

Na Sun

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11725612/publications.pdf>

Version: 2024-02-01

14
papers

960
citations

933447

10
h-index

1058476

14
g-index

14
all docs

14
docs citations

14
times ranked

1746
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell dissection of the human brain vasculature. <i>Nature</i> , 2022, 603, 893-899.	27.8	135
2	Immune genes outside immune cells for multiple sclerosis. <i>Neuron</i> , 2022, 110, 1090-1092.	8.1	2
3	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. <i>Cell Reports</i> , 2019, 29, 4568-4582.e5.	6.4	114
4	Accurate Drug Repositioning through Non-tissue-Specific Core Signatures from Cancer Transcriptomes. <i>Cell Reports</i> , 2018, 25, 523-535.e5.	6.4	20
5	Repression of human and mouse brain inflammaging transcriptome by broad gene-body histone hyperacetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7611-7616.	7.1	55
6	The system capacity view of aging and longevity. <i>Quantitative Biology</i> , 2017, 5, 251-259.	0.5	2
7	Inference of differentiation time for single cell transcriptomes using cell population reference data. <i>Nature Communications</i> , 2017, 8, 1856.	12.8	30
8	Spatial Transcriptome for the Molecular Annotation of Lineage Fates and Cell Identity in Mid-gastrula Mouse Embryo. <i>Developmental Cell</i> , 2016, 36, 681-697.	7.0	201
9	A Systems Approach to Reverse Engineer Lifespan Extension by Dietary Restriction. <i>Cell Metabolism</i> , 2016, 23, 529-540.	16.2	67
10	Genome-wide ChIP-seq and RNA-seq analyses of Pou3f1 during mouse pluripotent stem cell neural fate commitment. <i>Genomics Data</i> , 2015, 5, 375-377.	1.3	7
11	Single-cell-level spatial gene expression in the embryonic neural differentiation niche. <i>Genome Research</i> , 2015, 25, 570-581.	5.5	6
12	The transcription factor Pou3f1 promotes neural fate commitment via activation of neural lineage genes and inhibition of external signaling pathways. <i>ELife</i> , 2014, 3, .	6.0	213
13	Integrating Genomic, Epigenomic, and Transcriptomic Features Reveals Modular Signatures Underlying Poor Prognosis in Ovarian Cancer. <i>Cell Reports</i> , 2013, 4, 542-553.	6.4	88
14	A novel Bayesian network inference algorithm for integrative analysis of heterogeneous deep sequencing data. <i>Cell Research</i> , 2013, 23, 440-443.	12.0	20