

Sari Pennings

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

641
citations

840776

11
h-index

1058476

14
g-index

14
all docs

14
docs citations

14
times ranked

1418
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. <i>Genome Biology</i> , 2015, 16, 11. | 8.8 | 137 |
| 2 | Antagonistic remodelling by Swi5-Snf and Tup1-Ssn6 of an extensive chromatin region forms the background for FLO1 gene regulation. <i>EMBO Journal</i> , 2001, 20, 5219-5231. | 7.8 | 90 |
| 3 | Histone H4K20me3 and HP1± are late heterochromatin markers in development, but present in undifferentiated embryonic stem cells. <i>Journal of Cell Science</i> , 2011, 124, 1878-1890. | 2.0 | 79 |
| 4 | DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. <i>Cell Reports</i> , 2019, 29, 1974-1985.e6. | 6.4 | 76 |
| 5 | DNA methylation as a genomic marker of exposure to chemical and environmental agents. <i>Current Opinion in Chemical Biology</i> , 2018, 45, 48-56. | 6.1 | 55 |
| 6 | The Stem Cell Niche: Interactions between Stem Cells and Their Environment. <i>Stem Cells International</i> , 2018, 2018, 1-3. | 2.5 | 46 |
| 7 | The yeast Cyc8-Tup1 complex cooperates with Hda1p and Rpd3p histone deacetylases to robustly repress transcription of the subtelomeric FLO1 gene. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1242-1255. | 1.9 | 39 |
| 8 | Sas3 and Ada2(Gcn5)-dependent histone H3 acetylation is required for transcription elongation at the de-repressed FLO1 gene. <i>Nucleic Acids Research</i> , 2017, 45, gkx028. | 14.5 | 29 |
| 9 | Epigenetic silencing in embryogenesis. <i>Experimental Cell Research</i> , 2005, 309, 241-249. | 2.6 | 24 |
| 10 | Cardiac Stem Cells in the Postnatal Heart: Lessons from Development. <i>Stem Cells International</i> , 2018, 2018, 1-13. | 2.5 | 23 |
| 11 | Tup1-Ssn6 and Swi-Snf remodelling activities influence long-range chromatin organization upstream of the yeast SUC2 gene. <i>Nucleic Acids Research</i> , 2007, 35, 5520-5531. | 14.5 | 22 |
| 12 | Shoring up DNA methylation and H3K27me3 domain demarcation at developmental genes. <i>EMBO Journal</i> , 2017, 36, 3407-3408. | 7.8 | 9 |
| 13 | Antibody-Based Detection of Global Nuclear DNA Methylation in Cells, Tissue Sections, and Mammalian Embryos. <i>Methods in Molecular Biology</i> , 2018, 1708, 59-80. | 0.9 | 7 |
| 14 | Activation of transcription factor circuitry in 2i-induced ground state pluripotency is independent of repressive global epigenetic landscapes. <i>Nucleic Acids Research</i> , 2020, 48, 7748-7766. | 14.5 | 5 |