

Yohei Sasagawa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7059403/publications.pdf>

Version: 2024-02-01

13
papers

1,246
citations

1040056

9
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

2362
citing authors

#	ARTICLE	IF	CITATIONS
1	A common epigenetic mechanism across different cellular origins underlies systemic immune dysregulation in an idiopathic autism mouse model. <i>Molecular Psychiatry</i> , 2022, 27, 3343-3354.	7.9	4
2	Local states of chromatin compaction at transcription start sites control transcription levels. <i>Nucleic Acids Research</i> , 2021, 49, 8007-8023.	14.5	18
3	Developmental excitation-inhibition imbalance underlying psychoses revealed by single-cell analyses of discordant twins-derived cerebral organoids. <i>Molecular Psychiatry</i> , 2020, 25, 2695-2711.	7.9	73
4	Primed to Naive-Like Conversion of the Common Marmoset Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2020, 29, 761-773.	2.1	14
5	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	17.5	313
6	Strategies for Converting RNA to Amplifiable cDNA for Single-Cell RNA Sequencing Methods. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1129, 1-17.	1.6	6
7	Cell type-specific transcriptome analysis unveils secreted signaling molecule genes expressed in apical epithelial cap during appendage regeneration. <i>Development Growth and Differentiation</i> , 2019, 61, 447-456.	1.5	9
8	Polysaccharide hydrolase of the hadal zone amphipods <i>Hirondellea gigas</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2018, 82, 1123-1133.	1.3	10
9	Single-cell full-length total RNA sequencing uncovers dynamics of recursive splicing and enhancer RNAs. <i>Nature Communications</i> , 2018, 9, 619.	12.8	192
10	Chromatin remodeler CHD7 regulates the stem cell identity of human neural progenitors. <i>Genes and Development</i> , 2018, 32, 165-180.	5.9	28
11	Quartz-Seq2: a high-throughput single-cell RNA-sequencing method that effectively uses limited sequence reads. <i>Genome Biology</i> , 2018, 19, 29.	8.8	101
12	Constrained vertebrate evolution by pleiotropic genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 1722-1730.	7.8	72
13	Quartz-Seq: a highly reproducible and sensitive single-cell RNA sequencing method, reveals non-genetic gene-expression heterogeneity. <i>Genome Biology</i> , 2013, 14, R31.	8.8	378