

Integrative approaches for large-scale transcriptome-w

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Challenges and novel approaches for investigating molecular mediation. <i>Human Molecular Genetics</i> , 2016, 25, R149-R156.	1.4	104
2	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. <i>PLoS Genetics</i> , 2016, 12, e1006423.	1.5	143
3	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016, 8, 84.	3.6	91
4	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
5	Applications of integrative OMICs approaches to gene regulation studies. <i>Quantitative Biology</i> , 2016, 4, 283-301.	0.3	6
6	Genetics: From Molecule to Society. <i>Current Biology</i> , 2016, 26, R1194-R1196.	1.8	3
7	Colocalization of GWAS and eQTL Signals Detects Target Genes. <i>American Journal of Human Genetics</i> , 2016, 99, 1245-1260.	2.6	569
8	The road to precision psychiatry: translating genetics into disease mechanisms. <i>Nature Neuroscience</i> , 2016, 19, 1397-1407.	7.1	189
9	Translating genome-wide association findings into new therapeutics for psychiatry. <i>Nature Neuroscience</i> , 2016, 19, 1392-1396.	7.1	115
10	When size matters: CHD8 in autism. <i>Nature Neuroscience</i> , 2016, 19, 1430-1432.	7.1	14
11	Brains, genes and power. <i>Nature Neuroscience</i> , 2016, 19, 1428-1430.	7.1	2
12	Non-linear interactions between candidate genes of myocardial infarction revealed in mRNA expression profiles. <i>BMC Genomics</i> , 2016, 17, 738.	1.2	17
13	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.	9.4	1,757
14	Integrating gene variation and expression to understand complex traits. <i>Nature Reviews Genetics</i> , 2016, 17, 194-194.	7.7	18
15	Pathway analysis of complex diseases for GWAS, extending to consider rare variants, multi-omics and interactions. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 335-353.	1.1	54
16	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. <i>Journal of Lipid Research</i> , 2017, 58, 481-493.	2.0	147
17	Imaging Genetics and Genomics in Psychiatry: A Critical Review of Progress and Potential. <i>Biological Psychiatry</i> , 2017, 82, 165-175.	0.7	144
18	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 473-487.	2.6	248

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19	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. American Journal of Human Genetics, 2017, 100, 571-580.	2.6	101
20	TMEM175 deficiency impairs lysosomal and mitochondrial function and increases α -synuclein aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2389-2394.	3.3	164
21	Conditional eQTL analysis reveals allelic heterogeneity of gene expression. Human Molecular Genetics, 2017, 26, 1444-1451.	1.4	145
22	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
23	Multi-omics approaches to disease. Genome Biology, 2017, 18, 83.	3.8	1,439
24	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330
25	Non-coding variants contribute to the clinical heterogeneity of TTR amyloidosis. European Journal of Human Genetics, 2017, 25, 1055-1060.	1.4	23
26	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
27	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	9.4	130
28	Enhanced methods to detect haplotypic effects on gene expression. Bioinformatics, 2017, 33, 2307-2313.	1.8	5
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30	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	9.4	117
31	Backward genotype-transcript-phenotype association mapping. Methods, 2017, 129, 18-23.	1.9	4
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33	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. American Journal of Human Genetics, 2017, 101, 590-602.	2.6	65
34	Mendelian randomization with fine-mapped genetic data: Choosing from large numbers of correlated instrumental variables. Genetic Epidemiology, 2017, 41, 714-725.	0.6	122
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36	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. Carcinogenesis, 2017, 38, 1147-1154.	1.3	21

