Julie Brind'Amour

List of Publications by Year
in descending order

21 papers	1,561 citations	567281 15 h-index	794594 19 g-index
24 all docs	24 docs citations	24 times ranked	2617 citing authors

#	Article	IF	Citations
1	An ultra-low-input native ChIP-seq protocol for genome-wide profiling of rare cell populations. Nature Communications, 2015, 6, 6033.	12.8	322
2	Setdb1 is required for germline development and silencing of H3K9me3-marked endogenous retroviruses in primordial germ cells. Genes and Development, 2014, 28, 2041-2055.	5.9	228
3	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. Nature Genetics, 2019, 51, 844-856.	21.4	207
4	Role of poly(ADP-ribose) polymerase-1 in the removal of UV-induced DNA lesions by nucleotide excision repair. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1658-1663.	7.1	148
5	RTEL1 contributes to DNA replication and repair and telomere maintenance. Molecular Biology of the Cell, 2012, 23, 2782-2792.	2.1	100
6	Transcription shapes genome-wide histone acetylation patterns. Nature Communications, 2021, 12, 210.	12.8	84
7	Vertebrate diapause preserves organisms long term through Polycomb complex members. Science, 2020, 367, 870-874.	12.6	79
8	Activation of Endogenous Retroviruses in Dnmt1 â^'/â^' ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. Cell Stem Cell, 2016, 19, 81-94.	11.1	77
9	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. Nature Communications, 2018, 9, 3331.	12.8	65
10	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. Cell Reports, 2019, 27, 282-293.e4.	6.4	62
11	Histone H3K4 demethylation is negatively regulated by histone H3 acetylation in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18505-18510.	7.1	52
12	Evolution of imprinting via lineage-specific insertion of retroviral promoters. Nature Communications, 2019, 10, 5674.	12.8	39
13	Analysis of repetitive DNA in chromosomes by flow cytometry. Nature Methods, 2011, 8, 484-486.	19.0	23
14	Histone H3K4 and H3K36 Methylation Independently Recruit the NuA3 Histone Acetyltransferase in Saccharomyces cerevisiae. Genetics, 2017, 205, 1113-1123.	2.9	23
15	Epigenetic differences between sister chromatids?. Annals of the New York Academy of Sciences, 2012, 1266, 1-6.	3.8	18
16	Approaches to Detect PARP-1 Activation In Vivo, In Situ, and In Vitro. Methods in Molecular Biology, 2011, 780, 3-34.	0.9	15
17	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. Nature Communications, 2020, 11, 5417.	12.8	12
18	Reality check for transposon enhancers. ELife, 2019, 8, .	6.0	3

#	Article	IF	Citations
19	Setting the chromatin stage in oocytes. Nature Cell Biology, 2020, 22, 355-357.	10.3	1
20	Peptide nucleic acid (PNA) fluorescent in situ hybridization (FISH) on chromosomes in suspension for analysis of repetitive DNA by flow cytometry. Protocol Exchange, 0, , .	0.3	0
21	Ultra-low-input native ChIP-seq for rare cell populations. Protocol Exchange, 0, , .	0.3	0