Jennifer E Phillips-Cremins

List of Publications by Year
in descending order

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	Neuronal Yin Yang1 in the prefrontal cortex regulates transcriptional and behavioral responses to chronic stress in mice. Nature Communications, 2022, 13, 55.	12.8	14
2	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	14.8	25
3	Cohesin-dependence of neuronal gene expression relates to chromatin loop length. ELife, 2022, 11, .	6.0	40
4	Cohesin-mediated loop anchors confine the locations of human replication origins. Nature, 2022, 606, 812-819.	27.8	47
5	See(quence) and ye shall find: higher-order genome folding in intact single cells. Molecular Cell, 2021, 81, 1130-1132.	9.7	0
6	An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. IScience, 2021, 24, 103221.	4.1	27
7	On the existence and functionality of topologically associating domains. Nature Genetics, 2020, 52, 8-16.	21.4	242
8	3DeFDR: statistical methods for identifying cell type-specific looping interactions in 5C and Hi-C data. Genome Biology, 2020, 21, 219.	8.8	15
9	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	21.4	35
10	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
11	Three-dimensional genome restructuring across timescales of activity-induced neuronal gene expression. Nature Neuroscience, 2020, 23, 707-717.	14.8	99
12	A subset of topologically associating domains fold into mesoscale core-periphery networks. Scientific Reports, 2019, 9, 9526.	3.3	9
13	LADL: light-activated dynamic looping for endogenous gene expression control. Nature Methods, 2019, 16, 633-639.	19.0	108
14	Systematic Evaluation of Statistical Methods for Identifying Looping Interactions in 5C Data. Cell Systems, 2019, 8, 197-211.e13.	6.2	15
15	The importance of the whole: Topological data analysis for the network neuroscientist. Network Neuroscience, 2019, 3, 656-673.	2.6	122
16	Chromatin structure dynamics during the mitosis-to-G1 phase transition. Nature, 2019, 576, 158-162.	27.8	167
17	Detecting hierarchical genome folding with network modularity. Nature Methods, 2018, 15, 119-122.	19.0	106
18	Disease-Associated Short Tandem Repeats Co-localize with Chromatin Domain Boundaries. Cell, 2018, 175, 224-238.e15.	28.9	169

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19	5C-ID: Increased resolution Chromosome-Conformation-Capture-Carbon-Copy with in situ 3C and double alternating primer design. Methods, 2018, 142, 39-46.	3.8	17
20	YY1 and CTCF orchestrate a 3D chromatin looping switch during early neural lineage commitment. Genome Research, 2017, 27, 1139-1152.	5.5	249
21	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. Molecular Cell, 2017, 66, 102-116.*e7*.	9.7	114
22	Crossed wires: 3D genome misfolding in human disease. Journal of Cell Biology, 2017, 216, 3441-3452.	5.2	45
23	Dynamic Looping Interactions: Setting the 3D Stage for the Macrophage. Molecular Cell, 2017, 67, 901-903.	9.7	2
24	<scp>CRISPR</scp>/Cas9 genome editing throws descriptive 3â€D genome folding studies for a loop. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2016, 8, 286-299.	6.6	3
25	The Path to My Labâ€™s First Paper: Rong Lu, Alvaro Rada-Iglesias, and Jennifer Phillips-Cremins. Cell Stem Cell, 2016, 19, 683-685.	11.1	0
26	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. Cell Stem Cell, 2016, 18, 611-624.	11.1	112
27	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. Blood, 2016, 128, 1034-1034.	1.4	0
28	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. Genome Biology, 2015, 16, 237.	8.8	72
29	Unraveling architecture of the pluripotent genome. Current Opinion in Cell Biology, 2014, 28, 96-104.	5.4	29
30	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. Cell, 2013, 153, 1281-1295.	28.9	1,050
31	Chromatin Insulators: Linking Genome Organization to Cellular Function. Molecular Cell, 2013, 50, 461-474.	9.7	201
32	Human mesenchymal stem cell differentiation on self-assembled monolayers presenting different surface chemistries. Acta Biomaterialia, 2010, 6, 12-20.	8.3	171
33	Characterization of a small animal growth plate injury model using microcomputed tomography. Bone, 2010, 46, 1555-1563.	2.9	21
34	CTCF: Master Weaver of the Genome. Cell, 2009, 137, 1194-1211.	28.9	1,371
35	Engineering graded tissue interfaces. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12170-12175.	7.1	201
36	Genetic Engineering for Skeletal Regenerative Medicine. Annual Review of Biomedical Engineering, 2007, 9, 87-119.	12.3	35

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37	Dermal Fibroblasts Genetically Modified to Express Runx2/Cbfa1 as a Mineralizing Cell Source for Bone Tissue Engineering. Tissue Engineering, 2007, 13, 2029-2040.	4.6	29
38	Virus-based gene therapy strategies for bone regeneration. Biomaterials, 2007, 28, 211-229.	11.4	106
39	Glucocorticoid-induced osteogenesis is negatively regulated by Runx2/Cbfa1 serine phosphorylation. Journal of Cell Science, 2006, 119, 581-591.	2.0	115
40	Mineralization capacity of Runx2/Cbfa1-genetically engineered fibroblasts is scaffold dependent. Biomaterials, 2006, 27, 5535-5545.	11.4	43