

# Taiping Chen

## List of Publications by Year in descending order

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35  
papers

6,061  
citations

186265  
28  
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361022  
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times ranked

8461  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Essential Function of SETDB1 in Homologous Chromosome Pairing and Synapsis during Meiosis. <i>Cell Reports</i> , 2021, 34, 108575.	6.4	16
2	The inactive Dnmt3b3 isoform preferentially enhances Dnmt3b-mediated DNA methylation. <i>Genes and Development</i> , 2020, 34, 1546-1558.	5.9	44
3	The ZBTB24-CDCA7 axis regulates HELLS enrichment at centromeric satellite repeats to facilitate DNA methylation. <i>Protein and Cell</i> , 2020, 11, 214-218.	11.0	21
4	De novo identification of essential protein domains from CRISPR-Cas9 tiling-sgRNA knockout screens. <i>Nature Communications</i> , 2019, 10, 4541.	12.8	44
5	Structural basis of specific DNA binding by the transcription factor ZBTB24. <i>Nucleic Acids Research</i> , 2019, 47, 8388-8398.	14.5	29
6	DNA Methylation Reprogramming during Mammalian Development. <i>Genes</i> , 2019, 10, 257.	2.4	215
7	LRIG1 is a pleiotropic androgen receptor-regulated feedback tumor suppressor in prostate cancer. <i>Nature Communications</i> , 2019, 10, 5494.	12.8	13
8	DNMT3L facilitates DNA methylation partly by maintaining DNMT3A stability in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2019, 47, 152-167.	14.5	99
9	Identification of Rpl29 as a major substrate of the lysine methyltransferase Set7/9. <i>Journal of Biological Chemistry</i> , 2018, 293, 12770-12780.	3.4	24
10	DNMT3A and TET1 cooperate to regulate promoter epigenetic landscapes in mouse embryonic stem cells. <i>Genome Biology</i> , 2018, 19, 88.	8.8	120
11	Transcription and chromatin determinants of de novo DNA methylation timing in oocytes. <i>Epigenetics and Chromatin</i> , 2017, 10, 25.	3.9	69
12	Zscan4 Inhibits Maintenance DNA Methylation to Facilitate Telomere Elongation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2017, 20, 1936-1949.	6.4	81
13	The Arginine Methyltransferase PRMT6 Regulates DNA Methylation and Contributes to Global DNA Hypomethylation in Cancer. <i>Cell Reports</i> , 2017, 21, 3390-3397.	6.4	60
14	Negative regulation of DNMT3A de novo DNA methylation by frequently overexpressed UHRF family proteins as a mechanism for widespread DNA hypomethylation in cancer. <i>Cell Discovery</i> , 2016, 2, 16007.	6.7	74
15	Genetic Studies on Mammalian DNA Methyltransferases. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 123-150.	1.6	38
16	Maternal Setdb1 Is Required for Meiotic Progression and Preimplantation Development in Mouse. <i>PLoS Genetics</i> , 2016, 12, e1005970.	3.5	75
17	Dynamic changes in histone modifications precede de novo DNA methylation in oocytes. <i>Genes and Development</i> , 2015, 29, 2449-2462.	5.9	170
18	Genetic alterations of DNA methylation machinery in human diseases. <i>Epigenomics</i> , 2015, 7, 247-265.	2.1	209

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19	A DNMT3A mutation common in AML exhibits dominant-negative effects in murine ES cells. <i>Blood</i> , 2013, 122, 4086-4089.	1.4	153
20	Tet family of 5-methylcytosine dioxygenases in mammalian development. <i>Journal of Human Genetics</i> , 2013, 58, 421-427.	2.3	64
21	A Hypomorphic Lsd1 Allele Results in Heart Development Defects in Mice. <i>PLoS ONE</i> , 2013, 8, e60913.	2.5	23
22	Mechanistic and Functional Links Between Histone Methylation and DNA Methylation. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 335-348.	1.7	12
23	KMT1E Mediated H3K9 Methylation Is Required for the Maintenance of Embryonic Stem Cells by Repressing Trophoctoderm Differentiation. <i>Stem Cells</i> , 2010, 28, 201-212.	3.2	81
24	LSD1 demethylates histone and non-histone proteins. <i>Epigenetics</i> , 2009, 4, 129-132.	2.7	93
25	KDM1B is a histone H3K4 demethylase required to establish maternal genomic imprints. <i>Nature</i> , 2009, 461, 415-418.	27.8	465
26	The lysine demethylase LSD1 (KDM1) is required for maintenance of global DNA methylation. <i>Nature Genetics</i> , 2009, 41, 125-129.	21.4	721
27	A mammalian microRNA cluster controls DNA methylation and telomere recombination via Rbl2-dependent regulation of DNA methyltransferases. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 268-279.	8.2	348
28	Complete inactivation of DNMT1 leads to mitotic catastrophe in human cancer cells. <i>Nature Genetics</i> , 2007, 39, 391-396.	21.4	308
29	DNA methyltransferases control telomere length and telomere recombination in mammalian cells. <i>Nature Cell Biology</i> , 2006, 8, 416-424.	10.3	538
30	Lsh is involved in de novo methylation of DNA. <i>EMBO Journal</i> , 2006, 25, 335-345.	7.8	150
31	Inactivation of Dnmt3b in Mouse Embryonic Fibroblasts Results in DNA Hypomethylation, Chromosomal Instability, and Spontaneous Immortalization. <i>Journal of Biological Chemistry</i> , 2005, 280, 17986-17991.	3.4	237
32	The PWWP Domain of Dnmt3a and Dnmt3b Is Required for Directing DNA Methylation to the Major Satellite Repeats at Pericentric Heterochromatin. <i>Molecular and Cellular Biology</i> , 2004, 24, 9048-9058.	2.3	241
33	Structure and Function of Eukaryotic DNA Methyltransferases. <i>Current Topics in Developmental Biology</i> , 2004, 60, 55-89.	2.2	272
34	Establishment and Maintenance of Genomic Methylation Patterns in Mouse Embryonic Stem Cells by Dnmt3a and Dnmt3b. <i>Molecular and Cellular Biology</i> , 2003, 23, 5594-5605.	2.3	652
35	A Novel Dnmt3a Isoform Produced from an Alternative Promoter Localizes to Euchromatin and Its Expression Correlates with Active de Novo Methylation. <i>Journal of Biological Chemistry</i> , 2002, 277, 38746-38754.	3.4	302