

Sari Pennings

List of Publications by Year in descending order

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14
papers

641
citations

840776

11
h-index

1058476

14
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14
all docs

14
docs citations

14
times ranked

1418
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. <i>Cell Reports</i> , 2019, 29, 1974-1985.e6.	6.4	76
3	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
4	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
5	The Stem Cell Niche: Interactions between Stem Cells and Their Environment. <i>Stem Cells International</i> , 2018, 2018, 1-3.	2.5	46
6	Cardiac Stem Cells in the Postnatal Heart: Lessons from Development. <i>Stem Cells International</i> , 2018, 2018, 1-13.	2.5	23
7	Shoring up <sc>DNA</sc> methylation and H3K27me3 domain demarcation at developmental genes. <i>EMBO Journal</i> , 2017, 36, 3407-3408.	7.8	9
8	Sas3 and Ada2(Gcn5)-dependent histone H3 acetylation is required for transcription elongation at the de-repressed <i>FLO1</i> gene. <i>Nucleic Acids Research</i> , 2017, 45, gkx028.	14.5	29
9	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. <i>Genome Biology</i> , 2015, 16, 11.	8.8	137
10	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
11	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
12	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
13	Epigenetic silencing in embryogenesis. <i>Experimental Cell Research</i> , 2005, 309, 241-249.	2.6	24
14	Antagonistic remodelling by Swi–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