Petra C Schwalie

List of Publications by Year
in descending order

23 papers	3,733 citations	471509 17 h-index	642732 23 g-index
23 all docs	23 docs citations	23 times ranked	7635 citing authors

#	Article	IF	Citations
1	Five-Vertebrate ChIP-seq Reveals the Evolutionary Dynamics of Transcription Factor Binding. Science, 2010, 328, 1036-1040.	12.6	663
2	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
3	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. Cell, 2012, 148, 335-348.	28.9	528
4	A CTCF-independent role for cohesin in tissue-specific transcription. Genome Research, 2010, 20, 578-588.	5.5	331
5	A stromal cell population that inhibits adipogenesis in mammalian fat depots. Nature, 2018, 559, 103-108.	27.8	327
6	Insights into Negative Regulation by the Glucocorticoid Receptor from Genome-wide Profiling of Inflammatory Cistromes. Molecular Cell, 2013, 49, 158-171.	9.7	233
7	Cohesin regulates tissue-specific expression by stabilizing highly occupied *cis*-regulatory modules. Genome Research, 2012, 22, 2163-2175.	5.5	140
8	Reversible De-differentiation of Mature White Adipocytes into Preadipocyte-like Precursors during Lactation. Cell Metabolism, 2018, 28, 282-288.e3.	16.2	116
9	GLUT3 is induced during epithelial-mesenchymal transition and promotes tumor cell proliferation in non-small cell lung cancer. Cancer & Metabolism, 2014, 2, 11.	5.0	115
10	ASAP: a web-based platform for the analysis and interactive visualization of single-cell RNA-seq data. Bioinformatics, 2017, 33, 3123-3125.	4.1	112
11	Identification of the transcription factor ZEB1 as a central component of the adipogenic gene regulatory network. ELife, 2014, 3, e03346.	6.0	101
12	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	16.8	71
13	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. Genome Biology, 2013, 14, R148.	9.6	68
14	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	9.7	62
15	Mechanism and effects of pulsatile GABA secretion from cytosolic pools in the human beta cell. Nature Metabolism, 2019, 1, 1110-1126.	11.9	59
16	CAST-ChIP Maps Cell-Type-Specific Chromatin States in the Drosophila Central Nervous System. Cell Reports, 2013, 5, 271-282.	6.4	34
17	ZFP30 promotes adipogenesis through the KAP1-mediated activation of a retrotransposon-derived Pparg2 enhancer. Nature Communications, 2019, 10, 1809.	12.8	30
18	Dissecting the brown adipogenic regulatory network using integrative genomics. Scientific Reports, 2017, 7, 42130.	3.3	20

#	Article	IF	Citations
19	LncRNA *Ctcflos* orchestrates transcription and alternative splicing in thermogenic adipogenesis. EMBO Reports, 2021, 22, e51289.	4.5	19
20	Besca, a single-cell transcriptomics analysis toolkit to accelerate translational research. NAR Genomics and Bioinformatics, 2021, 3, lqab102.	3.2	13
21	Positive Selection in Tick Saliva Proteins of the Salp15 Family. Journal of Molecular Evolution, 2009, 68, 186-191.	1.8	12
22	Systems-Genetics-Based Inference of a Core Regulatory Network Underlying White Fat Browning. Cell Reports, 2019, 29, 4099-4113.e5.	6.4	10
23	Cross-Tissue Identification of Somatic Stem and Progenitor Cells Using a Single-Cell RNA-Sequencing Derived Gene Signature. Stem Cells, 2017, 35, 2390-2402.	3.2	6