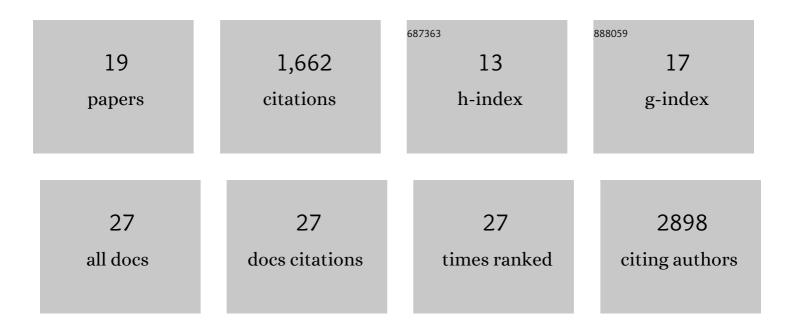
## Carlo Colantuoni

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/870095/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Two-stage linked component analysis for joint decomposition of multiple biologically related data sets. Biostatistics, 2022, 23, 1200-1217.	1.5	3
2	Single-Nucleus RNA-Seq Reveals Dysregulation of Striatal Cell Identity Due to Huntington's Disease Mutations. Journal of Neuroscience, 2021, 41, 5534-5552.	3.6	30
3	Plasma microRNAs are associated with domain-specific cognitive function in people with HIV. Aids, 2021, 35, 1795-1804.	2.2	1
4	gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration. Nature Methods, 2021, 18, 843-844.	19.0	100
5	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
6	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
7	Upregulation of Superoxide Dismutase 2 by Astrocytes in the SIV/Macaque Model of HIV-Associated Neurologic Disease. Journal of Neuropathology and Experimental Neurology, 2020, 79, 986-997.	1.7	4
8	Putative Autoantigen Leiomodin-1 Is Expressed in the Human Brain and in the Membrane Fraction of Newly Formed Neurons. Pathogens, 2020, 9, 1036.	2.8	11
9	projectR: an R/Bioconductor package for transfer learning via PCA, NMF, correlation and clustering. Bioinformatics, 2020, 36, 3592-3593.	4.1	45
10	Variation of Human Neural Stem Cells Generating Organizer States InÂVitro before Committing to Cortical Excitatory or Inhibitory Neuronal Fates. Cell Reports, 2020, 31, 107599.	6.4	20
11	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. Cell Systems, 2019, 8, 395-411.e8.	6.2	121
12	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. Cell Systems, 2019, 8, 122-135.e7.	6.2	45
13	Convergence of placenta biology and genetic risk for schizophrenia. Nature Medicine, 2018, 24, 792-801.	30.7	214
14	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. Nature Neuroscience, 2018, 21, 1117-1125.	14.8	300
15	PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. Bioinformatics, 2017, 33, 1892-1894.	4.1	39
16	Pattern Identification in Time-Course Gene Expression Data with the CoGAPS Matrix Factorization. Methods in Molecular Biology, 2014, 1101, 87-112.	0.9	9
17	Behaviorally Activated mRNA Expression Profiles Produce Signatures of Learning and Enhanced Inhibition in Aged Rats with Preserved Memory. PLoS ONE, 2013, 8, e83674.	2.5	34
18	Local Mean Normalization of Microarray Element Signal Intensities across an Array Surface: Quality Control and Correction of Spatially Systematic Artifacts. BioTechniques, 2002, 32, 1316-1320.	1.8	58

#	Article	IF	CITATIONS
19	High throughput analysis of gene expression in the human brain. , 2000, 59, 1-10.		71