Eric R Gamazon

List of Publications by Year in Descending Order

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	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. *International Journal of Cancer*, **2022**, 150, 80-90	7.5	2
193	Integrative transcriptomic, evolutionary, and causal inference framework for region-level analysis: Application to COVID-19.. *Npj Genomic Medicine*, **2022**, 7, 24	6.2	
192	CD36 maintains the gastric mucosa and associates with gastric disease. *Communications Biology*, **2021**, 4, 1247	6.7	1
191	Mapping the proteo-genomic convergence of human diseases. *Science*, **2021**, 374, eabj1541	33.3	11
190	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells. *Nature*, **2021**, 599, 136-140	50.4	7
189	Deep Learning Enables Fast and Accurate Imputation of Gene Expression. *Frontiers in Genetics*, **2021**, 12, 624128	4.5	0
188	Multi-omic analysis elucidates the genetic basis of hydrocephalus. *Cell Reports*, **2021**, 35, 109085	10.6	3
187	Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. *Npj Systems Biology and Applications*, **2021**, 7, 24	5	0
186	Revisiting Some Useful Statistical Guidelines in in Response to a Changing Landscape. *Circulation Research*, **2021**, 128, 1724-1727	15.7	0
185	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
184	Detecting context-dependent gene regulation. *Nature Computational Science*, **2021**, 1, 393-394		
183	Modeling mutational effects on biochemical phenotypes using convolutional neural networks: application to SARS-CoV-2 **2021**,		2
182	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. *Genome Biology*, **2021**, 22, 49	18.3	38
181	E-MAGMA: an eQTL-informed method to identify risk genes using genome-wide association study summary statistics. *Bioinformatics*, **2021**,	7.2	9
180	Contextualizing genetic risk score for disease screening and rare variant discovery. *Nature Communications*, **2021**, 12, 4418	17.4	2
179	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. *Human Molecular Genetics*, **2021**,	5.6	1
178	Integrative Network-Based Analysis Reveals Gene Networks and Novel Drug Repositioning Candidates for Alzheimer Disease. *Neurology: Genetics*, **2021**, 7, e622	3.8	2

177	A transcriptome-wide association study of Alzheimer's disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. *Genome Medicine*, **2021**, 13, 141	14.4	0
176	An integrative systems-based analysis of substance use: eQTL-informed gene-based tests, gene networks, and biological mechanisms. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2021**, 186, 162-172	3.5	1
175	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. *Translational Psychiatry*, **2021**, 11, 618	8.6	2
174	Tissue-specific genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and 30 novel loci. *Alzheimer's and Dementia*, **2020**, 16, e039475	1.2	
173	Genetic architecture of host proteins involved in SARS-CoV-2 infection. *Nature Communications*, **2020**, 11, 6397	17.4	22
172	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. *Nature Metabolism*, **2020**, 2, 487-498	14.6	10
171	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	12.9	2
170	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. *Nature Medicine*, **2020**, 26, 98-109	50.5	16
169	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	2.2	
168	Genetic architecture of host proteins interacting with SARS-CoV-2 **2020**,		5
167	Transcriptome-wide association analysis offers novel opportunities for clinical translation of genetic discoveries on mental disorders. *World Psychiatry*, **2020**, 19, 113-114	14.4	0
166	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	4.9	8
165	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. *Nature Genetics*, **2020**, 52, 1239-1246	36.3	35
164	Optimizing Genetic Analyses of Serum Lipids in Longitudinal Data. *Circulation Research*, **2020**, 127, 1337-1339	15.7	
163	A Quantitative Proteome Map of the Human Body. *Cell*, **2020**, 183, 269-283.e19	56.2	73
162	The GTEx Consortium atlas of genetic regulatory effects across human tissues. *Science*, **2020**, 369, 1318-1330	33.3	589
161	Transcriptomic signatures across human tissues identify functional rare genetic variation. *Science*, **2020**, 369,	33.3	36
160	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100

