Leonardo Collado-Torres

List of Publications by Year
in descending order

45 papers	5,331 citations	201385 27 h-index	243296 44 g-index
82 all docs	82 docs citations	82 times ranked	9189 citing authors

#	Article	IF	Citations
1	Genetics and Brain Transcriptomics of Completed Suicide. American Journal of Psychiatry, 2022, 179, 226-241.	4.0	17
2	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. Nature Neuroscience, 2022, 25, 381-389.	7.1	27
3	SpatialExperiment: infrastructure for spatially-resolvedÂtranscriptomics data in R using Bioconductor. Bioinformatics, 2022, 38, 3128-3131.	1.8	48
4	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. BMC Genomics, 2022, 23, .	1.2	50
5	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. Epigenetics, 2021, 16, 1-13.	1.3	19
6	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. Nature Neuroscience, 2021, 24, 425-436.	7.1	418
7	Megadepth: efficient coverage quantification for BigWigs and BAMs. Bioinformatics, 2021, 37, 3014-3016.	1.8	18
8	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. BMC Bioinformatics, 2021, 22, 224.	1.2	14
9	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. Biological Psychiatry, 2021, 90, 399-408.	0.7	10
10	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. Nature Communications, 2021, 12, 5251.	5.8	37
11	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. Neuron, 2021, 109, 3088-3103.e5.	3.8	95
12	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	3.8	103
13	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. Molecular Psychiatry, 2020, 25, 3267-3277.	4.1	16
14	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. Science Advances, 2020, 6, .	4.7	44
15	Programmatic access to bacterial regulatory networks with <i>regutools</i>. Bioinformatics, 2020, 36, 4532-4534.	1.8	4
16	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.	7.1	67
17	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041.	5.8	22
18	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	2.4	35

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19	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. Nature Communications, 2020, 11, 462.	5.8	96
20	SynGAP isoforms differentially regulate synaptic plasticity and dendritic development. ELife, 2020, 9, .	2.8	60
21	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. Genome Biology, 2019, 20, 196.	3.8	67
22	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. Acta Neuropathologica, 2019, 137, 557-569.	3.9	73
23	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. BMC Genomics, 2019, 20, 513.	1.2	65
24	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. Neuron, 2019, 103, 203-216.e8.	3.8	158
25	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. Proteomics, 2019, 19, e1800315.	1.3	16
26	Abstract 908: Comprehensive analysis of alternative polyadenylation across cancer phenotypes. , 2019, , .		0
27	Improving the value of public RNA-seq expression data by phenotype prediction. Nucleic Acids Research, 2018, 46, e54-e54.	6.5	49
28	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
29	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
30	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
31	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. Frontiers in Immunology, 2018, 9, 2679.	2.2	4
32	264. Unique Molecular Correlates of Schizophrenia and its Genetic Risk in the Hippocampus Compared to Frontal Cortex. Biological Psychiatry, 2018, 83, S107.	0.7	1
33	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. Nature Neuroscience, 2018, 21, 1117-1125.	7.1	300
34	Abstract 2297: Differential analysis of gene expression across the human genome using recount2 and FANTOM-CAT. , 2018, , .		2
35	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. Bioinformatics, 2017, 33, 4033-4040.	1.8	57
36	Reproducible RNA-seq analysis using recount2. Nature Biotechnology, 2017, 35, 319-321.	9.4	395

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37	Altered expression of histamine signaling genes in autism spectrum disorder. Translational Psychiatry, 2017, 7, e1126-e1126.	2.4	89
38	Flexible expressed region analysis for RNA-seq with `<tt>`derfinder`</tt>`. Nucleic Acids Research, 2017, 45, e9-e9.	6.5	54
39	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. F1000Research, 2017, 6, 1558.	0.8	50
40	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.	3.8	94
41	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. Nature Neuroscience, 2015, 18, 154-161.	7.1	142
42	regionReport: Interactive reports for region-based analyses. F1000Research, 2015, 4, 105.	0.8	5
43	regionReport: Interactive reports for region-level and feature-level genomic analyses. F1000Research, 2015, 4, 105.	0.8	4
44	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-D105.	6.5	315
45	Interspecies interactions that result in <i>Bacillus subtilis</i> 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.	3.3	94