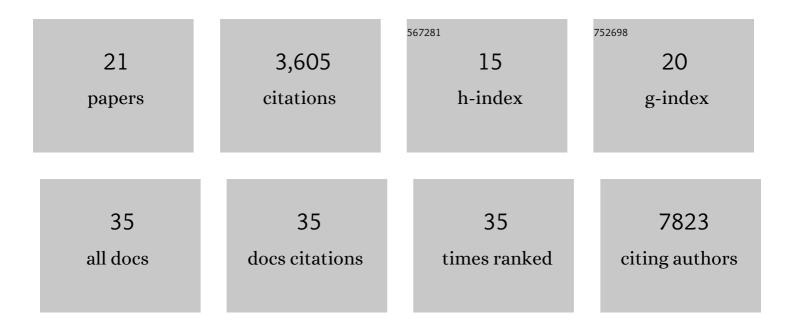
Alvaro N Barbeira

List of Publications by Year in descending order

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ALVADO N RADREIDA

#	Article	IF	CITATIONS
1	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
2	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. Nature Communications, 2021, 12, 1424.	12.8	23
3	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
4	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.7	6
5	Fineâ€mapping and QTL tissueâ€sharing information improves the reliability of causal gene identification. Genetic Epidemiology, 2020, 44, 854-867.	1.3	28
6	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
7	Cell type–specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
8	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
9	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. Genome Biology, 2020, 21, 232.	8.8	46
10	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. Science Advances, 2020, 6, .	10.3	83
11	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. Genome Biology, 2020, 21, 233.	8.8	64
12	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
13	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. Genome Biology, 2020, 21, 235.	8.8	18
14	Integrating predicted transcriptome from multiple tissues improves association detection. PLoS Genetics, 2019, 15, e1007889.	3.5	239
15	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	21.4	592
16	Imputed gene associations identify replicable <i>trans</i> â€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608.	1.3	19
17	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
18	Annotation-free quantification of RNA splicing using LeafCutter. Nature Genetics, 2018, 50, 151-158.	21.4	520

#	Article	IF	CITATIONS
19	Cancer expression quantitative trait loci (eQTLs) can be determined from heterogeneous tumor gene expression data by modeling variation in tumor purity. Genome Biology, 2018, 19, 130.	8.8	27
20	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	12.8	748
21	Generating A Database of Phenotypic Consequences of Gene Regulation Across 40 Human Tissues. European Neuropsychopharmacology, 2017, 27, S418.	0.7	Ο