159	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. *Cancer Research*, **2020**, 80, 4346-4354	10.1	7
158	A vast resource of allelic expression data spanning human tissues. *Genome Biology*, **2020**, 21, 234	18.3	18
157	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. *Genetics in Medicine*, **2020**, 22, 1191-1200	8.1	3
156	An analysis of genetically regulated gene expression across multiple tissues implicates novel gene candidates in Alzheimer's disease. *Alzheimer's Research and Therapy*, **2020**, 12, 43	9	11
155	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. *Nature Ecology and Evolution*, **2019**, 3, 1598-1606	12.3	22
154	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. *Nature Genetics*, **2019**, 51, 933-940	36.3	51
153	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	11	23
152	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
151	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. *Nature Genetics*, **2019**, 51, 659-674	36.3	99
150	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. *Clinical Cancer Research*, **2019**, 25, 4104-4116	12.9	15
149	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	6	36
148	243-LB: Characterization and Genetic Validation of Gene Expression Changes across Diabetes Development. *Diabetes*, **2019**, 68, 243-LB	0.9	
147	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	11	10
146	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. *Npj Genomic Medicine*, **2019**, 4, 29	6.2	3
145	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. *Pain*, **2019**, 160, 2328-2337	8	8
144	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. *Human Molecular Genetics*, **2019**, 28, 1212-1224	5.6	5
143	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	4.9	12
142	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. *Pharmacogenomics Journal*, **2018**, 18, 106-112	3.5	3

141	Shared Genetic Control of Brain Activity During Sleep and Insulin Secretion: A Laboratory-Based Family Study. *Diabetes*, **2018**, 67, 155-164	0.9	1
140	Regulation of Insulin Receptor Pathway and Glucose Metabolism by CD36 Signaling. *Diabetes*, **2018**, 67, 1272-1284	0.9	26
139	Bid maintains mitochondrial cristae structure and function and protects against cardiac disease in an integrative genomics study. *ELife*, **2018**, 7,	8.9	10
138	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	2.2	
137	An ancestry-based approach for detecting interactions. *Genetic Epidemiology*, **2018**, 42, 49-63	2.6	11
136	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. *Drug and Alcohol Dependence*, **2018**, 188, 94-101	4.9	7
135	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. *Nature Genetics*, **2018**, 50, 956-967	36.3	239
134	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. *Pharmacogenomics Journal*, **2017**, 17, 137-145	3.5	17
133	Variants in and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. *Clinical Cancer Research*, **2017**, 23, 3325-3333	12.9	47
132	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	5.4	2
131	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. *JAMA Oncology*, **2017**, 3, 1654-1662	13.4	146
130	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. *Clinical Cancer Research*, **2017**, 23, 5757-5768	12.9	40
129	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
128	Dynamic landscape and regulation of RNA editing in mammals. *Nature*, **2017**, 550, 249-254	50.4	286
127	Landscape of X chromosome inactivation across human tissues. *Nature*, **2017**, 550, 244-248	50.4	417
126	The impact of rare variation on gene expression across tissues. *Nature*, **2017**, 550, 239-243	50.4	146
125	Genetic effects on gene expression across human tissues. *Nature*, **2017**, 550, 204-213	50.4	2086
124	Identifying -mediators for -eQTLs across many human tissues using genomic mediation analysis. *Genome Research*, **2017**, 27, 1859-1871	9.7	38

123	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. *Genome Research*, **2017**, 27, 1843-1858	9.7	98
122	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. *Scientific Reports*, **2017**, 7, 5980	4.9	7
121	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	3.2	5
120	Differential expression of systemic inflammatory mediators in amputees with chronic residual limb pain. *Pain*, **2017**, 158, 68-74	8	11
119	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
118	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	3.7	111
117	Integrative genetic analysis suggests that skin color modifies the genetic architecture of melanoma. *PLoS ONE*, **2017**, 12, e0185730	3.7	7
116	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs. *Scientific Reports*, **2016**, 6, 19429	4.9	51
115	Alternative Splicing and Genome Evolution **2016**, 1-6		4
114	STAMS: STRING-assisted module search for genome wide association studies and application to autism. *Bioinformatics*, **2016**, 32, 3815-3822	7.2	11
113	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	2.2	1
112	Transcriptional regulation of PNPLA3 and its impact on susceptibility to nonalcoholic fatty liver Disease (NAFLD) in humans. *Aging*, **2016**, 9, 26-40	5.6	7
111	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
110	Consistency in large pharmacogenomic studies. *Nature*, **2016**, 540, E1-E2	50.4	35
109	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. *Nature Communications*, **2016**, 7, 10635	17.4	37
108	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. *American Journal of Human Genetics*, **2016**, 98, 697-708	11	25
107	Novel genetic predictors of venous thromboembolism risk in African Americans. *Blood*, **2016**, 127, 1923-9	9.2	28
106	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, 4835-4846	5.6	34

