

Melissa J Fullwood

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

25,810
citations

236612

25
h-index

288905

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. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
3	An oestrogen-receptor-bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	13.7	1,537
4	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
5	Roles, Functions, and Mechanisms of Long Non-coding RNAs in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 42-54.	3.0	789
6	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , 2009, 19, 521-532.	2.4	286
7	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010, 11, R22.	13.9	255
8	ChIP-based methods for the identification of long-range chromatin interactions. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 30-39.	1.2	246
9	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.	0.6	165
10	H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. <i>Nature Communications</i> , 2021, 12, 719.	5.8	140
11	Long-Range Chromatin Interactions Drive Mutant <i>TERT</i> Promoter Activation. <i>Cancer Discovery</i> , 2016, 6, 1276-1291.	7.7	127
12	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. <i>Nature Communications</i> , 2016, 7, 12983.	5.8	123
13	Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. <i>Nucleic Acids Research</i> , 2006, 34, e84-e84.	6.5	111
14	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	2.9	102
15	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.	0.6	92
16	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012, 58, 289-299.	1.9	83
17	NanoVar: accurate characterization of patients' genomic structural variants using low-depth nanopore sequencing. <i>Genome Biology</i> , 2020, 21, 56.	3.8	73
18	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. <i>Scientific Reports</i> , 2017, 7, 2186.	1.6	70

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19	Aberrant hyperediting of the myeloma transcriptome by ADAR1 confers oncogenicity and is a marker of poor prognosis. <i>Blood</i> , 2018, 132, 1304-1317.	0.6	67
20	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.	5.8	50
21	3D genome organization in health and disease: emerging opportunities in cancer translational medicine. <i>Nucleus</i> , 2015, 6, 382-393.	0.6	45
22	Inflated performance measures in enhancer-promoter interaction-prediction methods. <i>Nature Genetics</i> , 2019, 51, 1196-1198.	9.4	44
23	Chromatin Interaction Analysis Using Paired-End Tag Sequencing. <i>Current Protocols in Molecular Biology</i> , 2010, 89, Unit 21.15.1-25.	2.9	40
24	Targeting Phosphorylation of Eukaryotic Initiation Factor-2 to Treat Human Disease. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 106, 75-106.	0.9	36
25	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.	3.2	36
26	Chromatin interaction neural network (ChINN): a machine learning-based method for predicting chromatin interactions from DNA sequences. <i>Genome Biology</i> , 2021, 22, 226.	3.8	26
27	A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues. <i>Scientific Data</i> , 2015, 2, 150063.	2.4	24
28	<i>MYC</i> overexpression leads to increased chromatin interactions at super-enhancers and <i>MYC</i> binding sites. <i>Genome Research</i> , 2022, 32, 629-642.	2.4	24
29	Chromatin Interactions and Regulatory Elements in Cancer: From Bench to Bedside. <i>Trends in Genetics</i> , 2019, 35, 145-158.	2.9	22
30	Super Enhancer-Mediated Upregulation of <i>HJURP</i> Promotes Growth and Survival of t(4;14)-Positive Multiple Myeloma. <i>Cancer Research</i> , 2022, 82, 406-418.	0.4	18
31	Super-Enhancers, Phase-Separated Condensates, and 3D Genome Organization in Cancer. <i>Cancers</i> , 2022, 14, 2866.	1.7	16
32	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, .	0.2	15
33	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. <i>PLoS ONE</i> , 2011, 6, e26054.	1.1	11
34	Long-Distance Repression by Human Silencers: Chromatin Interactions and Phase Separation in Silencers. <i>Cells</i> , 2022, 11, 1560.	1.8	8
35	Expanding the effects of ERG on chromatin landscapes and dysregulated transcription in prostate cancer. <i>Nature Genetics</i> , 2017, 49, 1294-1295.	9.4	7
36	Chromatin loop anchors predict transcript and exon usage. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5

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37	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.	0.4	4
38	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.	1.1	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). <i>Oncogene</i> , 2022, 41, 2106-2121.	2.6	3
40	The use of multiple displacement amplification to amplify complex DNA libraries. <i>Nucleic Acids Research</i> , 2008, 36, e32.	6.5	2