Ana Viuela

List of Publications by Citations

57 papers	**3,078** citations	**28** h-index	**55** g-index
66 ext. papers	**4,231** ext. citations	**15.1** avg, IF	**4.37** L-index

#	Paper	IF	Citations
57	Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2	36.3	624
56	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. *Epigenetics*, **2014**, 9, 1382-96	5.7	222
55	Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biology*, **2013**, 14, R75	18.3	185
54	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. *Human Molecular Genetics*, **2012**, 21, 5385-94	5.6	162
53	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. *Nature Genetics*, **2015**, 47, 88-91	36.3	140
52	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
51	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100
50	Genome-wide gene expression regulation as a function of genotype and age in C. elegans. *Genome Research*, **2010**, 20, 929-37	9.7	95
49	Tensor decomposition for multiple-tissue gene expression experiments. *Nature Genetics*, **2016**, 48, 1094-100	36.3	87
48	Genetic interactions affecting human gene expression identified by variance association mapping. *ELife*, **2014**, 3, e01381	8.9	86
47	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. *Nature Communications*, **2014**, 5, 5719	17.4	85
46	Telomere length in circulating leukocytes is associated with lung function and disease. *European Respiratory Journal*, **2014**, 43, 983-92	13.6	83
45	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. *Nature Genetics*, **2018**, 50, 572-580	36.3	82
44	Circulating Proteomic Signatures of Chronological Age. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2015**, 70, 809-16	6.4	81
43	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81
42	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
41	A Quantitative Proteome Map of the Human Body. *Cell*, **2020**, 183, 269-283.e19	56.2	73

40	Cell type-specific genetic regulation of gene expression across human tissues. *Science*, **2020**, 369,	33.3	68
39	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. *Clinical Epigenetics*, **2018**, 10, 126	7.7	56
38	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. *Nature Genetics*, **2017**, 49, 1747-1751	36.3	55
37	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. *Human Molecular Genetics*, **2015**, 24, 5589-602	5.6	54
36	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. *Human Molecular Genetics*, **2018**, 27, 732-741	5.6	43
35	Aging Uncouples Heritability and Expression-QTL in Caenorhabditis elegans. *G3: Genes, Genomes, Genetics*, **2012**, 2, 597-605	3.2	43
34	The SIB Swiss Institute of Bioinformatics resources: focus on curated databases. *Nucleic Acids Research*, **2016**, 44, D27-37	20.1	41
33	Genome-wide gene expression analysis in response to organophosphorus pesticide chlorpyrifos and diazinon in C. elegans. *PLoS ONE*, **2010**, 5, e12145	3.7	40
32	Genome-Wide Association Shows that Pigmentation Genes Play a Role in Skin Aging. *Journal of Investigative Dermatology*, **2017**, 137, 1887-1894	4.3	30
31	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. *Nature Communications*, **2020**, 11, 4912	17.4	30
30	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
29	Mapping eQTLs with RNA-seq reveals novel susceptibility genes, non-coding RNAs and alternative-splicing events in systemic lupus erythematosus. *Human Molecular Genetics*, **2017**, 26, 1003-1017	5.6	28
28	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
27	Time-dependent genetic effects on gene expression implicate aging processes. *Genome Research*, **2017**, 27, 545-552	9.7	18
26	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. *PLoS Medicine*, **2020**, 17, e1003149	11.6	18
25	A vast resource of allelic expression data spanning human tissues. *Genome Biology*, **2020**, 21, 234	18.3	18
24	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. *American Journal of Human Genetics*, **2016**, 99, 567-579	11	17
23	Association of Forced Vital Capacity with the Developmental Gene NCOR2. *PLoS ONE*, **2016**, 11, e0147388	3.7	15

22	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. *Diabetologia*, **2019**, 62, 1601-1615	10.3	14
21	Gene expression modifications by temperature-toxicants interactions in Caenorhabditis elegans. *PLoS ONE*, **2011**, 6, e24676	3.7	13
20	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. *Journal of Hepatology*, **2019**, 71, 594-602	13.4	10
19	Influence of genetic variants on gene expression in human pancreatic islets Implications for type 2 diabetes		9
18	Cell type specific genetic regulation of gene expression across human tissues		7
17	Pathway-based factor analysis of gene expression data produces highly heritable phenotypes that associate with age. *G3: Genes, Genomes, Genetics*, **2015**, 5, 839-47	3.2	5
16	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. *Diabetologia*, **2020**, 63, 744-756	10.3	4
15	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort		4
14	Quantifying the degree of sharing of genetic and non-genetic causes of gene expression variability across four tissues		3
13	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. *PLoS ONE*, **2020**, 15, e0242360	3.7	2
12	Predicting causal variants affecting expression using whole genome sequence and RNA-seq from multiple human tissues		2
11	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. *EBioMedicine*, **2020**, 58, 102932	8.8	2
10	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, 80-90	5.6	2
9	A probabilistic model of biological ageing of the lungs for analysing the effects of smoking, asthma and COPD. *Respiratory Research*, **2013**, 14, 60	7.3	1
8	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study.. *Cell Reports Medicine*, **2022**, 3, 100477	18	1
7	Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study		1
6	Deletion of ABCB10 in beta-cells protects from high-fat diet induced insulin resistance. *Molecular Metabolism*, **2021**, 55, 101403	8.8	
5	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149		

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4   Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149

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