Diego Garrido-MartÃ-n

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. Nature Communications, 2021, 12, 727.	12.8	83
2	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
3	Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO!. Computational and Structural Biotechnology Journal, 2021, 19, 5800-5810.	4.1	4
4	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
5	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
6	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
7	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
8	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
9	Cell type–specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
10	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
11	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
12	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
13	Effect of the sequence data deluge on the performance of methods for detecting protein functional residues. BMC Bioinformatics, 2018, 19, 67.	2.6	4
14	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	12.8	748
15	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. PLoS Computational Biology, 2018, 14, e1006360.	3.2	159
16	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
17	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. Science Translational Medicine, 2017, 9, .	12.4	516
18	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

#	Article	IF	Citations
19	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495
20	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
21	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
22	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
23	Identifying <i>cis</i>-mediators for <i>trans</i>-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
24	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
25	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
26	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573