Jose Fernandez Navarro

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4327918/publications.pdf

Version: 2024-02-01

17	4,428	471061 17	887659 17
papers	citations	h-index	g-index

18	18	18	4956
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of early neurodegenerative pathways in progressive multiple sclerosis. Nature Neuroscience, 2022, 25, 944-955.	7.1	55
2	Single-cell and spatial transcriptomics enables probabilistic inference of cell type topography. Communications Biology, 2020, 3, 565.	2.0	252
3	Spatial Transcriptomics Reveals Genes Associated with Dysregulated Mitochondrial Functions and Stress Signaling in Alzheimer Disease. IScience, 2020, 23, 101556.	1.9	61
4	Spatial Transcriptomics and In Situ Sequencing to Study Alzheimerâ€™s Disease. Cell, 2020, 182, 976-991.e19.	13.5	491
5	Molecular atlas of the adult mouse brain. Science Advances, 2020, 6, eabb3446.	4.7	183
6	Identification and transfer of spatial transcriptomics signatures for cancer diagnosis. Breast Cancer Research, 2020, 22, 6.	2.2	54
7	ST viewer: a tool for analysis and visualization of spatial transcriptomics datasets. Bioinformatics, 2019, 35, 1058-1060.	1.8	30
8	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	9.0	708
9	ST Spot Detector: a web-based application for automatic spot and tissue detection for spatial Transcriptomics image datasets. Bioinformatics, 2018, 34, 1966-1968.	1.8	30
10	Barcoded solid-phase RNA capture for Spatial Transcriptomics profiling in mammalian tissue sections. Nature Protocols, 2018, 13, 2501-2534.	5.5	144
11	Spatially resolved transcriptome profiling in model plant species. Nature Plants, 2017, 3, 17061.	4.7	135
12	ST Pipeline: an automated pipeline for spatial mapping of unique transcripts. Bioinformatics, 2017, 33, 2591-2593.	1.8	81
13	Spatial detection of fetal marker genes expressed at low level in adult human heart tissue. Scientific Reports, 2017, 7, 12941.	1.6	62
14	Massive and parallel expression profiling using microarrayed single-cell sequencing. Nature Communications, 2016, 7, 13182.	5.8	44
15	An automated approach to prepare tissue-derived spatially barcoded RNA-sequencing libraries. Scientific Reports, 2016, 6, 37137.	1.6	52
16	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science, 2016, 353, 78-82.	6.0	1,983
17	Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics. Journal of Proteomics, 2013, 80, 123-131.	1.2	49