Mitchell Guttman

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Essential Roles for RNA in Shaping Nuclear Organization. Cold Spring Harbor Perspectives in Biology, 2022, 14, a039719.	5.5	19
2	Single-cell measurement of higher-order 3D genome organization with scSPRITE. Nature Biotechnology, 2022, 40, 64-73.	17.5	63
3	SPRITE: a genome-wide method for mapping higher-order 3D interactions in the nucleus using combinatorial split-and-pool barcoding. Nature Protocols, 2022, 17, 36-75.	12.0	24
4	Xist spatially amplifies SHARP/SPEN recruitment to balance chromosome-wide silencing and specificity to the X chromosome. Nature Structural and Molecular Biology, 2022, 29, 239-249.	8.2	46
5	Integrative genome modeling platform reveals essentiality of rare contact events in 3D genome organizations. Nature Methods, 2022, 19, 938-949.	19.0	20
6	Integrated spatial genomics reveals global architecture of single nuclei. Nature, 2021, 590, 344-350.	27.8	228
7	Nuclear compartmentalization as a mechanism of quantitative control of gene expression. Nature Reviews Molecular Cell Biology, 2021, 22, 653-670.	37.0	131
8	RNA promotes the formation of spatial compartments in the nucleus. Cell, 2021, 184, 5775-5790.e30.	28.9	192
9	Xist nucleates local protein gradients to propagate silencing across the X chromosome. Cell, 2021, 184, 6174-6192.e32.	28.9	62
10	High-Resolution Mapping of Multiway Enhancer-Promoter Interactions Regulating Pathogen Detection. Molecular Cell, 2020, 80, 359-373.e8.	9.7	21
11	SARS-CoV-2 Disrupts Splicing, Translation, and Protein Trafficking to Suppress Host Defenses. Cell, 2020, 183, 1325-1339.e21.	28.9	442
12	A protein assembly mediates Xist localization and gene silencing. Nature, 2020, 587, 145-151.	27.8	123
13	Xist drives spatial compartmentalization of DNA and protein to orchestrate initiation and maintenance of X inactivation. Current Opinion in Cell Biology, 2020, 64, 139-147.	5.4	38
14	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. Nature Genetics, 2019, 51, 1024-1034.	21.4	60
15	Phase separation drives X-chromosome inactivation: a hypothesis. Nature Structural and Molecular Biology, 2019, 26, 331-334.	8.2	98
16	Approaches for Understanding the Mechanisms of Long Noncoding RNA Regulation of Gene Expression. Cold Spring Harbor Perspectives in Biology, 2019, 11, a032151.	5.5	58
17	RAP-MS: A Method to Identify Proteins that Interact Directly with a Specific RNA Molecule in Cells. Methods in Molecular Biology, 2018, 1649, 473-488.	0.9	68
18	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. Nature, 2018, 561, 132-136.	27.8	303

MITCHELL GUTTMAN

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19	Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. Cell, 2018, 174, 744-757.e24.	28.9	649
20	Linking Protein and RNA Function within the Same Gene. Cell, 2017, 168, 753-755.	28.9	2
21	Response to Comment on "Xist recruits the X chromosome to the nuclear lamina to enable chromosome-wide silencing― Science, 2017, 356, .	12.6	5
22	Reâ€evaluating the foundations of lnc RNA –Polycomb function. EMBO Journal, 2017, 36, 964-966.	7.8	11
23	Quantitative predictions of protein interactions with long noncoding RNAs. Nature Methods, 2017, 14, 5-6.	19.0	113
24	The 4D nucleome project. Nature, 2017, 549, 219-226.	27.8	579
25	A Guide to Packing Your DNA. Cell, 2016, 165, 259-261.	28.9	2
26	m6A RNA methylation promotes XIST-mediated transcriptional repression. Nature, 2016, 537, 369-373.	27.8	1,250
27	Xist recruits the X chromosome to the nuclear lamina to enable chromosome-wide silencing. Science, 2016, 354, 468-472.	12.6	257
28	Long non-coding RNAs: spatial amplifiers that control nuclear structure and gene expression. Nature Reviews Molecular Cell Biology, 2016, 17, 756-770.	37.0	510
29	Local regulation of gene expression by IncRNA promoters, transcription and splicing. Nature, 2016, 539, 452-455.	27.8	1,056
30	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. Genome Biology, 2016, 17, 19.	8.8	141
31	Robust transcriptome-wide discovery of RNA-binding protein binding sites with enhanced CLIP (eCLIP). Nature Methods, 2016, 13, 508-514.	19.0	1,092
32	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	4.4	30
33	The Xist IncRNA interacts directly with SHARP to silence transcription through HDAC3. Nature, 2015, 521, 232-236.	27.8	946
34	Simultaneous generation of many RNA-seq libraries in a single reaction. Nature Methods, 2015, 12, 323-325.	19.0	256
35	Long noncoding RNAs: an emerging link between gene regulation and nuclear organization. Trends in Cell Biology, 2014, 24, 651-663.	7.9	286
36	Methods for comprehensive experimental identification of RNA-protein interactions. Genome Biology, 2014, 15, 203.	9.6	140

MITCHELL GUTTMAN

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37	RNA and dynamic nuclear organization. Science, 2014, 345, 1240-1241.	12.6	119
38	RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites. Cell, 2014, 159, 188-199.	28.9	425
39	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. Cell, 2014, 159, 148-162.	28.9	770
40	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. Nature Genetics, 2013, 45, 299-303.	21.4	237
41	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. Cell, 2013, 154, 240-251.	28.9	678
42	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. Cell, 2013, 153, 1149-1163.	28.9	419
43	The Xist IncRNA Exploits Three-Dimensional Genome Architecture to Spread Across the X Chromosome. Science, 2013, 341, 1237973.	12.6	846
44	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. Molecular Cell, 2012, 47, 810-822.	9.7	375
45	Modular regulatory principles of large non-coding RNAs. Nature, 2012, 482, 339-346.	27.8	2,036
46	lincRNAs act in the circuitry controlling pluripotency and differentiation. Nature, 2011, 477, 295-300.	27.8	1,749
47	Computational methods for transcriptome annotation and quantification using RNA-seq. Nature Methods, 2011, 8, 469-477.	19.0	919
48	Integrative genomics viewer. Nature Biotechnology, 2011, 29, 24-26.	17.5	11,708
49	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
50	Ab initio reconstruction of cell type–specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology, 2010, 28, 503-510.	17.5	1,251
51	Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. Nature Genetics, 2010, 42, 1113-1117.	21.4	902
52	Digital transcriptome profiling from attomole-level RNA samples. Genome Research, 2010, 20, 519-525.	5.5	56
53	A Large Intergenic Noncoding RNA Induced by p53 Mediates Global Gene Repression in the p53 Response. Cell, 2010, 142, 409-419.	28.9	1,919
54	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. Science, 2009, 326, 257-263.	12.6	473

MITCHELL GUTTMAN

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55	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	27.8	3,801
56	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11667-11672.	7.1	2,709
57	Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. PLoS Genetics, 2007, 3, e143.	3.5	41
58	N-cadherin Expression in Breast Cancer: Correlation with an Aggressive Histologic Variant – Invasive Micropapillary Carcinoma. Breast Cancer Research and Treatment, 2005, 94, 225-235.	2.5	78
59	A signaling pathway leading to metastasis is controlled by N-cadherin and the FGF receptor. Cancer Cell, 2002, 2, 301-314.	16.8	461