

Wanlu Liu

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,597
citations

304743

22
h-index

414414

32
g-index

33
all docs

33
docs citations

33
times ranked

3642
citing authors

#	ARTICLE	IF	CITATIONS
1	huARdb: human Antigen Receptor database for interactive clonotype-transcriptome analysis at the single-cell level. <i>Nucleic Acids Research</i> , 2022, 50, D1244-D1254.	14.5	10
2	Single cell analysis reveals inhibition of angiogenesis attenuates the progression of heterotopic ossification in Mx ^{Cre} /p ^{Cre} mice. <i>Bone Research</i> , 2022, 10, 4.	11.4	7
3	Human reproduction is regulated by retrotransposons derived from ancient Hominidae-specific viral infections. <i>Nature Communications</i> , 2022, 13, 463.	12.8	24
4	RAD: a web application to identify region associated differentially expressed genes. <i>Bioinformatics</i> , 2021, 37, 2741-2743.	4.1	11
5	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial SssI methyltransferase. <i>Nature Communications</i> , 2021, 12, 3130.	12.8	20
6	Early-Stage Primary Anti-inflammatory Therapy Enhances the Regenerative Efficacy of Platelet-Rich Plasma in a Rabbit Achilles Tendinopathy Model. <i>American Journal of Sports Medicine</i> , 2021, 49, 3357-3371.	4.2	6
7	Identification of SRSF3 target mRNAs using inducible TRIPE. <i>Biochemical and Biophysical Research Communications</i> , 2021, 578, 21-27.	2.1	1
8	DNA methylation-linked chromatin accessibility affects genomic architecture in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	70
9	Classification of four distinct osteoarthritis subtypes with a knee joint tissue transcriptome atlas. <i>Bone Research</i> , 2020, 8, 38.	11.4	57
10	Naive Human Embryonic Stem Cells Can Give Rise to Cells with a Trophoblast-like Transcriptome and Methyloome. <i>Stem Cell Reports</i> , 2020, 15, 198-213.	4.8	129
11	An Extended Culture System that Supports Human Primordial Germ Cell-like Cell Survival and Initiation of DNA Methylation Erasure. <i>Stem Cell Reports</i> , 2020, 14, 433-446.	4.8	30
12	Arabidopsis SWR1-associated protein methyl-CpG-binding domain 9 is required for histone H2A.Z deposition. <i>Nature Communications</i> , 2019, 10, 3352.	12.8	60
13	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019, 10, 3916.	12.8	31
14	Multi-level Modulation of Light Signaling by GIGANTEA Regulates Both the Output and Pace of the Circadian Clock. <i>Developmental Cell</i> , 2019, 49, 840-851.e8.	7.0	53
15	Co-targeting RNA Polymerases IV and V Promotes Efficient De Novo DNA Methylation in Arabidopsis. <i>Cell</i> , 2019, 176, 1068-1082.e19.	28.9	124
16	Site-specific manipulation of Arabidopsis loci using CRISPR-Cas9 SunTag systems. <i>Nature Communications</i> , 2019, 10, 729.	12.8	215
17	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. <i>Cell Reports</i> , 2019, 29, 4568-4582.e5.	6.4	114
18	A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. <i>Molecular Cell</i> , 2019, 73, 73-83.e6.	9.7	33

#	ARTICLE	IF	CITATIONS
19	TFAP2C regulates transcription in human naive pluripotency by opening enhancers. <i>Nature Cell Biology</i> , 2018, 20, 553-564.	10.3	134
20	Targeted DNA demethylation of the <i>Arabidopsis</i> genome using the human TET1 catalytic domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2125-E2134.	7.1	190
21	RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2018, 4, 181-188.	9.3	106
22	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1069-E1074.	7.1	51
23	The TFAP2C-Regulated OCT4 Naive Enhancer Is Involved in Human Germline Formation. <i>Cell Reports</i> , 2018, 25, 3591-3602.e5.	6.4	60
24	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
25	Primate Primordial Germ Cells Acquire Transplantation Potential by Carnegie Stage 23. <i>Stem Cell Reports</i> , 2017, 9, 329-341.	4.8	18
26	Germline competency of human embryonic stem cells depends on eomesodermin. <i>Biology of Reproduction</i> , 2017, 97, 850-861.	2.7	84
27	DNA methylome of the 20-gigabase Norway spruce genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8106-E8113.	7.1	85
28	Mouse MORC3 is a GHKL ATPase that localizes to H3K4me3 marked chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5108-16.	7.1	41
29	Naive Human Pluripotent Cells Feature a Methylation Landscape Devoid of Blastocyst or Germline Memory. <i>Cell Stem Cell</i> , 2016, 18, 323-329.	11.1	242
30	<i>Arabidopsis</i> AtMORC4 and AtMORC7 Form Nuclear Bodies and Repress a Large Number of Protein-Coding Genes. <i>PLoS Genetics</i> , 2016, 12, e1005998.	3.5	42
31	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. <i>Cell</i> , 2015, 163, 445-455.	28.9	260
32	MORC1 represses transposable elements in the mouse male germline. <i>Nature Communications</i> , 2014, 5, 5795.	12.8	108