

# Michael Weber

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

7,393  
citations

236612

25  
h-index

233125

45  
g-index

49  
all docs

49  
docs citations

49  
times ranked

10230  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. <i>Nature Genetics</i> , 2007, 39, 457-466.	9.4	1,922
2	Chromosome-wide and promoter-specific analyses identify sites of differential DNA methylation in normal and transformed human cells. <i>Nature Genetics</i> , 2005, 37, 853-862.	9.4	1,591
3	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. <i>Molecular Cell</i> , 2008, 30, 755-766.	4.5	802
4	Targets and dynamics of promoter DNA methylation during early mouse development. <i>Nature Genetics</i> , 2010, 42, 1093-1100.	9.4	527
5	Genomic patterns of DNA methylation: targets and function of an epigenetic mark. <i>Current Opinion in Cell Biology</i> , 2007, 19, 273-280.	2.6	338
6	Global profiling of DNA methylation erasure in mouse primordial germ cells. <i>Genome Research</i> , 2012, 22, 633-641.	2.4	289
7	Methylated DNA Immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , 2009, 507, 55-64.	0.4	203
8	Mechanisms of DNA methylation and demethylation in mammals. <i>Biochimie</i> , 2012, 94, 2202-2211.	1.3	144
9	Ontogeny of CpG island methylation and specificity of DNMT3 methyltransferases during embryonic development in the mouse. <i>Genome Biology</i> , 2014, 15, 545.	3.8	143
10	Reinforcement of STAT3 activity reprogrammes human embryonic stem cells to naive-like pluripotency. <i>Nature Communications</i> , 2015, 6, 7095.	5.8	137
11	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. <i>Blood</i> , 2009, 113, 2488-2497.	0.6	133
12	Functions of DNA Methylation and Hydroxymethylation in Mammalian Development. <i>Current Topics in Developmental Biology</i> , 2013, 104, 47-83.	1.0	133
13	Epigenomics: Mapping the Methylome. <i>Cell Cycle</i> , 2006, 5, 155-158.	1.3	117
14	Genome-wide analysis in the mouse embryo reveals the importance of DNA methylation for transcription integrity. <i>Nature Communications</i> , 2020, 11, 3153.	5.8	91
15	Exposure to Endocrine Disruptor Induces Transgenerational Epigenetic Deregulation of MicroRNAs in Primordial Germ Cells. <i>PLoS ONE</i> , 2015, 10, e0124296.	1.1	86
16	DNMT3AR882H mutant and Tet2 inactivation cooperate in the deregulation of DNA methylation control to induce lymphoid malignancies in mice. <i>Leukemia</i> , 2016, 30, 1388-1398.	3.3	67
17	EHMT2 directs DNA methylation for efficient gene silencing in mouse embryos. <i>Genome Research</i> , 2016, 26, 192-202.	2.4	60
18	Extensive tissue-specific variation of allelic methylation in the <i>Igf2</i> gene during mouse fetal development: relation to expression and imprinting. <i>Mechanisms of Development</i> , 2001, 101, 133-141.	1.7	54

