

Michael Weber

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. <i>Nature Genetics</i> , 2007, 39, 457-466. | 21.4 | 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. | 21.4 | 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. | 9.7 | 802 |
| 4 | Targets and dynamics of promoter DNA methylation during early mouse development. <i>Nature Genetics</i> , 2010, 42, 1093-1100. | 21.4 | 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. | 5.4 | 338 |
| 6 | Global profiling of DNA methylation erasure in mouse primordial germ cells. <i>Genome Research</i> , 2012, 22, 633-641. | 5.5 | 289 |
| 7 | Methylated DNA Immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , 2009, 507, 55-64. | 0.9 | 203 |
| 8 | Mechanisms of DNA methylation and demethylation in mammals. <i>Biochimie</i> , 2012, 94, 2202-2211. | 2.6 | 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. | 8.8 | 143 |
| 10 | Reinforcement of STAT3 activity reprogrammes human embryonic stem cells to naive-like pluripotency. <i>Nature Communications</i> , 2015, 6, 7095. | 12.8 | 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. | 1.4 | 133 |
| 12 | Functions of DNA Methylation and Hydroxymethylation in Mammalian Development. <i>Current Topics in Developmental Biology</i> , 2013, 104, 47-83. | 2.2 | 133 |
| 13 | Epigenomics: Mapping the Methylome. <i>Cell Cycle</i> , 2006, 5, 155-158. | 2.6 | 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. | 12.8 | 91 |
| 15 | Exposure to Endocrine Disruptor Induces Transgenerational Epigenetic Deregulation of MicroRNAs in Primordial Germ Cells. <i>PLoS ONE</i> , 2015, 10, e0124296. | 2.5 | 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. | 7.2 | 67 |
| 17 | EHMT2 directs DNA methylation for efficient gene silencing in mouse embryos. <i>Genome Research</i> , 2016, 26, 192-202. | 5.5 | 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. | 14.5 | 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. | 2.8 | 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. | 5.9 | 45 |
| 22 | Genomic Imprinting Controls Matrix Attachment Regions in the <i>Igf2</i> Gene. <i>Molecular and Cellular Biology</i> , 2003, 23, 8953-8959. | 2.3 | 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. | 2.5 | 41 |
| 24 | Dynamic regulation of DNA methylation during mammalian development. <i>Epigenomics</i> , 2009, 1, 81-98. | 2.1 | 40 |
| 25 | DNMT3A-dependent DNA methylation is required for spermatogonial stem cells to commit to spermatogenesis. <i>Nature Genetics</i> , 2022, 54, 469-480. | 21.4 | 39 |
| 26 | TFmotifView: a webserver for the visualization of transcription factor motifs in genomic regions. <i>Nucleic Acids Research</i> , 2020, 48, W208-W217. | 14.5 | 25 |
| 27 | Methylated DNA Immunoprecipitation (MeDIP) from Low Amounts of Cells. <i>Methods in Molecular Biology</i> , 2012, 925, 149-158. | 0.9 | 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. | 9.6 | 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. | 4.5 | 21 |
| 30 | E2F6 initiates stable epigenetic silencing of germline genes during embryonic development. <i>Nature Communications</i> , 2021, 12, 3582. | 12.8 | 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. | 2.4 | 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. | 8.8 | 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. | 0.9 | 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. | 3.8 | 12 |
| 35 | Pan-cancer predictions of transcription factors mediating aberrant DNA methylation. <i>Epigenetics and Chromatin</i> , 2022, 15, 10. | 3.9 | 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. | 1.1 | 7 |

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|----|---|------|-----------|
| 37 | Erase for a new start. Nature, 2012, 492, 363-364. | 27.8 | 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. Nature Methods, 2012, 9, 45-46. | 19.0 | 6 |
| 40 | DNA methylation: an identity card for brain cells. Genome Biology, 2013, 14, 131. | 9.6 | 6 |
| 41 | Distinct oncogenes drive different genome and epigenome alterations in human mammary epithelial cells. International Journal of Cancer, 2019, 145, 1299-1311. | 5.1 | 6 |
| 42 | TET2 regulates immune tolerance in chronically activated mast cells. JCI Insight, 2022, 7, . | 5.0 | 4 |
| 43 | Epigenetic traits of testicular cancer: from primordial germ cells to germ cell tumors. Epigenomics, 2014, 6, 253-255. | 2.1 | 3 |
| 44 | 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 |