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38	A Powerful Framework for Integrating eQTL and GWAS Summary Data. <i>Genetics</i> , 2017, 207, 893-902.	1.2	72
39	Imaging-wide association study: Integrating imaging endophenotypes in GWAS. <i>NeuroImage</i> , 2017, 159, 159-169.	2.1	57
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41	Mechanisms of Type 2 Diabetes Risk Loci. <i>Current Diabetes Reports</i> , 2017, 17, 72.	1.7	39
42	Prioritising Causal Genes at Type 2 Diabetes Risk Loci. <i>Current Diabetes Reports</i> , 2017, 17, 76.	1.7	25
43	Analysis of genome-wide association data highlights candidates for drug repositioning in psychiatry. <i>Nature Neuroscience</i> , 2017, 20, 1342-1349.	7.1	135
44	Genetic studies as a tool for identifying novel potential targets for treatment of COPD. <i>European Respiratory Journal</i> , 2017, 50, 1702042.	3.1	1
45	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. <i>Fertility and Sterility</i> , 2017, 108, 1056-1062.e4.	0.5	15
46	High-resolution mapping of cis-regulatory variation in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10736-E10744.	3.3	50
47	Cis-SNPs Set Testing and PrediXcan Analysis for Gene Expression Data using Linear Mixed Models. <i>Scientific Reports</i> , 2017, 7, 15237.	1.6	6
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50	Population diversity of the genetically determined TTR expression in human tissues and its implications in TTR amyloidosis. <i>BMC Genomics</i> , 2017, 18, 254.	1.2	17
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56	Translating natural genetic variation to gene expression in a computational model of the <i>Drosophila</i> gap gene regulatory network. <i>PLoS ONE</i> , 2017, 12, e0184657.	1.1	5
57	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease. <i>PLoS Genetics</i> , 2017, 13, e1006933.	1.5	96
58	A novel variant associated with HDL-C levels by modifying DAGLB expression levels: An annotation-based genome-wide association study. <i>European Journal of Human Genetics</i> , 2018, 26, 838-847.	1.4	7
59	A transcriptome-wide association study identifies PALMD as a susceptibility gene for calcific aortic valve stenosis. <i>Nature Communications</i> , 2018, 9, 988.	5.8	93
60	The genetics of adiposity. <i>Current Opinion in Genetics and Development</i> , 2018, 50, 86-95.	1.5	103
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68	Integrating eQTL data with GWAS summary statistics in pathway-based analysis with application to schizophrenia. <i>Genetic Epidemiology</i> , 2018, 42, 303-316.	0.6	20
69	Biosignature Discovery for Substance Use Disorders Using Statistical Learning. <i>Trends in Molecular Medicine</i> , 2018, 24, 221-235.	3.5	19
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72	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomics. <i>American Journal of Human Genetics</i> , 2018, 102, 904-919.	2.6	30

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77	Leveraging lung tissue transcriptome to uncover candidate causal genes in COPD genetic associations. <i>Human Molecular Genetics</i> , 2018, 27, 1819-1829.	1.4	37
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79	Proper joint analysis of summary association statistics requires the adjustment of heterogeneity in SNP coverage pattern. <i>Briefings in Bioinformatics</i> , 2018, 19, 1337-1343.	3.2	2
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81	How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?. , 2018, , .		20
82	Statistical and Machine Learning Approaches to Predict Gene Regulatory Networks From Transcriptome Datasets. <i>Frontiers in Plant Science</i> , 2018, 9, 1770.	1.7	54
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87	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	9.4	307
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90	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	5.8	121
91	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. <i>Circulation</i> , 2018, 138, 2469-2481.	1.6	42

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93	Transcriptome-wide association study identifies multiple genes and pathways associated with pancreatic cancer. <i>Cancer Medicine</i> , 2018, 7, 5727-5732.	1.3	26
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102	From lipid locus to drug target through human genomics. <i>Cardiovascular Research</i> , 2018, 114, 1258-1270.	1.8	17
103	Rare-Variant Studies to Complement Genome-Wide Association Studies. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 97-112.	2.5	34
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108	Using Genomic Data to Find Disease-Modifying Loci in Huntington's Disease (HD). <i>Methods in Molecular Biology</i> , 2018, 1780, 443-461.	0.4	2
109	Integration of summary data from GWAS and eQTL studies identified novel causal BMD genes with functional predictions. <i>Bone</i> , 2018, 113, 41-48.	1.4	29

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117	Integrative Bioinformatics Approaches for Identification of Drug Targets in Hypertension. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 25.	1.1	3
118	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 56.	1.1	21
119	Using Gene Expression to Annotate Cardiovascular GWAS Loci. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 59.	1.1	13
120	Comparison of methods for transcriptome imputation through application to two common complex diseases. <i>European Journal of Human Genetics</i> , 2018, 26, 1658-1667.	1.4	22
121	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	5.8	748
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125	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018, 9, 3097.	5.8	18
126	Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. <i>Behavior Genetics</i> , 2018, 48, 374-385.	1.4	12
127	Genomic insights into the causes of type 2 diabetes. <i>Lancet, The</i> , 2018, 391, 2463-2474.	6.3	110