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19	Long-range chromatin interactions at the mouse <i>Igf2/H19</i> locus reveal a novel paternally expressed long non-coding RNA. <i>Nucleic Acids Research</i> , 2011, 39, 5893-5906.	6.5	54
20	A multi-scale analysis of bull sperm methylome revealed both species peculiarities and conserved tissue-specific features. <i>BMC Genomics</i> , 2018, 19, 404.	1.2	52
21	H19 gene expression is up-regulated exclusively by stabilization of the RNA during muscle cell differentiation. <i>Oncogene</i> , 2000, 19, 5810-5816.	2.6	45
22	Genomic Imprinting Controls Matrix Attachment Regions in the <i>Igf2</i> Gene. <i>Molecular and Cellular Biology</i> , 2003, 23, 8953-8959.	1.1	43
23	H19 Antisense RNA Can Up-Regulate <i>Igf2</i> Transcription by Activation of a Novel Promoter in Mouse Myoblasts. <i>PLoS ONE</i> , 2012, 7, e37923.	1.1	41
24	Dynamic regulation of DNA methylation during mammalian development. <i>Epigenomics</i> , 2009, 1, 81-98.	1.0	40
25	DNMT3A-dependent DNA methylation is required for spermatogonial stem cells to commit to spermatogenesis. <i>Nature Genetics</i> , 2022, 54, 469-480.	9.4	39
26	TFmotifView: a webserver for the visualization of transcription factor motifs in genomic regions. <i>Nucleic Acids Research</i> , 2020, 48, W208-W217.	6.5	25
27	Methylated DNA Immunoprecipitation (MeDIP) from Low Amounts of Cells. <i>Methods in Molecular Biology</i> , 2012, 925, 149-158.	0.4	23
28	Modulated contact frequencies at gene-rich loci support a statistical helix model for mammalian chromatin organization. <i>Genome Biology</i> , 2011, 12, R42.	13.9	22
29	Turnover of primary transcripts is a major step in the regulation of mouse H19 gene expression. <i>EMBO Reports</i> , 2002, 3, 774-779.	2.0	21
30	E2F6 initiates stable epigenetic silencing of germline genes during embryonic development. <i>Nature Communications</i> , 2021, 12, 3582.	5.8	21
31	A real-time polymerase chain reaction assay for quantification of allele ratios and correction of amplification bias. <i>Analytical Biochemistry</i> , 2003, 320, 252-258.	1.1	18
32	Single-CpG resolution mapping of 5-hydroxymethylcytosine by chemical labeling and exonuclease digestion identifies evolutionarily unconserved CpGs as TET targets. <i>Genome Biology</i> , 2016, 17, 56.	3.8	14
33	Loss of <i>Apc</i> Rapidly Impairs DNA Methylation Programs and Cell Fate Decisions in <i>Lgr5+</i> Intestinal Stem Cells. <i>Cancer Research</i> , 2020, 80, 2101-2113.	0.4	13
34	A comparative methylome analysis reveals conservation and divergence of DNA methylation patterns and functions in vertebrates. <i>BMC Biology</i> , 2022, 20, 70.	1.7	12
35	Pan-cancer predictions of transcription factors mediating aberrant DNA methylation. <i>Epigenetics and Chromatin</i> , 2022, 15, 10.	1.8	10
36	The 3' portion of the mouse <i>H19</i> Imprinting-Control Region is required for proper tissue-specific expression of the <i>Igf2</i> gene. <i>Cytogenetic and Genome Research</i> , 2006, 113, 230-237.	0.6	7

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37	Erase for a new start. <i>Nature</i> , 2012, 492, 363-364.	13.7	7
38	Epigenetic Regulation of Mammalian Imprinted Genes: From Primary to Functional Imprints. , 2005, 38, 207-236.		6
39	Tracking genomic hydroxymethylation by the base. <i>Nature Methods</i> , 2012, 9, 45-46.	9.0	6
40	DNA methylation: an identity card for brain cells. <i>Genome Biology</i> , 2013, 14, 131.	13.9	6
41	Distinct oncogenes drive different genome and epigenome alterations in human mammary epithelial cells. <i>International Journal of Cancer</i> , 2019, 145, 1299-1311.	2.3	6
42	TET2 regulates immune tolerance in chronically activated mast cells. <i>JCI Insight</i> , 2022, 7, .	2.3	4
43	Epigenetic traits of testicular cancer: from primordial germ cells to germ cell tumors. <i>Epigenomics</i> , 2014, 6, 253-255.	1.0	3
44	Studying DNA Methylation Genome-Wide by Bisulfite Sequencing from Low Amounts of DNA in Mammals. <i>Methods in Molecular Biology</i> , 2021, 2214, 207-220.	0.4	2