

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	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	17.5	1,710
2	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
3	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
4	Interplay between the Cancer Genome and Epigenome. <i>Cell</i> , 2013, 153, 38-55.	28.9	733
5	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017, 45, gkw967.	14.5	466
6	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
7	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018, 50, 591-602.	21.4	258
8	SeSAmE: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , 2018, 46, e123.	14.5	213
9	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105.	9.6	178
10	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	16.8	151
11	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.2	103
12	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
13	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
14	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
15	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. <i>Cell Genomics</i> , 2022, 2, 100144.	6.5	37
16	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
17	Evaluation of whole-genome DNA methylation sequencing library preparation protocols. <i>Epigenetics and Chromatin</i> , 2021, 14, 28.	3.9	29