	Cytotoxic and Pathogenic Properties of Klebsiella oxytoca Isolated from Laboratory Animals. PLoS ONE, 2014, 9, e100542.	2.5	39
110	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
111	Linking the genetic architecture of cytosine modifications with human complex traits. Human Molecular Genetics, 2014, 23, 5893-5905.	2.9	36
112	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
113	Poly-Omic Prediction of Complex Traits: OmicKriging. Genetic Epidemiology, 2014, 38, 402-415.	1.3	41
114	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
115	A pharmacogenetic study of aldehyde oxidase I in patients treated with XK469. Pharmacogenetics and Genomics, 2014, 24, 129-132.	1.5	10
116	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
117	Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 2014, 507, 371-375.	27.8	1,079
118	The impact of microRNA expression on cellular proliferation. Human Genetics, 2014, 133, 931-938.	3.8	40
119	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
120	Ethnicity-specific pharmacogenetics: the case of warfarin in African Americans. Pharmacogenomics Journal, 2014, 14, 223-228.	2.0	59
121	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
122	Structural Architecture of SNP Effects on Complex Traits. American Journal of Human Genetics, 2014, 95, 477-489.	6.2	24
123	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
124	Discovery and Functional Assessment of Gene Variants in the Vascular Endothelial Growth Factor Pathway. Human Mutation, 2014, 35, 227-235.	2.5	12
125	Genetic association signal near <scp>NTN</scp>4 in <scp>T</scp>ourette syndrome. Annals of Neurology, 2014, 76, 310-315.	5.3	53
126	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	3.8	103

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127	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
128	Genetic factors affecting gene transcription and catalytic activity of UDP-glucuronosyltransferases in human liver. Human Molecular Genetics, 2014, 23, 5558-5569.	2.9	50
129	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. Blood, 2014, 124, 2298-2305.	1.4	57
130	A genome-wide integrative study of microRNAs in human liver. BMC Genomics, 2013, 14, 395.	2.8	39
131	SCAN: A Systems Biology Approach to Pharmacogenomic Discovery. Methods in Molecular Biology, 2013, 1015, 213-224.	0.9	8
132	Genome-wide association study of Tourette's syndrome. Molecular Psychiatry, 2013, 18, 721-728.	7.9	161
133	Translating pharmacogenomics discoveries into the clinic: an implementation framework. Genome Medicine, 2013, 5, 94.	8.2	6
134	Genome-wide association study of obsessive-compulsive disorder. Molecular Psychiatry, 2013, 18, 788-798.	7.9	312
135	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
136	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. Lancet, The, 2013, 382, 790-796.	13.7	237
137	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
138	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
139	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
140	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
141	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. Pharmacogenomics Journal, 2013, 13, 35-43.	2.0	49
142	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	3.5	241
143	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
144	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

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145	Mixed Effects Modeling of Proliferation Rates in Cell-Based Models: Consequence for Pharmacogenomics and Cancer. PLoS Genetics, 2012, 8, e1002525.	3.5	26
146	Variants Affecting Exon Skipping Contribute to Complex Traits. PLoS Genetics, 2012, 8, e1002998.	3.5	53
147	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. Human Molecular Genetics, 2012, 21, 1470-1480.	2.9	16
148	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
149	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
150	Small Science: High Stakes. Science, 2012, 338, 883-883.	12.6	0
151	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
152	Genome-wide approaches in pharmacogenomics: heritability estimation and pharmacoethnicity as primary challenges. Pharmacogenomics, 2012, 13, 1101-1104.	1.3	11
153	The limits of genome-wide methods for pharmacogenomic testing. Pharmacogenetics and Genomics, 2012, 22, 261-272.	1.5	29
154	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. Pharmacogenetics and Genomics, 2012, 22, 498-507.	1.5	28
155	Clinical Translation of Cell-Based Pharmacogenomic Discovery. Clinical Pharmacology and Therapeutics, 2012, 92, 425-427.	4.7	24
156	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
157	Response to Knoppers etÂal.. American Journal of Human Genetics, 2012, 91, 579.	6.2	0
158	Genetic Risk Factors for Type 2 Diabetes: A Trans-Regulatory Genetic Architecture?. American Journal of Human Genetics, 2012, 91, 466-477.	6.2	31
159	An Exponential Combination Procedure for Set-Based Association Tests in Sequencing Studies. American Journal of Human Genetics, 2012, 91, 977-986.	6.2	34
160	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
161	The regulatory effect of miRNAs is a heritable genetic trait in humans. BMC Genomics, 2012, 13, 383.	2.8	23
162	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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163	Identification of novel germline polymorphisms governing capecitabine sensitivity. Cancer, 2012, 118, 4063-4073.	4.1	25
164	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
165	Genetic Architecture of MicroRNA Expression: Implications for the Transcriptome and Complex Traits. American Journal of Human Genetics, 2012, 90, 1046-1063.	6.2	92
166	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
167	Integrative Genomics: Quantifying Significance of Phenotype-Genotype Relationships from Multiple Sources of High-Throughput Data. Frontiers in Genetics, 2012, 3, 202.	2.3	14
168	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
169	Copy number polymorphisms and anticancer pharmacogenomics. Genome Biology, 2011, 12, R46.	9.6	25
170	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
171	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
172	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
173	Population differences in microRNA expression and biological implications. RNA Biology, 2011, 8, 692-701.	3.1	138
174	Comprehensive Evaluation of the Contribution of X Chromosome Genes to Platinum Sensitivity. Molecular Cancer Therapeutics, 2011, 10, 472-480.	4.1	5
175	A Study of CNVs As Trait-Associated Polymorphisms and As Expression Quantitative Trait Loci. PLoS Genetics, 2011, 7, e1001292.	3.5	50
176	Identification, Replication, and Functional Fine-Mapping of Expression Quantitative Trait Loci in Primary Human Liver Tissue. PLoS Genetics, 2011, 7, e1002078.	3.5	191
177	Genome-Wide Local Ancestry Approach Identifies Genes and Variants Associated with Chemotherapeutic Susceptibility in African Americans. PLoS ONE, 2011, 6, e21920.	2.5	25
178	Population differences in platinum toxicity as a means to identify novel genetic susceptibility variants. Pharmacogenetics and Genomics, 2010, 20, 327-337.	1.5	30
179	Comprehensive Survey of SNPs in the Affymetrix Exon Array Using the 1000 Genomes Dataset. PLoS ONE, 2010, 5, e9366.	2.5	18
180	Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS. PLoS Genetics, 2010, 6, e1000888.	3.5	1,161

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