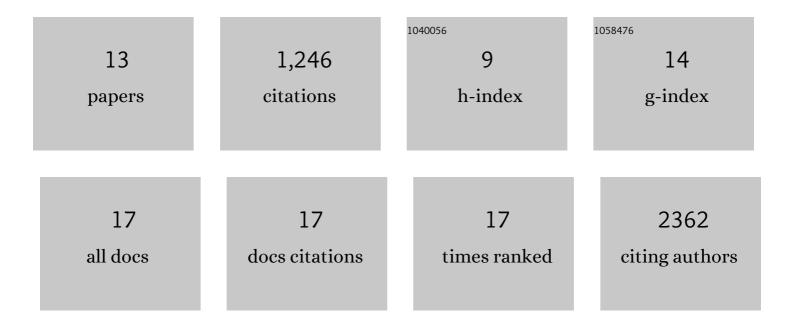
Yohei Sasagawa

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7059403/publications.pdf Version: 2024-02-01



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