105	MicroRNA biogenesis and cellular proliferation. *Translational Research*, **2015**, 166, 145-51	11	16
104	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. *PLoS Computational Biology*, **2015**, 11, e1004220	5	104
103	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	6	76
102	The impact of human copy number variation on gene expression. *Briefings in Functional Genomics*, **2015**, 14, 352-7	4.9	69
101	Enrichment of inflammatory bowel disease and colorectal cancer risk variants in colon expression quantitative trait loci. *BMC Genomics*, **2015**, 16, 138	4.5	29
100	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
99	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
98	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. *Biopreservation and Biobanking*, **2015**, 13, 311-9	2.1	432
97	A gene-based association method for mapping traits using reference transcriptome data. *Nature Genetics*, **2015**, 47, 1091-8	36.3	850
96	Identification of a variant in KDR associated with serum VEGFR2 and pharmacodynamics of Pazopanib. *Clinical Cancer Research*, **2015**, 21, 365-72	12.9	24
95	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. *Scientific Reports*, **2015**, 5, 15145	4.9	128
94	SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	17
93	A genome-wide sib-pair scan for quantitative language traits reveals linkage to chromosomes 10 and 13. *Genes, Brain and Behavior*, **2015**, 14, 387-97	3.6	5
92	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	4.5	7
91	Cross-disorder genome-wide analyses suggest a complex genetic relationship between Tourette's syndrome and OCD. *American Journal of Psychiatry*, **2015**, 172, 82-93	11.9	101
90	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, 658-69	4	63
89	Obesity-associated variants within FTO form long-range functional connections with IRX3. *Nature*, **2014**, 507, 371-5	50.4	835
88	The impact of microRNA expression on cellular proliferation. *Human Genetics*, **2014**, 133, 931-8	6.3	29

87	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, 5968-73	11.5	15
86	Ethnicity-specific pharmacogenetics: the case of warfarin in African Americans. *Pharmacogenomics Journal*, **2014**, 14, 223-8	3.5	50
85	Cross-tissue and tissue-specific eQTLs: partitioning the heritability of a complex trait. *American Journal of Human Genetics*, **2014**, 95, 521-34	11	61
84	Structural architecture of SNP effects on complex traits. *American Journal of Human Genetics*, **2014**, 95, 477-89	11	20
83	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, 644-52	6.1	7
82	Discovery and functional assessment of gene variants in the vascular endothelial growth factor pathway. *Human Mutation*, **2014**, 35, 227-35	4.7	11
81	Genetic association signal near NTN4 in Tourette syndrome. *Annals of Neurology*, **2014**, 76, 310-5	9.4	42
80	Genomics of alternative splicing: evolution, development and pathophysiology. *Human Genetics*, **2014**, 133, 679-87	6.3	71
79	Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. *BMC Genomics*, **2014**, 15, 292	4.5	19
78	Genetic factors affecting gene transcription and catalytic activity of UDP-glucuronosyltransferases in human liver. *Human Molecular Genetics*, **2014**, 23, 5558-69	5.6	44
77	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. *Blood*, **2014**, 124, 2298-305	2.2	49
76	Cytotoxic and pathogenic properties of Klebsiella oxytoca isolated from laboratory animals. *PLoS ONE*, **2014**, 9, e100542	3.7	33
75	Gastric colonisation with a restricted commensal microbiota replicates the promotion of neoplastic lesions by diverse intestinal microbiota in the Helicobacter pylori INS-GAS mouse model of gastric carcinogenesis. *Gut*, **2014**, 63, 54-63	19.2	160
74	Linking the genetic architecture of cytosine modifications with human complex traits. *Human Molecular Genetics*, **2014**, 23, 5893-905	5.6	30
73	Genome-wide interrogation of longitudinal FEV1 in children with asthma. *American Journal of Respiratory and Critical Care Medicine*, **2014**, 190, 619-27	10.2	14
72	Poly-omic prediction of complex traits: OmicKriging. *Genetic Epidemiology*, **2014**, 38, 402-15	2.6	34
71	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, 13127-32	11.5	121
70	A pharmacogenetic study of aldehyde oxidase I in patients treated with XK469. *Pharmacogenetics and Genomics*, **2014**, 24, 129-32	1.9	9

