

# Hui Shen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2283012/publications.pdf>

Version: 2024-02-01

17  
papers

6,610  
citations

471509

17  
h-index

888059

17  
g-index

24  
all docs

24  
docs citations

24  
times ranked

15300  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. <i>Cell Genomics</i> , 2022, 2, 100144.  | 6.5  | 37        |
| 2  | Evaluation of whole-genome DNA methylation sequencing library preparation protocols. <i>Epigenetics and Chromatin</i> , 2021, 14, 28.   | 3.9  | 29        |
| 3  | Epigenomic Reprogramming toward Mesenchymal-Epithelial Transition in Ovarian-Cancer-Associated Mesenchymal Stem Cells Drives Metastasis. <i>Cell Reports</i> , 2020, 33, 108473.                                    | 6.4  | 34        |
| 4  | Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.   | 16.8 | 151       |
| 5  | Phase II clinical trial of metformin as a cancer stem cell-targeting agent in ovarian cancer. <i>JCI Insight</i> , 2020, 5, .   | 5.0  | 74        |
| 6  | Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.  | 6.2  | 103       |
| 7  | Integrated Epigenome, Exome, and Transcriptome Analyses Reveal Molecular Subtypes and Homeotic Transformation in Uterine Fibroids. <i>Cell Reports</i> , 2019, 29, 4069-4085.e6.                                    | 6.4  | 49        |
| 8  | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.  | 28.9 | 1,417     |
| 9  | DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018, 50, 591-602.  | 21.4 | 258       |
| 10 | The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .   | 12.6 | 781       |
| 11 | SeSAmE: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , 2018, 46, e123.   | 14.5 | 213       |
| 12 | Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017, 45, gkw967.  | 14.5 | 466       |
| 13 | Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.  | 16.8 | 309       |
| 14 | Identification of activated enhancers and linked transcription factors in breast, prostate, and kidney tumors by tracing enhancer networks using epigenetic traits. <i>Epigenetics and Chromatin</i> , 2016, 9, 50. | 3.9  | 53        |
| 15 | Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105.  | 9.6  | 178       |
| 16 | Interplay between the Cancer Genome and Epigenome. <i>Cell</i> , 2013, 153, 38-55.  | 28.9 | 733       |
| 17 | Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.  | 17.5 | 1,710     |