Michael Weber

List of Publications by Year in descending order

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44

papers

7,393

citations

236925

25

h-index

233421

45

g-index

49

all docs

49

docs citations

49

times ranked

10230

citing authors

#	Article	IF	Citations
1	Pan-cancer predictions of transcription factors mediating aberrant DNA methylation. Epigenetics and Chromatin, 2022, 15, 10.	3.9	10
2	A comparative methylome analysis reveals conservation and divergence of DNA methylation patterns and functions in vertebrates. BMC Biology, 2022, 20, 70.	3.8	12
3	TET2 regulates immune tolerance in chronically activated mast cells. JCI Insight, 2022, 7, .	5.0	4
4	DNMT3A-dependent DNA methylation is required for spermatogonial stem cells to commit to spermatogenesis. Nature Genetics, 2022, 54, 469-480.	21.4	39
5	E2F6 initiates stable epigenetic silencing of germline genes during embryonic development. Nature Communications, 2021, 12, 3582.	12.8	21
6	Studying DNA Methylation Genome-Wide by Bisulfite Sequencing from Low Amounts of DNA in Mammals. Methods in Molecular Biology, 2021, 2214, 207-220.	0.9	2
7	Genome-wide analysis in the mouse embryo reveals the importance of DNA methylation for transcription integrity. Nature Communications, 2020, 11, 3153.	12.8	91
8	Loss of Apc Rapidly Impairs DNA Methylation Programs and Cell Fate Decisions in Lgr5+ Intestinal Stem Cells. Cancer Research, 2020, 80, 2101-2113.	0.9	13
9	TFmotifView: a webserver for the visualization of transcription factor motifs in genomic regions. Nucleic Acids Research, 2020, 48, W208-W217.	14.5	25
10	Distinct oncogenes drive different genome and epigenome alterations in human mammary epithelial cells. International Journal of Cancer, 2019, 145, 1299-1311.	5.1	6
11	A multi-scale analysis of bull sperm methylome revealed both species peculiarities and conserved tissue-specific features. BMC Genomics, 2018, 19, 404.	2.8	52
12	Single-CpG resolution mapping of 5-hydroxymethylcytosine by chemical labeling and exonuclease digestion identifies evolutionarily unconserved CpGs as TET targets. Genome Biology, 2016, 17, 56.	8.8	14
13	EHMT2 directs DNA methylation for efficient gene silencing in mouse embryos. Genome Research, 2016, 26, 192-202.	5.5	60
14	DNMT3AR882H mutant and Tet2 inactivation cooperate in the deregulation of DNA methylation control to induce lymphoid malignancies in mice. Leukemia, 2016, 30, 1388-1398.	7.2	67
15	Exposure to Endocrine Disruptor Induces Transgenerational Epigenetic Deregulation of MicroRNAs in Primordial Germ Cells. PLoS ONE, 2015, 10, e0124296.	2.5	86
16	Reinforcement of STAT3 activity reprogrammes human embryonic stem cells to naive-like pluripotency. Nature Communications, 2015, 6, 7095.	12.8	137
17	Ontogeny of CpG island methylation and specificity of DNMT3 methyltransferases during embryonic development in the mouse. Genome Biology, 2014, 15, 545.	8.8	143
18	Epigenetic traits of testicular cancer: from primordial germ cells to germ cell tumors. Epigenomics, 2014, 6, 253-255.	2.1	3

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19	DNA methylation: an identity card for brain cells. Genome Biology, 2013, 14, 131.	9.6	6
20	Functions of DNA Methylation and Hydroxymethylation in Mammalian Development. Current Topics in Developmental Biology, 2013, 104, 47-83.	2.2	133
21	Global profiling of DNA methylation erasure in mouse primordial germ cells. Genome Research, 2012, 22, 633-641.	5.5	289
22	H19 Antisense RNA Can Up-Regulate Igf2 Transcription by Activation of a Novel Promoter in Mouse Myoblasts. PLoS ONE, 2012, 7, e37923.	2.5	41
23	Erase for a new start. Nature, 2012, 492, 363-364.	27.8	7
24	Methylated DNA Immunoprecipitation (MeDIP) from Low Amounts of Cells. Methods in Molecular Biology, 2012, 925, 149-158.	0.9	23
25	Mechanisms of DNA methylation and demethylation in mammals. Biochimie, 2012, 94, 2202-2211.	2.6	144
26	Tracking genomic hydroxymethylation by the base. Nature Methods, 2012, 9, 45-46.	19.0	6
27	Modulated contact frequencies at gene-rich loci support a statistical helix model for mammalian chromatin organization. Genome Biology, 2011, 12, R42.	9.6	22
28	Long-range chromatin interactions at the mouse Igf2/H19 locus reveal a novel paternally expressed long non-coding RNA. Nucleic Acids Research, 2011, 39, 5893-5906.	14.5	54
29	Targets and dynamics of promoter DNA methylation during early mouse development. Nature Genetics, 2010, 42, 1093-1100.	21.4	527
30	Dynamic regulation of DNA methylation during mammalian development. Epigenomics, 2009, 1, 81-98.	2.1	40
31	Methylated DNA Immunoprecipitation (MeDIP). Methods in Molecular Biology, 2009, 507, 55-64.	0.9	203
32	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. Blood, 2009, 113, 2488-2497.	1.4	133
33	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. Molecular Cell, 2008, 30, 755-766.	9.7	802
34	Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. Nature Genetics, 2007, 39, 457-466.	21.4	1,922
35	Genomic patterns of DNA methylation: targets and function of an epigenetic mark. Current Opinion in Cell Biology, 2007, 19, 273-280.	5.4	338
36	The 3â€² portion of the mouse <i>H19</i> Imprinting-Control Region is required for proper tissue-specific expression of the <i>Igf2 </i>gene. Cytogenetic and Genome Research, 2006, 113, 230-237.	1.1	7

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37	Epigenomics: Mapping the Methylome. Cell Cycle, 2006, 5, 155-158.	2.6	117
38	Chromosome-wide and promoter-specific analyses identify sites of differential DNA methylation in normal and transformed human cells. Nature Genetics, 2005, 37, 853-862.	21.4	1,591
39	Epigenetic Regulation of Mammalian Imprinted Genes: From Primary to Functional Imprints. , 2005, 38, 207-236.		6
40	A real-time polymerase chain reaction assay for quantification of allele ratios and correction of amplification bias. Analytical Biochemistry, 2003, 320, 252-258.	2.4	18
41	Genomic Imprinting Controls Matrix Attachment Regionsin the <i>Igf2</i>Gene. Molecular and Cellular Biology, 2003, 23, 8953-8959.	2.3	43
42	Turnover of primary transcripts is a major step in the regulation of mouseH19gene expression. EMBO Reports, 2002, 3, 774-779.	4.5	21
43	Extensive tissue-specific variation of allelic methylation in the Igf2 gene during mouse fetal development: relation to expression and imprinting. Mechanisms of Development, 2001, 101, 133-141.	1.7	54
44	H19 gene expression is up-regulated exclusively by stabilization of the RNA during muscle cell differentiation. Oncogene, 2000, 19, 5810-5816.	5.9	45