

Jennifer E Phillips-Cremins

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

5,280
citations

257450

24
h-index

315739

38
g-index

55
all docs

55
docs citations

55
times ranked

7470
citing authors

#	ARTICLE	IF	CITATIONS
1	CTCF: Master Weaver of the Genome. <i>Cell</i> , 2009, 137, 1194-1211.	28.9	1,371
2	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. <i>Cell</i> , 2013, 153, 1281-1295.	28.9	1,050
3	YY1 and CTCF orchestrate a 3D chromatin looping switch during early neural lineage commitment. <i>Genome Research</i> , 2017, 27, 1139-1152.	5.5	249
4	On the existence and functionality of topologically associating domains. <i>Nature Genetics</i> , 2020, 52, 8-16.	21.4	242
5	Engineering graded tissue interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12170-12175.	7.1	201
6	Chromatin Insulators: Linking Genome Organization to Cellular Function. <i>Molecular Cell</i> , 2013, 50, 461-474.	9.7	201
7	Human mesenchymal stem cell differentiation on self-assembled monolayers presenting different surface chemistries. <i>Acta Biomaterialia</i> , 2010, 6, 12-20.	8.3	171
8	Disease-Associated Short Tandem Repeats Co-localize with Chromatin Domain Boundaries. <i>Cell</i> , 2018, 175, 224-238.e15.	28.9	169
9	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	27.8	167
10	The importance of the whole: Topological data analysis for the network neuroscientist. <i>Network Neuroscience</i> , 2019, 3, 656-673.	2.6	122
11	Glucocorticoid-induced osteogenesis is negatively regulated by Runx2/Cbfa1 serine phosphorylation. <i>Journal of Cell Science</i> , 2006, 119, 581-591.	2.0	115
12	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. <i>Molecular Cell</i> , 2017, 66, 102-116.e7.	9.7	114
13	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016, 18, 611-624.	11.1	112
14	LADL: light-activated dynamic looping for endogenous gene expression control. <i>Nature Methods</i> , 2019, 16, 633-639.	19.0	108
15	Virus-based gene therapy strategies for bone regeneration. <i>Biomaterials</i> , 2007, 28, 211-229.	11.4	106
16	Detecting hierarchical genome folding with network modularity. <i>Nature Methods</i> , 2018, 15, 119-122.	19.0	106
17	Three-dimensional genome restructuring across timescales of activity-induced neuronal gene expression. <i>Nature Neuroscience</i> , 2020, 23, 707-717.	14.8	99
18	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. <i>Genome Biology</i> , 2015, 16, 237.	8.8	72

#	ARTICLE	IF	CITATIONS
19	Cohesin-mediated loop anchors confine the locations of human replication origins. <i>Nature</i> , 2022, 606, 812-819.	27.8	47
20	Crossed wires: 3D genome misfolding in human disease. <i>Journal of Cell Biology</i> , 2017, 216, 3441-3452.	5.2	45
21	Mineralization capacity of Runx2/Cbfa1-genetically engineered fibroblasts is scaffold dependent. <i>Biomaterials</i> , 2006, 27, 5535-5545.	11.4	43
22	Cohesin-dependence of neuronal gene expression relates to chromatin loop length. <i>ELife</i> , 2022, 11, .	6.0	40
23	Genetic Engineering for Skeletal Regenerative Medicine. <i>Annual Review of Biomedical Engineering</i> , 2007, 9, 87-119.	12.3	35
24	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	21.4	35
25	Dermal Fibroblasts Genetically Modified to Express Runx2/Cbfa1 as a Mineralizing Cell Source for Bone Tissue Engineering. <i>Tissue Engineering</i> , 2007, 13, 2029-2040.	4.6	29
26	Unraveling architecture of the pluripotent genome. <i>Current Opinion in Cell Biology</i> , 2014, 28, 96-104.	5.4	29
27	An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. <i>IScience</i> , 2021, 24, 103221.	4.1	27
28	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. <i>Nature Neuroscience</i> , 2022, 25, 474-483.	14.8	25
29	Characterization of a small animal growth plate injury model using microcomputed tomography. <i>Bone</i> , 2010, 46, 1555-1563.	2.9	21
30	5C-ID: Increased resolution Chromosome-Conformation-Capture-Carbon-Copy with in situ 3C and double alternating primer design. <i>Methods</i> , 2018, 142, 39-46.	3.8	17
31	Systematic Evaluation of Statistical Methods for Identifying Looping Interactions in 5C Data. <i>Cell Systems</i> , 2019, 8, 197-211.e13.	6.2	15
32	3DeFDR: statistical methods for identifying cell type-specific looping interactions in 5C and Hi-C data. <i>Genome Biology</i> , 2020, 21, 219.	8.8	15
33	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice. <i>Nature Communications</i> , 2022, 13, 55.	12.8	14
34	A subset of topologically associating domains fold into mesoscale core-periphery networks. <i>Scientific Reports</i> , 2019, 9, 9526.	3.3	9
35	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020, 11, 2061.	12.8	8
36	<scp>CRISPR</scp>/Cas9 genome editing throws descriptive 3D genome folding studies for a loop. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, 286-299.	6.6	3

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37	Dynamic Looping Interactions: Setting the 3D Stage for the Macrophage. <i>Molecular Cell</i> , 2017, 67, 901-903.	9.7	2
38	The Path to My Lab's First Paper: Rong Lu, Alvaro Rada-Iglesias, and Jennifer Phillips-Cremins. <i>Cell Stem Cell</i> , 2016, 19, 683-685.	11.1	0
39	See(quence) and ye shall find: higher-order genome folding in intact single cells. <i>Molecular Cell</i> , 2021, 81, 1130-1132.	9.7	0
40	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. <i>Blood</i> , 2016, 128, 1034-1034.	1.4	0