

Tao P Wu

List of Publications by Year in descending order

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27
papers

2,044
citations

516710

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27
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all docs

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docs citations

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times ranked

2958
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation on N6-adenine in mammalian embryonic stem cells. <i>Nature</i> , 2016, 532, 329-333.	27.8	554
2	N-methyladenine DNA Modification in Glioblastoma. <i>Cell</i> , 2018, 175, 1228-1243.e20.	28.9	236
3	Transcriptional inhibition of Hoxd4 expression by miRNA-10a in human breast cancer cells. <i>BMC Molecular Biology</i> , 2009, 10, 12.	3.0	167
4	Types of nuclear localization signals and mechanisms of protein import into the nucleus. <i>Cell Communication and Signaling</i> , 2021, 19, 60.	6.5	155
5	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	11.1	137
6	Rif1 Maintains Telomere Length Homeostasis of ESCs by Mediating Heterochromatin Silencing. <i>Developmental Cell</i> , 2014, 29, 7-19.	7.0	102
7	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006, 34, D150-D152.	14.5	93
8	Extensive Nuclear Reprogramming Underlies Lineage Conversion into Functional Trophoblast Stem-like Cells. <i>Cell Stem Cell</i> , 2015, 17, 543-556.	11.1	80
9	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. <i>Genome Research</i> , 2018, 28, 1067-1078.	5.5	80
10	Mammalian ALKBH1 serves as an N6-mA demethylase of unpairing DNA. <i>Cell Research</i> , 2020, 30, 197-210.	12.0	71
11	Histone Variant H2A.X Deposition Pattern Serves as a Functional Epigenetic Mark for Distinguishing the Developmental Potentials of iPSCs. <i>Cell Stem Cell</i> , 2014, 15, 281-294.	11.1	58
12	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , 2007, 17, 1471-1477.	5.5	53
13	N6-methyladenine in DNA antagonizes SATB1 in early development. <i>Nature</i> , 2020, 583, 625-630.	27.8	53
14	Human MettL3-MettL14 complex is a sequence-specific DNA adenine methyltransferase active on single-strand and unpaired DNA in vitro. <i>Cell Discovery</i> , 2019, 5, 63.	6.7	45
15	Engineering an Artificial Membrane Vesicle Trafficking System (AMVTS) for the Excretion of β -Carotene in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 1037-1046.	3.8	36
16	Integrated analysis of multiple data sources reveals modular structure of biological networks. <i>Biochemical and Biophysical Research Communications</i> , 2006, 345, 302-309.	2.1	33
17	The exploration of N6-deoxyadenosine methylation in mammalian genomes. <i>Protein and Cell</i> , 2021, 12, 756-768.	11.0	16
18	Dynamic Changes in Subgraph Preference Profiles of Crucial Transcription Factors. <i>PLoS Computational Biology</i> , 2006, 2, e47.	3.2	14

#	ARTICLE	IF	CITATIONS
19	Identifying Hfq-binding small RNA targets in Escherichia coli. Biochemical and Biophysical Research Communications, 2006, 343, 950-955.	2.1	13
20	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
21	Enzymatic characterization of mRNA cap adenosine-N6 methyltransferase PCIF1 activity on uncapped RNAs. Journal of Biological Chemistry, 2022, 298, 101751.	3.4	8
22	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
23	Enzymatic Characterization of In Vitro Activity of RNA Methyltransferase PCIF1 on DNA. Biochemistry, 2022, 61, 1005-1013.	2.5	6
24	Estimating developmental states of tumors and normal tissues using a linear time-ordered model. BMC Bioinformatics, 2011, 12, 53.	2.6	4
25	NT-seq: a chemical-based sequencing method for genomic methylome profiling. Genome Biology, 2022, 23, .	8.8	4
26	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
27	Estimating the Quality of Reprogrammed Cells Using ES Cell Differentiation Expression Patterns. PLoS ONE, 2011, 6, e15336.	2.5	2