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128	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	13.5	623
129	Principled multi-omic analysis reveals gene regulatory mechanisms of phenotype variation. <i>Genome Research</i> , 2018, 28, 1207-1216.	2.4	19
130	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	5.8	294
131	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
132	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. <i>Reproductive Sciences</i> , 2019, 26, 496-502.	1.1	13
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135	Candidate Genes and MiRNAs Linked to the Inverse Relationship Between Cancer and Alzheimer's Disease: Insights From Data Mining and Enrichment Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 846.	1.1	16
136	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. <i>American Journal of Human Genetics</i> , 2019, 105, 456-476.	2.6	175
137	CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. <i>Cell</i> , 2019, 178, 887-900.e14.	13.5	301
138	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
139	Case-Only Analysis of Gene-Environment Interactions Using Polygenic Risk Scores. <i>American Journal of Epidemiology</i> , 2019, 188, 2013-2020.	1.6	15
140	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.	1.5	74
141	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. <i>Science</i> , 2019, 365, .	6.0	152
142	Integrative analysis revealed potential causal genetic and epigenetic factors for multiple sclerosis. <i>Journal of Neurology</i> , 2019, 266, 2699-2709.	1.8	34
143	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	15.2	177
144	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. <i>Nature Communications</i> , 2019, 10, 3300.	5.8	193
145	iFunMed: Integrative functional mediation analysis of GWAS and eQTL studies. <i>Genetic Epidemiology</i> , 2019, 43, 742-760.	0.6	1

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147	Genome-Wide Assessment for Resting Heart Rate and Shared Genetics With Cardiometabolic Traits and Type 2 Diabetes. <i>Journal of the American College of Cardiology</i> , 2019, 74, 2162-2174.	1.2	28
148	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. <i>Cell</i> , 2019, 179, 750-771.e22.	13.5	174
149	Informing disease modelling with brain-relevant functional genomic annotations. <i>Brain</i> , 2019, 142, 3694-3712.	3.7	8
150	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. <i>Science</i> , 2019, 366, 351-356.	6.0	99
151	CoMM: A Collaborative Mixed Model That Integrates GWAS and eQTL Data Sets to Investigate the Genetic Architecture of Complex Traits. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221988143.	1.0	5
152	Systems genetics applications in metabolism research. <i>Nature Metabolism</i> , 2019, 1, 1038-1050.	5.1	35
153	Shared genetics of asthma and mental health disorders: a large-scale genome-wide cross-trait analysis. <i>European Respiratory Journal</i> , 2019, 54, 1901507.	3.1	106
154	An integrative analysis of transcriptome-wide association study and mRNA expression profile identified candidate genes for attention-deficit/hyperactivity disorder. <i>Psychiatry Research</i> , 2019, 282, 112639.	1.7	16
155	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. <i>Nature Communications</i> , 2019, 10, 4788.	5.8	59
156	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. <i>Nature Communications</i> , 2019, 10, 3842.	5.8	90
157	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. <i>Science</i> , 2019, 365, .	6.0	245
158	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019, 10, 3834.	5.8	68
159	Integrating transcriptome-wide study and mRNA expression profiles yields novel insights into the biological mechanism of chondropathies. <i>Arthritis Research and Therapy</i> , 2019, 21, 194.	1.6	7
160	The Length of the Expressed 3' UTR Is an Intermediate Molecular Phenotype Linking Genetic Variants to Complex Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 714.	1.1	23
161	Transcriptome Analysis of the Effects of Fasting Caecotrophy on Hepatic Lipid Metabolism in New Zealand Rabbits. <i>Animals</i> , 2019, 9, 648.	1.0	10
162	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimer's Disease. <i>Frontiers in Genetics</i> , 2019, 10, 726.	1.1	18
163	Transcriptome-wide association study of attention deficit hyperactivity disorder identifies associated genes and phenotypes. <i>Nature Communications</i> , 2019, 10, 4450.	5.8	56

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164	The expression tractability of biological traits shaped by natural selection. <i>Journal of Genetics and Genomics</i> , 2019, 46, 397-404.	1.7	0
165	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. <i>Scientific Data</i> , 2019, 6, 180.	2.4	149
166	The Human Cell Atlas: making "cell space"™ for disease. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	9
167	Integrating predicted transcriptome from multiple tissues improves association detection. <i>PLoS Genetics</i> , 2019, 15, e1007889.	1.5	239
168	Prioritizing Crohn's™ disease genes by integrating association signals with gene expression implicates monocyte subsets. <i>Genes and Immunity</i> , 2019, 20, 577-588.	2.2	16
169	Association mapping in plants in the post-GWAS genomics era. <i>Advances in Genetics</i> , 2019, 104, 75-154.	0.8	100
170	The virtuous cycle of human genetics and mouse models in drug discovery. <i>Nature Reviews Drug Discovery</i> , 2019, 18, 255-272.	21.5	44
171	Prediction of Alzheimer's™ Disease-Associated Genes by Integration of GWAS Summary Data and Expression Data. <i>Frontiers in Genetics</i> , 2018, 9, 653.	1.1	34
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