

Leonardo Collado-Torres

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Genetics and Brain Transcriptomics of Completed Suicide.. <i>American Journal of Psychiatry</i> , 2022 , 179, 226-241	11.9	0
59	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. <i>Nature Neuroscience</i> , 2022 , 25, 381-389	25.5	2
58	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor.. <i>Bioinformatics</i> , 2022 ,	7.2	2
57	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. <i>BMC Genomics</i> , 2022 , 23,	4.5	2
56	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021 , 22, 323	18.3	3
55	Megadepth: efficient coverage quantification for BigWigs and BAMs. <i>Bioinformatics</i> , 2021 ,	7.2	3
54	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. <i>BMC Bioinformatics</i> , 2021 , 22, 224	3.6	3
53	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. <i>Epigenetics</i> , 2021 , 16, 1-13	5.7	9
52	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. <i>Nature Neuroscience</i> , 2021 , 24, 425-436	25.5	69
51	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. <i>Biological Psychiatry</i> , 2021 , 90, 399-408	7.9	3
50	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. <i>Nature Communications</i> , 2021 , 12, 5251	17.4	3
49	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. <i>Neuron</i> , 2021 , 109, 3088-3103.e5	13.9	8
48	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. <i>Science Advances</i> , 2020 , 6,	14.3	15
47	Programmatic access to bacterial regulatory networks with regutools. <i>Bioinformatics</i> , 2020 , 36, 4532-4534	7.2	0
46	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. <i>Nature Neuroscience</i> , 2020 , 23, 510-519	25.5	30
45	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020 , 11, 1041	17.4	6
44	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020 , 30, 1073-1081	9.7	13

43	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. <i>Nature Communications</i> , 2020 , 11, 462	17.4	37
42	SynGAP isoforms differentially regulate synaptic plasticity and dendritic development. <i>ELife</i> , 2020 , 9,	8.9	14
41	Author response: SynGAP isoforms differentially regulate synaptic plasticity and dendritic development 2020 ,		2
40	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. <i>Molecular Psychiatry</i> , 2020 , 25, 3267-3277	15.1	4
39	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. <i>Genome Biology</i> , 2019 , 20, 196	18.3	42
38	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2019 , 137, 557-569	14.3	30
37	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. <i>BMC Genomics</i> , 2019 , 20, 513	4.5	36
36	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. <i>Neuron</i> , 2019 , 103, 203-216.e8	13.9	67
35	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019 , 19, e1800315	4.8	8
34	Improving the value of public RNA-seq expression data by phenotype prediction. <i>Nucleic Acids Research</i> , 2018 , 46, e54	20.1	31
33	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. <i>Nature Neuroscience</i> , 2018 , 21, 1117-1125	25.5	176
32	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277
31	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018 , 362,	33.3	434
30	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018 , 362,	33.3	319
29	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. <i>Frontiers in Immunology</i> , 2018 , 9, 2679	8.4	2
28	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017 , 35, 319-321	44.5	211
27	Altered expression of histamine signaling genes in autism spectrum disorder. <i>Translational Psychiatry</i> , 2017 , 7, e1126	8.6	49
26	Flexible expressed region analysis for RNA-seq with derfinder. <i>Nucleic Acids Research</i> , 2017 , 45, e9	20.1	32

25	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. <i>F1000Research</i> , 2017 , 6, 1558	3.6	30
24	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. <i>Bioinformatics</i> , 2017 , 33, 4033-4040	7.2	33
23	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. <i>Genome Biology</i> , 2016 , 17, 266	18.3	65
22	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. <i>Nature Neuroscience</i> , 2015 , 18, 154-161	25.5	110
21	regionReport: Interactive reports for region-based analyses. <i>F1000Research</i> , 2015 , 4, 105	3.6	4
20	regionReport: Interactive reports for region-level and feature-level genomic analyses. <i>F1000Research</i> , 2015 , 4, 105	3.6	4
19	RegulonDB version 7.0: transcriptional regulation of Escherichia coli K-12 integrated within genetic sensory response units (Gensor Units). <i>Nucleic Acids Research</i> , 2011 , 39, D98-105	20.1	275
18	Interspecies interactions that result in Bacillus subtilis forming biofilms are mediated mainly by members of its own genus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1236-43	11.5	75
17	Rail-RNA: Scalable analysis of RNA-seq splicing and coverage		5
16	recount: A large-scale resource of analysis-ready RNA-seq expression data		5
15	Improving the value of public RNA-seq expression data by phenotype prediction		2
14	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex		16
13	Widespread methylation quantitative trait loci and their role in schizophrenia risk		1
12	Single-nucleus transcriptome analysis reveals cell type-specific molecular signatures across reward circuitry in the human brain		4
11	Megadepth: efficient coverage quantification for BigWigs and BAMs		1
10	RNA-seq transcript quantification from reduced-representation data in recount2		2
9	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs		3
8	Regional heterogeneity in gene expression, regulation and coherence in hippocampus and dorsolateral prefrontal cortex across development and in schizophrenia		4

7	Divergent neuronal DNA methylation patterns across human cortical development: Critical periods and a unique role of CpH methylation	1
6	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods	1
5	recount-brain: a curated repository of human brain RNA-seq datasets metadata	3
4	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex	1
3	Flexible expressed region analysis for RNA-seq with derfinder	6
2	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data	2
1	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor	8