Diego Garrido-MartÃn

List of Publications by Year
in descending order

26 papers	12,177 citations	304743 22 h-index	552781 26 g-index
31 all docs	31 docs citations	31 times ranked	23469 citing authors

#	Article	IF	Citations
1	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
2	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
3	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
4	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
5	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	12.8	748
6	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
7	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. Science Translational Medicine, 2017, 9, .	12.4	516
8	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495
9	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
10	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
11	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
12	Cell type–specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
13	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. PLoS Computational Biology, 2018, 14, e1006360.	3.2	159
14	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
15	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
16	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
17	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
18	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89

#	Article	IF	Citations
19	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. Nature Communications, 2021, 12, 727.	12.8	83
20	Identifying *cis*-mediators for *trans*-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
21	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
22	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
23	Screening and Validation of Novel Biomarkers in Osteoarticular Pathologies by Comprehensive Combination of Protein Array Technologies. Journal of Proteome Research, 2017, 16, 1890-1899.	3.7	23
24	Effect of BDNF Val66Met on hippocampal subfields volumes and compensatory interaction with APOE-Îµ4 in middle-age cognitively unimpaired individuals from the ALFA study. Brain Structure and Function, 2020, 225, 2331-2345.	2.3	5
25	Effect of the sequence data deluge on the performance of methods for detecting protein functional residues. BMC Bioinformatics, 2018, 19, 67.	2.6	4
26	Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Letâ€™s MAMBO!. Computational and Structural Biotechnology Journal, 2021, 19, 5800-5810.	4.1	4