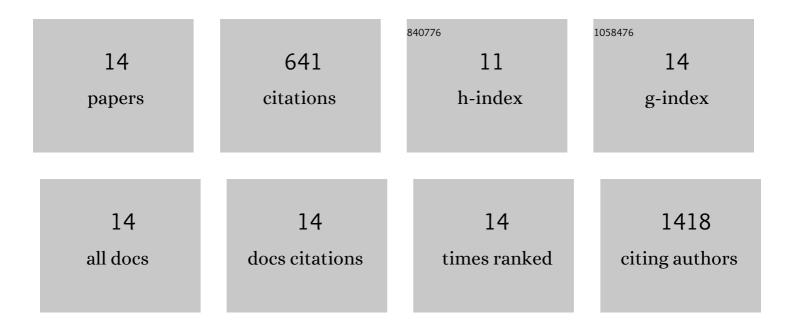
## Sari Pennings

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3709421/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11.	8.8	137
2	Antagonistic remodelling by Swi–Snf and Tup1–Ssn6 of an extensive chromatin region forms the background for FLO1 gene regulation. EMBO Journal, 2001, 20, 5219-5231.	7.8	90
3	Histone H4K20me3 and HP1 $\hat{l}\pm$ are late heterochromatin markers in development, but present in undifferentiated embryonic stem cells. Journal of Cell Science, 2011, 124, 1878-1890.	2.0	79
4	DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. Cell Reports, 2019, 29, 1974-1985.e6.	6.4	76
5	DNA methylation as a genomic marker of exposure to chemical and environmental agents. Current Opinion in Chemical Biology, 2018, 45, 48-56.	6.1	55
6	The Stem Cell Niche: Interactions between Stem Cells and Their Environment. Stem Cells International, 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. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 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 <i>FLO1</i> gene. Nucleic Acids Research, 2017, 45, gkx028.	14.5	29
9	Epigenetic silencing in embryogenesis. Experimental Cell Research, 2005, 309, 241-249.	2.6	24
10	Cardiac Stem Cells in the Postnatal Heart: Lessons from Development. Stem Cells International, 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. Nucleic Acids Research, 2007, 35, 5520-5531.	14.5	22
12	Shoring up <scp>DNA</scp> methylation and H3K27me3 domain demarcation at developmental genes. EMBO Journal, 2017, 36, 3407-3408.	7.8	9
13	Antibody-Based Detection of Clobal Nuclear DNA Methylation in Cells, Tissue Sections, and Mammalian Embryos. Methods in Molecular Biology, 2018, 1708, 59-80.	0.9	7
14	Activation of transcription factor circuity in 2i-induced ground state pluripotency is independent of repressive global epigenetic landscapes. Nucleic Acids Research, 2020, 48, 7748-7766.	14.5	5