

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