

Petra Hajkova

List of Publications by Year in descending order

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58
papers

8,940
citations

101496

36
h-index

161767

54
g-index

66
all docs

66
docs citations

66
times ranked

10788
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic reprogramming in mouse primordial germ cells. <i>Mechanisms of Development</i> , 2002, 117, 15-23.	1.7	1,091
2	Genetic and Epigenetic Regulators of Pluripotency. <i>Cell</i> , 2007, 128, 747-762.	13.5	611
3	Chromatin dynamics during epigenetic reprogramming in the mouse germ line. <i>Nature</i> , 2008, 452, 877-881.	13.7	611
4	Resistance of IAPs to methylation reprogramming may provide a mechanism for epigenetic inheritance in the mouse. <i>Genesis</i> , 2003, 35, 88-93.	0.8	599
5	Maternal microRNAs are essential for mouse zygotic development. <i>Genes and Development</i> , 2007, 21, 644-648.	2.7	496
6	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	6.0	469
7	Naive pluripotency is associated with global DNA hypomethylation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 311-316.	3.6	465
8	MicroRNA Biogenesis Is Required for Mouse Primordial Germ Cell Development and Spermatogenesis. <i>PLoS ONE</i> , 2008, 3, e1738.	1.1	442
9	Blimp1 associates with Prmt5 and directs histone arginine methylation in mouse germ cells. <i>Nature Cell Biology</i> , 2006, 8, 623-630.	4.6	425
10	Genome-Wide Reprogramming in the Mouse Germ Line Entails the Base Excision Repair Pathway. <i>Science</i> , 2010, 329, 78-82.	6.0	420
11	MicroRNA expression profiling of single whole embryonic stem cells. <i>Nucleic Acids Research</i> , 2006, 34, e9-e9.	6.5	306
12	Prmt5 is essential for early mouse development and acts in the cytoplasm to maintain ES cell pluripotency. <i>Genes and Development</i> , 2010, 24, 2772-2777.	2.7	287
13	De novo DNA methylation drives 5hmC accumulation in mouse zygotes. <i>Nature Cell Biology</i> , 2016, 18, 225-233.	4.6	205
14	Epigenetic reprogramming enables the transition from primordial germ cell to gonocyte. <i>Nature</i> , 2018, 555, 392-396.	13.7	185
15	Epigenetic modifications in an imprinting cluster are controlled by a hierarchy of DMRs suggesting long-range chromatin interactions. <i>Human Molecular Genetics</i> , 2003, 12, 295-305.	1.4	159
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	Reprogramming of cell fate: epigenetic memory and the erasure of memories past. <i>EMBO Journal</i> , 2015, 34, 1296-1308.	3.5	139
18	DNA demethylation, Tet proteins and 5-hydroxymethylcytosine in epigenetic reprogramming: An emerging complex story. <i>Genomics</i> , 2014, 104, 324-333.	1.3	135

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19	Continuous Histone Replacement by Hira Is Essential for Normal Transcriptional Regulation and De Novo DNA Methylation during Mouse Oogenesis. <i>Molecular Cell</i> , 2015, 60, 611-625.	4.5	110
20	220-plex microRNA expression profile of a single cell. <i>Nature Protocols</i> , 2006, 1, 1154-1159.	5.5	97
21	Epigenetic reprogramming in the germline: towards the ground state of the epigenome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 2266-2273.	1.8	91
22	DNA-Methylation Analysis by the Bisulfite-Assisted Genomic Sequencing Method. , 2002, 200, 143-154.		89
23	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
24	Different Roles for Tet1 and Tet2 Proteins in Reprogramming-Mediated Erasure of Imprints Induced by EGC Fusion. <i>Molecular Cell</i> , 2013, 49, 1023-1033.	4.5	86
25	TET2 Regulates the Neuroinflammatory Response in Microglia. <i>Cell Reports</i> , 2019, 29, 697-713.e8.	2.9	74
26	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
27	Analysis of Esg1 Expression in Pluripotent Cells and the Germline Reveals Similarities with Oct4 and Sox2 and Differences Between Human Pluripotent Cell Lines. <i>Stem Cells</i> , 2005, 23, 1436-1442.	1.4	70
28	Oxidative stress in sperm affects the epigenetic reprogramming in early embryonic development. <i>Epigenetics and Chromatin</i> , 2018, 11, 60.	1.8	70
29	A Critical Control Element for Interleukin-4 Memory Expression in T Helper Lymphocytes. <i>Journal of Biological Chemistry</i> , 2005, 280, 28177-28185.	1.6	65
30	Influence of sex chromosome constitution on the genomic imprinting of germ cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11184-11188.	3.3	64
31	DNA methylation in the IGF2 intragenic DMR is re-established in a sex-specific manner in bovine blastocysts after somatic cloning. <i>Genomics</i> , 2009, 94, 63-69.	1.3	59
32	The bovine IGF2 gene is differentially methylated in oocyte and sperm DNA. <i>Genomics</i> , 2006, 88, 222-229.	1.3	55
33	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
34	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
35	Germ Line, Stem Cells, and Epigenetic Reprogramming. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2008, 73, 9-15.	2.0	53
36	Epigenetic reprogramming "taking a lesson from the embryo. <i>Current Opinion in Cell Biology</i> , 2010, 22, 342-350.	2.6	48

