

Petra Hajkova

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

8,940
citations

101384

36
h-index

161609

54
g-index

66
all docs

66
docs citations

66
times ranked

10788
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Specification and epigenomic resetting of the pig germline exhibit conservation with the human lineage. <i>Cell Reports</i> , 2021, 34, 108735. | 2.9 | 43 |
| 2 | Sex-specific chromatin remodelling safeguards transcription in germ cells. <i>Nature</i> , 2021, 600, 737-742. | 13.7 | 24 |
| 3 | TBPL2/TFIIA complex establishes the maternal transcriptome through oocyte-specific promoter usage. <i>Nature Communications</i> , 2020, 11, 6439. | 5.8 | 23 |
| 4 | Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. <i>Cell</i> , 2020, 180, 263-277.e20. | 13.5 | 87 |
| 5 | TET2 Regulates the Neuroinflammatory Response in Microglia. <i>Cell Reports</i> , 2019, 29, 697-713.e8. | 2.9 | 74 |
| 6 | Oral vitamin C supplementation to patients with myeloid cancer on azacitidine treatment: Normalization of plasma vitamin C induces epigenetic changes. <i>Clinical Epigenetics</i> , 2019, 11, 143. | 1.8 | 55 |
| 7 | Mechanistic Insights into Cytosine-N3 Methylation by DNA Methyltransferase DNMT3A. <i>Journal of Molecular Biology</i> , 2019, 431, 3139-3145. | 2.0 | 17 |
| 8 | Eggs sense high-fat diet. <i>Nature Genetics</i> , 2018, 50, 318-319. | 9.4 | 1 |
| 9 | Epigenetic reprogramming enables the transition from primordial germ cell to gonocyte. <i>Nature</i> , 2018, 555, 392-396. | 13.7 | 185 |
| 10 | Evolutionary analysis indicates that DNA alkylation damage is a byproduct of cytosine DNA methyltransferase activity. <i>Nature Genetics</i> , 2018, 50, 452-459. | 9.4 | 71 |
| 11 | SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956. | 2.4 | 33 |
| 12 | Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340. | 6.0 | 469 |
| 13 | Oxidative stress in sperm affects the epigenetic reprogramming in early embryonic development. <i>Epigenetics and Chromatin</i> , 2018, 11, 60. | 1.8 | 70 |
| 14 | Oral Vitamin C Supplementation to Azacitidine in Patients with Myeloid Cancer: Normalization of Plasma Vitamin C Induces Epigenetic Changes. <i>Blood</i> , 2018, 132, 3079-3079. | 0.6 | 0 |
| 15 | Overexpression of TET dioxygenases in seminomas associates with low levels of DNA methylation and hydroxymethylation. <i>Molecular Carcinogenesis</i> , 2017, 56, 1837-1850. | 1.3 | 17 |
| 16 | Methylation of DNA Ligase 1 by G9a/GLP Recruits UHRF1 to Replicating DNA and Regulates DNA Methylation. <i>Molecular Cell</i> , 2017, 67, 550-565.e5. | 4.5 | 151 |
| 17 | Dynamic changes in H1 subtype composition during epigenetic reprogramming. <i>Journal of Cell Biology</i> , 2017, 216, 3017-3028. | 2.3 | 17 |
| 18 | Characterization of the Epigenetic Changes During Human Gonadal Primordial Germ Cells Reprogramming. <i>Stem Cells</i> , 2016, 34, 2418-2428. | 1.4 | 38 |

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|----|--|------|-----------|
| 19 | DNA (De)Methylation: The Passive Route to Naïveté?. Trends in Genetics, 2016, 32, 592-595. | 2.9 | 5 |
| 20 | De novo DNA methylation drives 5hmC accumulation in mouse zygotes. Nature Cell Biology, 2016, 18, 225-233. | 4.6 | 205 |
| 21 | Reprogramming of cell fate: epigenetic memory and the erasure of memories past. EMBO Journal, 2015, 34, 1296-1308. | 3.5 | 139 |
| 22 | Continuous Histone Replacement by Hira Is Essential for Normal Transcriptional Regulation and De Novo DNA Methylation during Mouse Oogenesis. Molecular Cell, 2015, 60, 611-625. | 4.5 | 110 |
| 23 | Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585. | 1.5 | 31 |
| 24 | DNA demethylation, Tet proteins and 5-hydroxymethylcytosine in epigenetic reprogramming: An emerging complex story. Genomics, 2014, 104, 324-333. | 1.3 | 135 |
| 25 | Current technological advances in mapping new DNA modifications. Drug Discovery Today: Disease Models, 2014, 12, 15-26. | 1.2 | 0 |
| 26 | Naive pluripotency is associated with global DNA hypomethylation. Nature Structural and Molecular Biology, 2013, 20, 311-316. | 3.6 | 465 |
| 27 | Different Roles for Tet1 and Tet2 Proteins in Reprogramming-Mediated Erasure of Imprints Induced by EGC Fusion. Molecular Cell, 2013, 49, 1176. | 4.5 | 4 |
| 28 | Different Roles for Tet1 and Tet2 Proteins in Reprogramming-Mediated Erasure of Imprints Induced by EGC Fusion. Molecular Cell, 2013, 49, 1023-1033. | 4.5 | 86 |
| 29 | The impact of culture on epigenetic properties of pluripotent stem cells and pre-implantation embryos. Biochemical Society Transactions, 2013, 41, 711-719. | 1.6 | 25 |
| 30 | Epigenetic reprogramming in the germline: towards the ground state of the epigenome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 2266-2273. | 1.8 | 91 |
| 31 | Epigenetic Reprogramming of Mouse Germ Cells toward Totipotency. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 211-218. | 2.0 | 46 |
| 32 | Epigenetic reprogramming "taking a lesson from the embryo. Current Opinion in Cell Biology, 2010, 22, 342-350. | 2.6 | 48 |
| 33 | Prmt5 is essential for early mouse development and acts in the cytoplasm to maintain ES cell pluripotency. Genes and Development, 2010, 24, 2772-2777. | 2.7 | 287 |
| 34 | Genome-Wide Reprogramming in the Mouse Germ Line Entails the Base Excision Repair Pathway. Science, 2010, 329, 78-82. | 6.0 | 420 |
| 35 | DNA methylation in the IGF2 intragenic DMR is re-established in a sex-specific manner in bovine blastocysts after somatic cloning. Genomics, 2009, 94, 63-69. | 1.3 | 59 |
| 36 | Chromatin dynamics during epigenetic reprogramming in the mouse germ line. Nature, 2008, 452, 877-881. | 13.7 | 611 |

