

Stefan Schoenfelder

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

7,918
citations

218677

26
h-index

395702

33
g-index

43
all docs

43
docs citations

43
times ranked

10123
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. <i>Nature</i> , 2013, 502, 59-64.	27.8	1,347
2	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. <i>Nature Genetics</i> , 2015, 47, 598-606.	21.4	857
3	Long-range enhancer-promoter contacts in gene expression control. <i>Nature Reviews Genetics</i> , 2019, 20, 437-455.	16.3	735
4	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , 2010, 42, 53-61.	21.4	652
5	Topologically associating domains and chromatin loops depend on cohesin and are regulated by CTCF, WAPL, and PDS5 proteins. <i>EMBO Journal</i> , 2017, 36, 3573-3599.	7.8	620
6	HiCUP: pipeline for mapping and processing Hi-C data. <i>F1000Research</i> , 2015, 4, 1310.	1.6	485
7	The pluripotent regulatory circuitry connecting promoters to their long-range interacting elements. <i>Genome Research</i> , 2015, 25, 582-597.	5.5	402
8	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. <i>Genome Biology</i> , 2016, 17, 127.	8.8	344
9	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. <i>Nature Genetics</i> , 2015, 47, 1179-1186.	21.4	330
10	Global Reorganization of the Nuclear Landscape in Senescent Cells. <i>Cell Reports</i> , 2015, 10, 471-483.	6.4	282
11	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. <i>Genome Research</i> , 2014, 24, 1854-1868.	5.5	219
12	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <i>Nature Communications</i> , 2015, 6, 6178.	12.8	186
13	Capture Hi-C reveals novel candidate genes and complex long-range interactions with related autoimmune risk loci. <i>Nature Communications</i> , 2015, 6, 10069.	12.8	161
14	Comparison of Hi-C results using in-solution versus in-nucleus ligation. <i>Genome Biology</i> , 2015, 16, 175.	8.8	157
15	Hi-C as a tool for precise detection and characterisation of chromosomal rearrangements and copy number variation in human tumours. <i>Genome Biology</i> , 2017, 18, 125.	8.8	136
16	Global reorganisation of cis-regulatory units upon lineage commitment of human embryonic stem cells. <i>ELife</i> , 2017, 6, .	6.0	130
17	ESCO1 and CTCF enable formation of long chromatin loops by protecting cohesin-STAG1 from WAPL. <i>ELife</i> , 2020, 9, .	6.0	116
18	Cohesin-Dependent and -Independent Mechanisms Mediate Chromosomal Contacts between Promoters and Enhancers. <i>Cell Reports</i> , 2020, 32, 107929.	6.4	106

#	ARTICLE	IF	CITATIONS
19	Long-Range Enhancer Interactions Are Prevalent in Mouse Embryonic Stem Cells and Are Reorganized upon Pluripotent State Transition. <i>Cell Reports</i> , 2018, 22, 2615-2627.	6.4	99
20	Capture Hi-C identifies a novel causal gene, IL20RA, in the pan-autoimmune genetic susceptibility region 6q23. <i>Genome Biology</i> , 2016, 17, 212.	8.8	85
21	Promoter Capture Hi-C: High-resolution, Genome-wide Profiling of Promoter Interactions. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	66
22	GOTHIC, a probabilistic model to resolve complex biases and to identify real interactions in Hi-C data. <i>PLoS ONE</i> , 2017, 12, e0174744.	2.5	58
23	Divergent wiring of repressive and active chromatin interactions between mouse embryonic and trophoblast lineages. <i>Nature Communications</i> , 2018, 9, 4189.	12.8	51
24	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <i>Blood</i> , 2016, 127, e12-e23.	1.4	49
25	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. <i>Nature Communications</i> , 2020, 11, 6049.	12.8	42
26	Thrombopoietin signaling to chromatin elicits rapid and pervasive epigenome remodeling within poised chromatin architectures. <i>Genome Research</i> , 2018, 28, 295-309.	5.5	39
27	Widespread reorganisation of pluripotent factor binding and gene regulatory interactions between human pluripotent states. <i>Nature Communications</i> , 2021, 12, 2098.	12.8	30
28	Genome organization and chromatin analysis identify transcriptional downregulation of insulin-like growth factor signaling as a hallmark of aging in developing B cells. <i>Genome Biology</i> , 2018, 19, 126.	8.8	29
29	Identifying Causal Genes at the Multiple Sclerosis Associated Region 6q23 Using Capture Hi-C. <i>PLoS ONE</i> , 2016, 11, e0166923.	2.5	28
30	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. <i>PLoS Pathogens</i> , 2021, 17, e1009875.	4.7	18
31	Locus-specific induction of gene expression from heterochromatin loci during cellular senescence. <i>Nature Aging</i> , 2022, 2, 31-45.	11.6	12
32	Cis-Regulatory Control of Mammalian Sex Determination. <i>Sexual Development</i> , 2021, 15, 317-334.	2.0	6
33	High-resolution three-dimensional chromatin profiling of the Chinese hamster ovary cell genome. <i>Biotechnology and Bioengineering</i> , 2021, 118, 784-796.	3.3	5