

Ruijie Liu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3108338/publications.pdf>

Version: 2024-02-01

15
papers

1,401
citations

840776

11
h-index

996975

15
g-index

20
all docs

20
docs citations

20
times ranked

3731
citing authors

#	ARTICLE	IF	CITATIONS
1	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015, 43, e97-e97.	14.5	430
2	The Molecular Signature of Tissue Resident Memory CD8 T Cells Isolated from the Brain. <i>Journal of Immunology</i> , 2012, 189, 3462-3471.	0.8	310
3	Id2 expression delineates differential checkpoints in the genetic program of CD8 ⁺ and CD103 ⁺ dendritic cell lineages. <i>EMBO Journal</i> , 2011, 30, 2690-2704.	7.8	121
4	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017, 19, 164-176.	10.3	99
5	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. <i>Cell Reports</i> , 2017, 18, 406-418.	6.4	95
6	Genome-wide binding and mechanistic analyses of Smchd1-mediated epigenetic regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3535-44.	7.1	83
7	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 16.	3.9	63
8	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. <i>Cell Stem Cell</i> , 2019, 25, 258-272.e9.	11.1	60
9	Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. <i>BMC Bioinformatics</i> , 2011, 12, 68.	2.6	38
10	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017, 45, e30-e30.	14.5	34
11	Isolation of tissues and preservation of <i>scRNA</i> from intact, germinated barley grain. <i>Plant Journal</i> , 2017, 91, 754-765.	5.7	28
12	Allele-specific expression analysis methods for high-density SNP microarray data. <i>Bioinformatics</i> , 2012, 28, 1102-1108.	4.1	15
13	Transcriptional profiling of the epigenetic regulator Smchd1. <i>Genomics Data</i> , 2016, 7, 144-147.	1.3	13
14	KRLMM: an adaptive genotype calling method for common and low frequency variants. <i>BMC Bioinformatics</i> , 2014, 15, 158.	2.6	4
15	Distinctive gene expression patterns and imprinting signatures revealed in reciprocal crosses between cattle sub-species. <i>BMC Genomics</i> , 2021, 22, 410.	2.8	4