Melissa J Fullwood

List of Publications by Year
in descending order

40 papers	25,810 citations	236925 25 h-index	289244 40 g-index
46 all docs	46 docs citations	46 times ranked	43999 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
3	An oestrogen-receptor-α-bound human chromatin interactome. Nature, 2009, 462, 58-64.	27.8	1,537
4	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
5	Roles, Functions, and Mechanisms of Long Non-coding RNAs in Cancer. Genomics, Proteomics and Bioinformatics, 2016, 14, 42-54.	6.9	789
6	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. Genome Research, 2009, 19, 521-532.	5.5	286
7	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	9.6	255
8	ChIP-based methods for the identification of long-range chromatin interactions. Journal of Cellular Biochemistry, 2009, 107, 30-39.	2.6	246
9	Super-Enhancer-Driven Long Non-Coding RNA LINC01503, Regulated by TP63, Is Over-Expressed and Oncogenic in Squamous Cell Carcinoma. Gastroenterology, 2018, 154, 2137-2151.e1.	1.3	165
10	H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. Nature Communications, 2021, 12, 719.	12.8	140
11	Long-Range Chromatin Interactions Drive Mutant *TERT* Promoter Activation. Cancer Discovery, 2016, 6, 1276-1291.	9.4	127
12	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	12.8	123
13	Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. Nucleic Acids Research, 2006, 34, e84-e84.	14.5	111
14	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	6.4	102
15	TP63, SOX2, and KLF5 Establish a Core Regulatory Circuitry That Controls Epigenetic and Transcription Patterns in Esophageal Squamous Cell Carcinoma Cell Lines. Gastroenterology, 2020, 159, 1311-1327.e19.	1.3	92
16	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	3.8	83
17	NanoVar: accurate characterization of patients' genomic structural variants using low-depth nanopore sequencing. Genome Biology, 2020, 21, 56.	8.8	73
18	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. Scientific Reports, 2017, 7, 2186.	3.3	70

#	Article	IF	Citations
19	Aberrant hyperediting of the myeloma transcriptome by ADAR1 confers oncogenicity and is a marker of poor prognosis. Blood, 2018, 132, 1304-1317.	1.4	67
20	Interplay and cooperation between SREBF1 and master transcription factors regulate lipid metabolism and tumor-promoting pathways in squamous cancer. Nature Communications, 2021, 12, 4362.	12.8	50
21	3D genome organization in health and disease: emerging opportunities in cancer translational medicine. Nucleus, 2015, 6, 382-393.	2.2	45
22	Inflated performance measures in enhancer–promoter interaction-prediction methods. Nature Genetics, 2019, 51, 1196-1198.	21.4	44
23	Chromatin Interaction Analysis Using Paired-End Tag Sequencing. Current Protocols in Molecular Biology, 2010, 89, Unit 21.15.1-25.	2.9	40
24	Targeting Phosphorylation of Eukaryotic Initiation Factor-2α to Treat Human Disease. Progress in Molecular Biology and Translational Science, 2012, 106, 75-106.	1.7	36
25	DeepCPP: a deep neural network based on nucleotide bias information and minimum distribution similarity feature selection for RNA coding potential prediction. Briefings in Bioinformatics, 2021, 22, 2073-2084.	6.5	36
26	Chromatin interaction neural network (ChINN): a machine learning-based method for predicting chromatin interactions from DNA sequences. Genome Biology, 2021, 22, 226.	8.8	26
27	A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues. Scientific Data, 2015, 2, 150063.	5.3	24
28	*MYC* overexpression leads to increased chromatin interactions at super-enhancers and MYC binding sites. Genome Research, 2022, 32, 629-642.	5.5	24
29	Chromatin Interactions and Regulatory Elements in Cancer: From Bench to Bedside. Trends in Genetics, 2019, 35, 145-158.	6.7	22
30	Super Enhancer-Mediated Upregulation of *HJURP* Promotes Growth and Survival of t(4;14)-Positive Multiple Myeloma. Cancer Research, 2022, 82, 406-418.	0.9	18
31	Super-Enhancers, Phase-Separated Condensates, and 3D Genome Organization in Cancer. Cancers, 2022, 14, 2866.	3.7	16
32	Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET) for Mapping Chromatin Interactions and Understanding Transcription Regulation. Journal of Visualized Experiments, 2012, , .	0.3	15
33	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. PLoS ONE, 2011, 6, e26054.	2.5	11
34	Long-Distance Repression by Human Silencers: Chromatin Interactions and Phase Separation in Silencers. Cells, 2022, 11, 1560.	4.1	8
35	Expanding the effects of ERG on chromatin landscapes and dysregulated transcription in prostate cancer. Nature Genetics, 2017, 49, 1294-1295.	21.4	7
36	Chromatin loop anchors predict transcript and exon usage. Briefings in Bioinformatics, 2021, 22, .	6.5	5

#	Article	IF	Citations
37	Deciphering Noncoding RNA and Chromatin Interactions: Multiplex Chromatin Interaction Analysis by Paired-End Tag Sequencing (mChIA-PET). Methods in Molecular Biology, 2017, 1468, 63-89.	0.9	4
38	Profiling of 3D Genome Organization in Nasopharyngeal Cancer Needle Biopsy Patient Samples by a Modified Hi-C Approach. Frontiers in Genetics, 2021, 12, 673530.	2.3	4
39	p53-NEIL1 co-abnormalities induce genomic instability and promote synthetic lethality with Chk1 inhibition in multiple myeloma having concomitant 17p13(del) and 1q21(gain). Oncogene, 2022, 41, 2106-2121.	5.9	3
40	The use of multiple displacement amplification to amplify complex DNA libraries. Nucleic Acids Research, 2008, 36, e32.	14.5	2