

# Steven W Wingett

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

7,638  
citations

236612

25  
h-index

377514

34  
g-index

42  
all docs

42  
docs citations

42  
times ranked

12009  
citing authors

#	ARTICLE	IF	CITATIONS
1	FastQ Screen: A tool for multi-genome mapping and quality control. F1000Research, 2018, 7, 1338.	0.8	905
2	FastQ Screen: A tool for multi-genome mapping and quality control. F1000Research, 2018, 7, 1338.	0.8	865
3	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
4	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. Nature Genetics, 2015, 47, 598-606.	9.4	857
5	Cell-cycle dynamics of chromosomal organization at single-cell resolution. Nature, 2017, 547, 61-67.	13.7	636
6	HiCUP: pipeline for mapping and processing Hi-C data. F1000Research, 2015, 4, 1310.	0.8	485
7	The pluripotent regulatory circuitry connecting promoters to their long-range interacting elements. Genome Research, 2015, 25, 582-597.	2.4	402
8	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. Genome Biology, 2016, 17, 127.	3.8	344
9	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. Nature Genetics, 2015, 47, 1179-1186.	9.4	330
10	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	9.4	255
11	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. Genome Research, 2014, 24, 1854-1868.	2.4	219
12	Comparison of Hi-C results using in-solution versus in-nucleus ligation. Genome Biology, 2015, 16, 175.	3.8	157
13	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
14	Hi-C as a tool for precise detection and characterisation of chromosomal rearrangements and copy number variation in human tumours. Genome Biology, 2017, 18, 125.	3.8	136
15	Single-cell Hi-C for genome-wide detection of chromatin interactions that occur simultaneously in a single cell. Nature Protocols, 2015, 10, 1986-2003.	5.5	135
16	Global reorganisation of cis-regulatory units upon lineage commitment of human embryonic stem cells. ELife, 2017, 6, .	2.8	130
17	Long-Range Enhancer Interactions Are Prevalent in Mouse Embryonic Stem Cells and Are Reorganized upon Pluripotent State Transition. Cell Reports, 2018, 22, 2615-2627.	2.9	99
18	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. Nature Communications, 2018, 9, 1028.	5.8	98

#	ARTICLE	IF	CITATIONS
19	The adjuvant GLA-SE promotes human Tfh cell expansion and emergence of public TCR <sup>β</sup> clonotypes. <i>Journal of Experimental Medicine</i> , 2019, 216, 1857-1873.	4.2	87
20	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. <i>Genome Biology</i> , 2017, 18, 165.	3.8	68
21	Promoter Capture Hi-C: High-resolution, Genome-wide Profiling of Promoter Interactions. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	66
22	Active and repressed biosynthetic gene clusters have spatially distinct chromosome states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13800-13809.	3.3	66
23	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
24	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. <i>Nature Communications</i> , 2018, 9, 2526.	5.8	48
25	RNA proximity sequencing reveals the spatial organization of the transcriptome in the nucleus. <i>Nature Biotechnology</i> , 2019, 37, 793-802.	9.4	30
26	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.	3.8	29
27	The global and promoter-centric 3D genome organization temporally resolved during a circadian cycle. <i>Genome Biology</i> , 2021, 22, 162.	3.8	21
28	Detecting chromosomal interactions in Capture Hi-C data with CHiCAGO and companion tools. <i>Nature Protocols</i> , 2021, 16, 4144-4176.	5.5	21
29	Capturing Three-Dimensional Genome Organization in Individual Cells by Single-Cell Hi-C. <i>Methods in Molecular Biology</i> , 2017, 1654, 79-97.	0.4	17
30	Neuronal HSF-1 coordinates the propagation of fat desaturation across tissues to enable adaptation to high temperatures in <i>C. elegans</i> . <i>PLoS Biology</i> , 2021, 19, e3001431.	2.6	15
31	Cellular responses to halofuginone reveal a vulnerability of the GCN2 branch of the integrated stress response. <i>EMBO Journal</i> , 2022, 41, e109985.	3.5	7
32	RNA proximity sequencing data and analysis pipeline from a human neuroblastoma nuclear transcriptome. <i>Scientific Data</i> , 2020, 7, 35.	2.4	2
33	Proximity : A Sequencing Method to Identify Co-localization of. <i>Methods in Molecular Biology</i> , 2020, 2161, 175-194.	0.4	1