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|----|--|------|-----------|
| 37 | Germ Line, Stem Cells, and Epigenetic Reprogramming. Cold Spring Harbor Symposia on Quantitative Biology, 2008, 73, 9-15. | 2.0 | 53 |
| 38 | MicroRNAs are tightly associated with RNA-induced gene silencing complexes in vivo. Biochemical and Biophysical Research Communications, 2008, 372, 24-29. | 1.0 | 26 |
| 39 | MicroRNA Biogenesis Is Required for Mouse Primordial Germ Cell Development and Spermatogenesis. PLoS ONE, 2008, 3, e1738. | 1.1 | 442 |
| 40 | Maternal microRNAs are essential for mouse zygotic development. Genes and Development, 2007, 21, 644-648. | 2.7 | 496 |
| 41 | Genetic and Epigenetic Regulators of Pluripotency. Cell, 2007, 128, 747-762. | 13.5 | 611 |
| 42 | The bovine IGF2 gene is differentially methylated in oocyte and sperm DNA. Genomics, 2006, 88, 222-229. | 1.3 | 55 |
| 43 | Blimp1 associates with Prmt5 and directs histone arginine methylation in mouse germ cells. Nature Cell Biology, 2006, 8, 623-630. | 4.6 | 425 |
| 44 | 220-plex microRNA expression profile of a single cell. Nature Protocols, 2006, 1, 1154-1159. | 5.5 | 97 |
| 45 | The continuing quest to comprehend genomic imprinting. Cytogenetic and Genome Research, 2006, 113, 6-11. | 0.6 | 29 |
| 46 | Influence of sex chromosome constitution on the genomic imprinting of germ cells. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11184-11188. | 3.3 | 64 |
| 47 | MicroRNA expression profiling of single whole embryonic stem cells. Nucleic Acids Research, 2006, 34, e9-e9. | 6.5 | 306 |
| 48 | Analysis of Esg1 Expression in Pluripotent Cells and the Germline Reveals Similarities with Oct4 and Sox2 and Differences Between Human Pluripotent Cell Lines. Stem Cells, 2005, 23, 1436-1442. | 1.4 | 70 |
| 49 | A Critical Control Element for Interleukin-4 Memory Expression in T Helper Lymphocytes. Journal of Biological Chemistry, 2005, 280, 28177-28185. | 1.6 | 65 |
| 50 | DEVELOPMENT: Enhanced: Programming the X Chromosome. Science, 2004, 303, 633-634. | 6.0 | 18 |
| 51 | Resistance of IAPs to methylation reprogramming may provide a mechanism for epigenetic inheritance in the mouse. Genesis, 2003, 35, 88-93. | 0.8 | 599 |
| 52 | Demethylation of host-cell DNA at the site of avian retrovirus integration. Biochemical and Biophysical Research Communications, 2003, 311, 641-648. | 1.0 | 9 |
| 53 | Epigenetic modifications in an imprinting cluster are controlled by a hierarchy of DMRs suggesting long-range chromatin interactions. Human Molecular Genetics, 2003, 12, 295-305. | 1.4 | 159 |
| 54 | Bisulfite-Based Methylation Analysis of Imprinted Genes. , 2002, 181, 217-228. | | 11 |

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|----|--|-----|-----------|
| 55 | Epigenetic reprogramming in mouse primordial germ cells. <i>Mechanisms of Development</i> , 2002, 117, 15-23. | 1.7 | 1,091 |
| 56 | DNA-Methylation Analysis by the Bisulfite-Assisted Genomic Sequencing Method. , 2002, 200, 143-154. | | 89 |
| 57 | CpG island protects Rous sarcoma virus-derived vectors integrated into nonpermissive cells from DNA methylation and transcriptional suppression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 565-569. | 3.3 | 53 |
| 58 | The LTR, v-src, LTR provirus in H-19 hamster tumor cell line is integrated adjacent to the negative regulatory region. <i>Gene</i> , 1996, 174, 9-17. | 1.0 | 11 |