69	A genome-wide integrative study of microRNAs in human liver. *BMC Genomics*, **2013**, 14, 395	4.5	31
68	SCAN: a systems biology approach to pharmacogenomic discovery. *Methods in Molecular Biology*, **2013**, 1015, 213-24	1.4	8
67	Genome-wide association study of Tourette's syndrome. *Molecular Psychiatry*, **2013**, 18, 721-8	15.1	138
66	Translating pharmacogenomics discoveries into the clinic: an implementation framework. *Genome Medicine*, **2013**, 5, 94	14.4	6
65	Genome-wide association study of obsessive-compulsive disorder. *Molecular Psychiatry*, **2013**, 18, 788-98	15.1	244
64	Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. *Molecular Psychiatry*, **2013**, 18, 340-6	15.1	134
63	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. *Lancet, The*, **2013**, 382, 790-6	40	191
62	Genome-wide discovery of genetic variants affecting tamoxifen sensitivity and their clinical and functional validation. *Annals of Oncology*, **2013**, 24, 1867-1873	10.3	9
61	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, 619-29	8.6	35
60	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, 491-9	12.9	45
59	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. *Carcinogenesis*, **2013**, 34, 1520-8	4.6	24
58	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. *Pharmacogenomics Journal*, **2013**, 13, 35-43	3.5	45
57	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics*, **2013**, 9, e1003864	6	189
56	The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, **2013**, 45, 580-5	36.3	4179
55	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. *Blood*, **2013**, 121, 4366-76	2.2	36
54	Trans-population analysis of genetic mechanisms of ethnic disparities in neuroblastoma survival. *Journal of the National Cancer Institute*, **2013**, 105, 302-9	9.7	25
53	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	2.3	78
52	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	6.5	27

51	Response to Knoppers et al.. *American Journal of Human Genetics*, **2012**, 91, 579	11	78
50	Genetic risk factors for type 2 diabetes: a trans-regulatory genetic architecture?. *American Journal of Human Genetics*, **2012**, 91, 466-77	11	28
49	An exponential combination procedure for set-based association tests in sequencing studies. *American Journal of Human Genetics*, **2012**, 91, 977-86	11	30
48	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	11.5	47
47	The regulatory effect of miRNAs is a heritable genetic trait in humans. *BMC Genomics*, **2012**, 13, 383	4.5	21
46	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	3.7	96
45	Identification of novel germline polymorphisms governing capecitabine sensitivity. *Cancer*, **2012**, 118, 4063-73	6.4	23
44	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, 591-8	11	61
43	Genetic architecture of microRNA expression: implications for the transcriptome and complex traits. *American Journal of Human Genetics*, **2012**, 90, 1046-63	11	80
42	Integrative genomics: quantifying significance of phenotype-genotype relationships from multiple sources of high-throughput data. *Frontiers in Genetics*, **2012**, 3, 202	4.5	13
41	Mixed effects modeling of proliferation rates in cell-based models: consequence for pharmacogenomics and cancer. *PLoS Genetics*, **2012**, 8, e1002525	6	24
40	Variants affecting exon skipping contribute to complex traits. *PLoS Genetics*, **2012**, 8, e1002998	6	47
39	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. *Human Molecular Genetics*, **2012**, 21, 1470-80	5.6	12
38	Genetic susceptibility to type 2 diabetes and breast cancer risk in women of European and African ancestry. *Cancer Epidemiology Biomarkers and Prevention*, **2012**, 21, 552-6	4	10
37	Small science: high stakes. *Science*, **2012**, 338, 883	33.3	
36	Genetic variation that predicts platinum sensitivity reveals the role of miR-193b* in chemotherapeutic susceptibility. *Molecular Cancer Therapeutics*, **2012**, 11, 2054-61	6.1	33
35	The limits of genome-wide methods for pharmacogenomic testing. *Pharmacogenetics and Genomics* , **2012**, 22, 261-72	1.9	23
34	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. *Pharmacogenetics and Genomics*, **2012**, 22, 498-507	1.9	21

