

Melissa J Fullwood

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38

papers

19,183

citations

23

h-index

46

g-index

46

ext. papers

23,414

ext. citations

14.9

avg, IF

8.11

L-index

#	Paper	IF	Citations
38	overexpression leads to increased chromatin interactions at superenhancers and MYC binding sites.. <i>Genome Research</i> , 2022 ,	9.7	5
37	Chromatin loop anchors predict transcript and exon usage. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
36	DeepCPP: a deep neural network based on nucleotide bias information and minimum distribution similarity feature selection for RNA coding potential prediction. <i>Briefings in Bioinformatics</i> , 2021 , 22, 2073-2084	13.4	11
35	H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. <i>Nature Communications</i> , 2021 , 12, 719	17.4	24
34	Interplay and cooperation between SREBF1 and master transcription factors regulate lipid metabolism and tumor-promoting pathways in squamous cancer. <i>Nature Communications</i> , 2021 , 12, 4362	17.4	8
33	Chromatin interaction neural network (ChINN): a machine learning-based method for predicting chromatin interactions from DNA sequences. <i>Genome Biology</i> , 2021 , 22, 226	18.3	1
32	Profiling of 3D Genome Organization in Nasopharyngeal Cancer Needle Biopsy Patient Samples by a Modified Hi-C Approach. <i>Frontiers in Genetics</i> , 2021 , 12, 673530	4.5	1
31	Super enhancer-mediated upregulation of HJURP promotes growth and survival of t(4;14)-positive multiple myeloma. <i>Cancer Research</i> , 2021 ,	10.1	1
30	NanoVar: accurate characterization of patients' genomic structural variants using low-depth nanopore sequencing. <i>Genome Biology</i> , 2020 , 21, 56	18.3	27
29	TP63, SOX2, and KLF5 Establish a Core Regulatory Circuitry That Controls Epigenetic and Transcription Patterns in Esophageal Squamous Cell Carcinoma Cell Lines. <i>Gastroenterology</i> , 2020 , 159, 1311-1327.e19	13.3	29
28	Inflated performance measures in enhancer-promoter interaction-prediction methods. <i>Nature Genetics</i> , 2019 , 51, 1196-1198	36.3	24
27	Chromatin Interactions and Regulatory Elements in Cancer: From Bench to Bedside. <i>Trends in Genetics</i> , 2019 , 35, 145-158	8.5	11
26	Super-Enhancer-Driven Long Non-Coding RNA LINC01503, Regulated by TP63, Is Over-Expressed and Oncogenic in Squamous Cell Carcinoma. <i>Gastroenterology</i> , 2018 , 154, 2137-2151.e1	13.3	108
25	Aberrant hyperediting of the myeloma transcriptome by ADAR1 confers oncogenicity and is a marker of poor prognosis. <i>Blood</i> , 2018 , 132, 1304-1317	2.2	36
24	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. <i>Scientific Reports</i> , 2017 , 7, 2186	4.9	40
23	Deciphering Noncoding RNA and Chromatin Interactions: Multiplex Chromatin Interaction Analysis by Paired-End Tag Sequencing (mChIA-PET). <i>Methods in Molecular Biology</i> , 2017 , 1468, 63-89	1.4	2
22	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. <i>Nature Communications</i> , 2016 , 7, 12983	17.4	78

21	Roles, Functions, and Mechanisms of Long Non-coding RNAs in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2016 , 14, 42-54	6.5	526
20	Long-Range Chromatin Interactions Drive Mutant TERT Promoter Activation. <i>Cancer Discovery</i> , 2016 , 6, 1276-1291	24.4	96
19	A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues. <i>Scientific Data</i> , 2015 , 2, 150063	8.2	17
18	3D genome organization in health and disease: emerging opportunities in cancer translational medicine. <i>Nucleus</i> , 2015 , 6, 382-93	3.9	29
17	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012 , 58, 289-99	4.6	69
16	Large-scale functional organization of long-range chromatin interaction networks. <i>Cell Reports</i> , 2012 , 2, 1207-19	10.6	84
15	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
14	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
13	Targeting phosphorylation of eukaryotic initiation factor-2 to treat human disease. <i>Progress in Molecular Biology and Translational Science</i> , 2012 , 106, 75-106	4	34
12	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
11	Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET) for mapping chromatin interactions and understanding transcription regulation. <i>Journal of Visualized Experiments</i> , 2012 ,	1.6	14
10	Next-generation sequencing of apoptotic DNA breakpoints reveals association with actively transcribed genes and gene translocations. <i>PLoS ONE</i> , 2011 , 6, e26054	3.7	9
9	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010 , 11, R22	18.3	199
8	Chromatin interaction analysis using paired-end tag sequencing. <i>Current Protocols in Molecular Biology</i> , 2010 , Chapter 21, Unit 21.15.1-25	2.9	34
7	ChIP-based methods for the identification of long-range chromatin interactions. <i>Journal of Cellular Biochemistry</i> , 2009 , 107, 30-9	4.7	186
6	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , 2009 , 462, 58-64	50.4	1243
5	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , 2009 , 19, 521-32	9.7	252
4	The use of multiple displacement amplification to amplify complex DNA libraries. <i>Nucleic Acids Research</i> , 2008 , 36, e32	20.1	1

- 3 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 20.1 96
- 2 Three-dimensional Genome Organization Maps in Normal Haematopoietic Stem Cells and Acute Myeloid Leukemia 1
- 1 MYC overexpression leads to increased chromatin interactions at superenhancers and c-Myc binding sites 1