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37	Epigenetic Reprogramming of Mouse Germ Cells toward Totipotency. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 211-218.	2.0	46
38	Specification and epigenomic resetting of the pig germline exhibit conservation with the human lineage. Cell Reports, 2021, 34, 108735.	2.9	43
39	Characterization of the Epigenetic Changes During Human Gonadal Primordial Germ Cells Reprogramming. Stem Cells, 2016, 34, 2418-2428.	1.4	38
40	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. Genome Research, 2018, 28, 1943-1956.	2.4	33
41	Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585.	1.5	31
42	The continuing quest to comprehend genomic imprinting. Cytogenetic and Genome Research, 2006, 113, 6-11.	0.6	29
43	MicroRNAs are tightly associated with RNA-induced gene silencing complexes in vivo. Biochemical and Biophysical Research Communications, 2008, 372, 24-29.	1.0	26
44	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
45	Sex-specific chromatin remodelling safeguards transcription in germ cells. Nature, 2021, 600, 737-742.	13.7	24
46	TBPL2/TFIIA complex establishes the maternal transcriptome through oocyte-specific promoter usage. Nature Communications, 2020, 11, 6439.	5.8	23
47	DEVELOPMENT: Enhanced: Programming the X Chromosome. Science, 2004, 303, 633-634.	6.0	18
48	Overexpression of TET dioxygenases in seminomas associates with low levels of DNA methylation and hydroxymethylation. Molecular Carcinogenesis, 2017, 56, 1837-1850.	1.3	17
49	Dynamic changes in H1 subtype composition during epigenetic reprogramming. Journal of Cell Biology, 2017, 216, 3017-3028.	2.3	17
50	Mechanistic Insights into Cytosine-N3 Methylation by DNA Methyltransferase DNMT3A. Journal of Molecular Biology, 2019, 431, 3139-3145.	2.0	17
51	The LTR, v-src, LTR provirus in H-19 hamster tumor cell line is integrated adjacent to the negative regulatory region. Gene, 1996, 174, 9-17.	1.0	11
52	Bisulfite-Based Methylation Analysis of Imprinted Genes. , 2002, 181, 217-228.		11
53	Demethylation of host-cell DNA at the site of avian retrovirus integration. Biochemical and Biophysical Research Communications, 2003, 311, 641-648.	1.0	9
54	DNA (De)Methylation: The Passive Route to Na ⁺ vety?. Trends in Genetics, 2016, 32, 592-595.	2.9	5

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55	Different Roles for Tet1 and Tet2 Proteins in Reprogramming-Mediated Erasure of Imprints Induced by EGC Fusion. <i>Molecular Cell</i> , 2013, 49, 1176.	4.5	4
56	Eggs sense high-fat diet. <i>Nature Genetics</i> , 2018, 50, 318-319.	9.4	1
57	Current technological advances in mapping new DNA modifications. <i>Drug Discovery Today: Disease Models</i> , 2014, 12, 15-26.	1.2	0
58	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