Tao P Wu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Enzymatic characterization of mRNA cap adenosine-N6 methyltransferase PCIF1 activity on uncapped RNAs. Journal of Biological Chemistry, 2022, 298, 101751.	3.4	8
2	Enzymatic Characterization of In Vitro Activity of RNA Methyltransferase PCIF1 on DNA. Biochemistry, 2022, 61, 1005-1013.	2.5	6
3	NT-seq: a chemical-based sequencing method for genomic methylome profiling. Genome Biology, 2022, 23, .	8.8	4
4	Types of nuclear localization signals and mechanisms of protein import into the nucleus. Cell Communication and Signaling, 2021, 19, 60.	6.5	155
5	The exploration of N6-deoxyadenosine methylation in mammalian genomes. Protein and Cell, 2021, 12, 756-768.	11.0	16
6	Analysis of Internal and External Microorganism Community of Wild Cicada Flowers and Identification of the Predominant Cordyceps cicadae Fungus. Frontiers in Microbiology, 2021, 12, 752791.	3.5	3
7	New Insights Into the Biosynthesis of Typical Bioactive Components in the Traditional Chinese Medicinal Fungus Cordyceps militaris. Frontiers in Bioengineering and Biotechnology, 2021, 9, 801721.	4.1	8
8	N6-methyladenine in DNA antagonizes SATB1 in early development. Nature, 2020, 583, 625-630.	27.8	53
9	Mammalian ALKBH1 serves as an N6-mA demethylase of unpairing DNA. Cell Research, 2020, 30, 197-210.	12.0	71
10	Engineering an Artificial Membrane Vesicle Trafficking System (AMVTS) for the Excretion of β-Carotene in <i>Escherichia coli</i> . ACS Synthetic Biology, 2019, 8, 1037-1046.	3.8	36
11	Human MettL3–MettL14 complex is a sequence-specific DNA adenine methyltransferase active on single-strand and unpaired DNA in vitro. Cell Discovery, 2019, 5, 63.	6.7	45
12	N-methyladenine DNA Modification in Glioblastoma. Cell, 2018, 175, 1228-1243.e20.	28.9	236
13	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. Genome Research, 2018, 28, 1067-1078.	5.5	80
14	DNA methylation on N6-adenine in mammalian embryonic stem cells. Nature, 2016, 532, 329-333.	27.8	554
15	Extensive Nuclear Reprogramming Underlies Lineage Conversion into Functional Trophoblast Stem-like Cells. Cell Stem Cell, 2015, 17, 543-556.	11.1	80
16	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. Cell Stem Cell, 2014, 15, 295-309.	11.1	137
17	Histone Variant H2A.X Deposition Pattern Serves as a Functional Epigenetic Mark for Distinguishing the Developmental Potentials of iPSCs. Cell Stem Cell, 2014, 15, 281-294.	11.1	58
18	Rif1 Maintains Telomere Length Homeostasis of ESCs by Mediating Heterochromatin Silencing. Developmental Cell, 2014, 29, 7-19.	7.0	102

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19	Estimating the Quality of Reprogrammed Cells Using ES Cell Differentiation Expression Patterns. PLoS ONE, 2011, 6, e15336.	2.5	2
20	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. BMC Bioinformatics, 2011, 12, 53.	2.6	4
21	Genome-scale identification of Caenorhabditis elegans regulatory elements by tiling-array mapping of DNase I hypersensitive sites. BMC Genomics, 2009, 10, 92.	2.8	13
22	Transcriptional inhibiton of Hoxd4 expression by miRNA-10a in human breast cancer cells. BMC Molecular Biology, 2009, 10, 12.	3.0	167
23	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. Genome Research, 2007, 17, 1471-1477.	5.5	53
24	Identifying Hfq-binding small RNA targets in Escherichia coli. Biochemical and Biophysical Research Communications, 2006, 343, 950-955.	2.1	13
25	Integrated analysis of multiple data sources reveals modular structure of biological networks. Biochemical and Biophysical Research Communications, 2006, 345, 302-309.	2.1	33
26	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. Nucleic Acids Research, 2006, 34, D150-D152.	14.5	93
27	Dynamic Changes in Subgraph Preference Profiles of Crucial Transcription Factors. PLoS Computational Biology, 2006, 2, e47.	3.2	14