

Ni Huang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1844291/publications.pdf>

Version: 2024-02-01

18
papers

2,550
citations

623734

14
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

5143
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254. | 27.8 | 495 |
| 2 | Large, rare chromosomal deletions associated with severe early-onset obesity. <i>Nature</i> , 2010, 463, 666-670. | 27.8 | 487 |
| 3 | Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83. | 14.5 | 363 |
| 4 | Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197. | 12.6 | 265 |
| 5 | Developmental cell programs are co-opted in inflammatory skin disease. <i>Science</i> , 2021, 371, . | 12.6 | 264 |
| 6 | Human Spermatogenic Failure Purges Deleterious Mutation Load from the Autosomes and Both Sex Chromosomes, including the Gene DMRT1. <i>PLoS Genetics</i> , 2013, 9, e1003349. | 3.5 | 118 |
| 7 | Putative cell type discovery from single-cell gene expression data. <i>Nature Methods</i> , 2020, 17, 621-628. | 19.0 | 91 |
| 8 | A team of heterochromatin factors collaborates with small RNA pathways to combat repetitive elements and germline stress. <i>ELife</i> , 2017, 6, . | 6.0 | 87 |
| 9 | Chromatin accessibility dynamics across <i>C. elegans</i> development and ageing. <i>ELife</i> , 2018, 7, . | 6.0 | 76 |
| 10 | Stable <i>Caenorhabditis elegans</i> chromatin domains separate broadly expressed and developmentally regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7020-E7029. | 7.1 | 73 |
| 11 | Physical and functional interaction between SET1/COMPASS complex component CFP-1 and a Sin3S HDAC complex in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2019, 47, 11164-11180. | 14.5 | 54 |
| 12 | A Screen for Genomic Disorders of Infertility Identifies MAST2 Duplications Associated with Nonobstructive Azoospermia in Humans ¹ . <i>Biology of Reproduction</i> , 2015, 93, 61. | 2.7 | 30 |
| 13 | User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328. | 19.0 | 26 |
| 14 | Rare mutations in the complement regulatory gene CSMD1 are associated with male and female infertility. <i>Nature Communications</i> , 2019, 10, 4626. | 12.8 | 24 |
| 15 | Transcriptional characterization of human megakaryocyte polyploidization and lineage commitment. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 1236-1249. | 3.8 | 15 |
| 16 | A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020, 9, . | 6.4 | 14 |
| 17 | DREAM represses distinct targets by cooperating with different THAP domain proteins. <i>Cell Reports</i> , 2021, 37, 109835. | 6.4 | 6 |
| 18 | Accessible Region Conformation Capture (ARC-C) gives high-resolution insights into genome architecture and regulation. <i>Genome Research</i> , 2022, 32, 357-366. | 5.5 | 6 |