Leonardo Collado-Torres

List of Publications by Citations

60 papers	2,607 citations	21 h-index	50 g-index
82 ext. papers	4,184 ext. citations	14.3 avg, IF	4.45 L-index

#	Paper	IF	Citations
60	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
59	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
58	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
57	RegulonDB version 7.0: transcriptional regulation of Escherichia coli K-12 integrated within genetic sensory response units (Gensor Units). *Nucleic Acids Research*, **2011**, 39, D98-105	20.1	275
56	Reproducible RNA-seq analysis using recount2. *Nature Biotechnology*, **2017**, 35, 319-321	44.5	211
55	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. *Nature Neuroscience*, **2018**, 21, 1117-1125	25.5	176
54	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. *Nature Neuroscience*, **2015**, 18, 154-161	25.5	110
53	Interspecies interactions that result in Bacillus subtilis forming biofilms are mediated mainly by members of its own genus. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E1236-43	11.5	75
52	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. *Nature Neuroscience*, **2021**, 24, 425-436	25.5	69
51	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. *Neuron*, **2019**, 103, 203-216.e8	13.9	67
50	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. *Genome Biology*, **2016**, 17, 266	18.3	65
49	Altered expression of histamine signaling genes in autism spectrum disorder. *Translational Psychiatry*, **2017**, 7, e1126	8.6	49
48	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. *Genome Biology*, **2019**, 20, 196	18.3	42
47	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. *Nature Communications*, **2020**, 11, 462	17.4	37
46	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. *BMC Genomics*, **2019**, 20, 513	4.5	36
45	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. *Bioinformatics*, **2017**, 33, 4033-4040	7.2	33
44	Flexible expressed region analysis for RNA-seq with derfinder. *Nucleic Acids Research*, **2017**, 45, e9	20.1	32

#	Reference		
43	Improving the value of public RNA-seq expression data by phenotype prediction. *Nucleic Acids Research*, **2018**, 46, e54	20.1	31
42	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. *Acta Neuropathologica*, **2019**, 137, 557-569	14.3	30
41	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. *Nature Neuroscience*, **2020**, 23, 510-519	25.5	30
40	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. *F1000Research*, **2017**, 6, 1558	3.6	30
39	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex		16
38	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. *Science Advances*, **2020**, 6,	14.3	15
37	SynGAP isoforms differentially regulate synaptic plasticity and dendritic development. *ELife*, **2020**, 9,	8.9	14
36	Recounting the FANTOM CAGE-Associated Transcriptome. *Genome Research*, **2020**, 30, 1073-1081	9.7	13
35	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. *Epigenetics*, **2021**, 16, 1-13	5.7	9
34	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. *Proteomics*, **2019**, 19, e1800315	4.8	8
33	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor		8
32	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. *Neuron*, **2021**, 109, 3088-3103.e5	13.9	8
31	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. *Nature Communications*, **2020**, 11, 1041	17.4	6
30	Flexible expressed region analysis for RNA-seq with derfinder		6
29	Rail-RNA: Scalable analysis of RNA-seq splicing and coverage		5
28	recount: A large-scale resource of analysis-ready RNA-seq expression data		5
27	regionReport: Interactive reports for region-based analyses. *F1000Research*, **2015**, 4, 105	3.6	4
26	regionReport: Interactive reports for region-level and feature-level genomic analyses. *F1000Research*, **2015**, 4, 105	3.6	4

25	Single-nucleus transcriptome analysis reveals cell type-specific molecular signatures across reward circuitry in the human brain		4
24	Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia		4
23	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. *Molecular Psychiatry*, **2020**, 25, 3267-3277	15.1	4
22	recount3: summaries and queries for large-scale RNA-seq expression and splicing. *Genome Biology*, **2021**, 22, 323	18.3	3
21	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs		3
20	recount-brain: a curated repository of human brain RNA-seq datasets metadata		3
19	Megadepth: efficient coverage quantification for BigWigs and BAMs. *Bioinformatics*, **2021**,	7.2	3
18	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. *BMC Bioinformatics*, **2021**, 22, 224	3.6	3
17	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. *Biological Psychiatry*, **2021**, 90, 399-408	7.9	3
16	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. *Nature Communications*, **2021**, 12, 5251	17.4	3
15	Author response: SynGAP isoforms differentially regulate synaptic plasticity and dendritic development **2020**,		2
14	Improving the value of public RNA-seq expression data by phenotype prediction		2
13	RNA-seq transcript quantification from reduced-representation data in recount2		2
12	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data		2
11	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. *Frontiers in Immunology*, **2018**, 9, 2679	8.4	2
10	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. *Nature Neuroscience*, **2022**, 25, 381-389	25.5	2
9	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor.. *Bioinformatics*, **2022**,	7.2	2
8	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. *BMC Genomics*, **2022**, 23,	4.5	2

List of Publications

7	Widespread methylation quantitative trait loci and their role in schizophrenia risk		1
6	Megadepth: efficient coverage quantification for BigWigs and BAMs		1
5	Divergent neuronal DNA methylation patterns across human cortical development: Critical periods and a unique role of CpH methylation		1
4	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods		1
3	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex		1
2	Programmatic access to bacterial regulatory networks with regutools. *Bioinformatics*, **2020**, 36, 4532-4534	7.4	0
1	Genetics and Brain Transcriptomics of Completed Suicide.. *American Journal of Psychiatry*, **2022**, 179, 226-241	11.9	0