

Integration of summary data from GWAS and eQTL studies to identify potential drug targets

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Challenges and novel approaches for investigating molecular mediation. Human Molecular Genetics, 2016, 25, R149-R156.	2.9	104
3	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	3.5	143
4	Personalized medicine in rheumatology. Reumatologia, 2016, 54, 177-186.	1.1	14
5	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.	8.2	91
6	Expanding the Immunology Toolbox: Embracing Public-Data Reuse and Crowdsourcing. Immunity, 2016, 45, 1191-1204.	14.3	19
7	Endometriosis risk alleles at 1p36.12 act through inverse regulation of CDC42 and LINC00339. Human Molecular Genetics, 2016, 25, ddw320.	2.9	56
8	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome Medicine, 2016, 8, 78.	8.2	135
9	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	28.9	863
10	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
11	GLITTER: a web-based application for gene link inspection through tissue-specific coexpression. Scientific Reports, 2016, 6, 33460.	3.3	3
12	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	8.2	137
13	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	21.4	134
14	Sparse Simultaneous Signal Detection for Identifying Genetically Controlled Disease Genes. Journal of the American Statistical Association, 2017, 112, 1032-1046.	3.1	9
15	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	6.2	248
16	A functional SNP associated with atopic dermatitis controls cell type-specific methylation of the VSTM1 gene locus. Genome Medicine, 2017, 9, 18.	8.2	30
17	Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. Nature Genetics, 2017, 49, 600-605.	21.4	205
18	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 2017, 66, 1713-1722.	0.6	32
19	Genome-wide association study identifies four novel loci associated with Alzheimer's endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	7.7	199

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20	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	6.2	141
21	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.	7.1	164
22	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
23	Genetic regulation of gene expression in the epileptic human hippocampus. Human Molecular Genetics, 2017, 26, 1759-1769.	2.9	20
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25	Systems biology in the central nervous system: A brief perspective on essential recent advancements. Current Opinion in Systems Biology, 2017, 3, 67-76.	2.6	8
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27	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	14.8	330
28	Pleiotropic Effects of Trait-Associated Genetic Variation on DNA Methylation: Utility for Refining GWAS Loci. American Journal of Human Genetics, 2017, 100, 954-959.	6.2	77
29	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. Nature Communications, 2017, 8, 15353.	12.8	92
30	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
31	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	6.2	91
32	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	21.4	130
33	Integrating genome-wide association study and expression quantitative trait loci data identifies multiple genes and gene set associated with neuroticism. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 78, 149-152.	4.8	12
34	Genetics of rheumatoid arthritis susceptibility, severity, and treatment response. Seminars in Immunopathology, 2017, 39, 395-408.	6.1	73
35	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	21.4	117
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39	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. Nature Genetics, 2017, 49, 1576-1583.	21.4	395
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44	A Dementia-Associated Risk Variant near TMEM106B Alters Chromatin Architecture and Gene Expression. American Journal of Human Genetics, 2017, 101, 643-663.	6.2	87
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47	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	2.9	72
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61	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
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96	Polygenic Risk Scores in Clinical Psychology: Bridging Genomic Risk to Individual Differences. Annual Review of Clinical Psychology, 2018, 14, 119-157.	12.3	110
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129	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	12.8	121
130	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	12.8	181
131	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. <i>American Journal of Human Genetics</i> , 2018, 103, 654-665.	6.2	126
132	eQTL discovery and their association with severe equine asthma in European Warmblood horses. <i>BMC Genomics</i> , 2018, 19, 581.	2.8	13
133	Coronary artery disease genes SMAD3 and TCF21 promote opposing interactive genetic programs that regulate smooth muscle cell differentiation and disease risk. <i>PLoS Genetics</i> , 2018, 14, e1007681.	3.5	41
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135	Distinguishing genetic correlation from causation across 52 diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1728-1734.	21.4	262
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144	Stratification of candidate genes for Parkinsonâ€™s disease using weighted protein-protein interaction network analysis. <i>BMC Genomics</i> , 2018, 19, 452.	2.8	35
145	Convergence of placenta biology and genetic risk for schizophrenia. <i>Nature Medicine</i> , 2018, 24, 792-801.	30.7	214

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158	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
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163	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	21.4	893

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166	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
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169	Role of the Complement System in Chronic Central Serous Chorioretinopathy. <i>JAMA Ophthalmology</i> , 2018, 136, 1128.	2.5	49
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171	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 56.	2.4	21
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173	Empirical Bayes Estimation of Semi-parametric Hierarchical Mixture Models for Unbiased Characterization of Polygenic Disease Architectures. <i>Frontiers in Genetics</i> , 2018, 9, 115.	2.3	10
174	Comparison of methods for transcriptome imputation through application to two common complex diseases. <i>European Journal of Human Genetics</i> , 2018, 26, 1658-1667.	2.8	22
175	A coding and non-coding transcriptomic perspective on the genomics of human metabolic disease. <i>Nucleic Acids Research</i> , 2018, 46, 7772-7792.	14.5	41
176	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
177	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.	3.5	117
178	Genetic Regulatory Mechanisms of Smooth Muscle Cells Map to Coronary Artery Disease Risk Loci. <i>American Journal of Human Genetics</i> , 2018, 103, 377-388.	6.2	76
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1462	GWAS and meta-analysis identifies 49 genetic variants underlying critical COVID-19. <i>Nature</i> , 2023, 617, 764-768.	27.8	38
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