

Stephen J Clark

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

2,636
citations

567281

15
h-index

996975

15
g-index

25
all docs

25
docs citations

25
times ranked

4136
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. <i>Nature Communications</i> , 2022, 13, 1779.	12.8	25
2	Spatial profiling of early primate gastrulation in utero. <i>Nature</i> , 2022, 609, 136-143.	27.8	56
3	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021, 12, 5771.	12.8	20
4	Increased transcriptome variation and localised DNA methylation changes in oocytes from aged mice revealed by parallel single-cell analysis. <i>Aging Cell</i> , 2020, 19, e13278.	6.7	27
5	Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. <i>Nature Communications</i> , 2019, 10, 4361.	12.8	157
6	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. <i>Genome Biology</i> , 2019, 20, 30.	8.8	61
7	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491.	27.8	307
8	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. <i>Nature Communications</i> , 2018, 9, 781.	12.8	513
9	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. <i>Cell Systems</i> , 2018, 7, 63-76.e12.	6.2	70
10	Genome-wide base-resolution mapping of DNA methylation in single cells using single-cell bisulfite sequencing (scBS-seq). <i>Nature Protocols</i> , 2017, 12, 534-547.	12.0	199
11	Single-cell epigenomics: powerful new methods for understanding gene regulation and cell identity. <i>Genome Biology</i> , 2016, 17, 72.	8.8	253
12	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016, 13, 229-232.	19.0	602
13	Continuous Histone Replacement by Hira Is Essential for Normal Transcriptional Regulation and De Novo DNA Methylation during Mouse Oogenesis. <i>Molecular Cell</i> , 2015, 60, 611-625.	9.7	110
14	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. <i>Cell Reports</i> , 2014, 9, 1990-2000.	6.4	116
15	Association of Sirtuin 1 (<i>SIRT1</i>) Gene SNPs and Transcript Expression Levels With Severe Obesity. <i>Obesity</i> , 2012, 20, 178-185.	3.0	68