33	Clinical translation of cell-based pharmacogenomic discovery. *Clinical Pharmacology and Therapeutics*, **2012**, 92, 425-7	6.1	20
32	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. *Translational Research*, **2011**, 157, 265-72	11	37
31	Copy number polymorphisms and anticancer pharmacogenomics. *Genome Biology*, **2011**, 12, R46	18.3	23
30	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, 408-15	6.1	94
29	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, 2047-55	10.3	90
28	Platinum sensitivity-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, 5490-500	12.9	55
27	Population differences in microRNA expression and biological implications. *RNA Biology*, **2011**, 8, 692-70	4.8	115
26	Comprehensive evaluation of the contribution of X chromosome genes to platinum sensitivity. *Molecular Cancer Therapeutics*, **2011**, 10, 472-80	6.1	4
25	A study of CNVs as trait-associated polymorphisms and as expression quantitative trait loci. *PLoS Genetics*, **2011**, 7, e1001292	6	46
24	Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. *PLoS Genetics*, **2011**, 7, e1002078	6	171
23	Genome-wide local ancestry approach identifies genes and variants associated with chemotherapeutic susceptibility in African Americans. *PLoS ONE*, **2011**, 6, e21920	3.7	21
22	Comprehensive survey of SNPs in the Affymetrix exon array using the 1000 Genomes dataset. *PLoS ONE*, **2010**, 5, e9366	3.7	16
21	Trait-associated SNPs are more likely to be eQTLs: annotation to enhance discovery from GWAS. *PLoS Genetics*, **2010**, 6, e1000888	6	941
20	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, 9287-92	11.5	96
19	SCAN: SNP and copy number annotation. *Bioinformatics*, **2010**, 26, 259-62	7.2	203
18	Population differences in platinum toxicity as a means to identify novel genetic susceptibility variants. *Pharmacogenetics and Genomics*, **2010**, 20, 327-37	1.9	25
17	Exprtarget: an integrative approach to predicting human microRNA targets. *PLoS ONE*, **2010**, 5, e13534	3.7	65
16	PACdb: a database for cell-based pharmacogenomics. *Pharmacogenetics and Genomics*, **2010**, 20, 269-73	1.9	35

15	A pharmacogene database enhanced by the 1000 Genomes Project. *Pharmacogenetics and Genomics*, **2009**, 19, 829-32	1.9	16
14	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
13	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3
12	SNP-based heritability estimation: measurement noise, population stratification, and stability		5
11	Distant regulatory effects of genetic variation in multiple human tissues		6
10	Local genetic effects on gene expression across 44 human tissues		22
9	Gene Expression Imputation with Generative Adversarial Imputation Nets		1
8	Gene expression imputation across multiple brain regions reveals schizophrenia risk throughout development		6
7	Transcriptomic Imputation of Bipolar Disorder and Bipolar subtypes reveals 29 novel associated genes		9
6	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation		1
5	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
4	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81
3	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci		21
2	An Integrative Network-based Analysis Reveals Gene Networks, Biological Mechanisms, and Novel Drug Targets in Alzheimer's Disease		1
1	SLC25A39 is necessary for mitochondrial glutathione import in mammalian cells		1